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Sir:

Transmitted herewith for filing is the patent application of:

Inventors: Markum Pompejus *et al.*For: "*Corynebacterium Glutamicum* Genes Encoding Novel Proteins"

Enclosed are:

- ☒ 58 pages of specification, 5 pages of claims and 1 page of abstract;
- ☒ 26 pages of Table 1;
- ☒ 16 pages of Table 2;
- ☒ 6 pages of Table 3;
- ☒ 95 pages of Table 4;
- ☒ 535 pages of Appendix A;
- ☒ 162 pages of Appendix B;
- ☒ 3331 pages of Sequence Listing;
- ☒ Zip Disk Containing Sequence Listing;
- ☒ Transmittal Letter for Zip Disk Containing Sequence Listing;
- ☒ An *unexecuted* Declaration, Petition and Power of Attorney;
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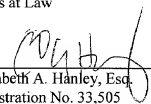
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***CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING NOVEL
PROTEINS**

Related Applications

- 5 This application claims priority to prior filed U.S. Provisional Patent Application Serial No. 60/142764, filed July 8, 1999, and U.S. Provisional Patent Application Serial No. 60/152,318, filed September 3, 1999. The entire contents of both of the aforementioned applications are hereby expressly incorporated herein by reference.

Background of the Invention

- Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids,
- 15 nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through the large-scale culture of bacteria developed to produce and secrete large quantities of one or more desired molecules. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive,
- 20 nonpathogenic bacterium. Through strain selection, a number of mutant strains have been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

Summary of the Invention

- The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C. glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related
- 30 bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as marker and fine chemical production (MCP) proteins.

- C. glutamicum* is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the
- 35 degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The MCP nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, e.g., by

fermentation processes. Modulation of the expression of the MCP nucleic acids of the invention, or modification of the sequence of the MCP nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a microorganism (e.g., to improve the yield or production of one or more fine chemicals from a *Corynebacterium* or *Brevibacterium* species).

The MCP nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

The MCP nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms. Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered *Corynebacterium* or *Brevibacterium* species.

The MCP proteins encoded by the novel nucleic acid molecules of the invention may be involved, for example, in the direct or indirect production of one or more fine chemicals from *C. glutamicum*. The MCP proteins of the invention may also participate in the degradation of hydrocarbons or the oxidation of terpenoids. These proteins may also be utilized for the identification of *Corynebacterium glutamicum* or organisms related to *C. glutamicum*; the presence of an MCP protein specific to *C. glutamicum* and related species in a mixture of proteins may indicate the presence of one of these bacteria in the sample. Further, these MCP proteins may have homologues in plants or animals which are involved in a disease state or condition; these proteins thus may serve as useful pharmaceutical targets for drug screening and the development of therapeutic compounds.

Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (e.g., *lactofermentum*) (Yoshihama *et al.*, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be

utilized in the genetic engineering of this organism to modulate the production of one or more fine chemicals. This modulation may be due to a direct effect of manipulation of a gene of the invention, or it may be due to an indirect effect of such manipulation. For example, by modifying the activity of a protein involved in the biosynthesis or degradation of a fine chemical (*i.e.*, through mutagenesis of the corresponding gene), one may directly modulate the ability of the cell to synthesize or to degrade this compound, thereby modulating the yield and/or efficiency of production of the fine chemical. Similarly, by modulating the activity of a protein which regulates a fine chemical metabolic pathway, one may directly influence whether the production of the desired compound is up- or down-regulated, either of which will modulate the yield or efficiency of production of the fine chemical from the cell.

Indirect modulation of fine chemical production may also result by modifying the activity of a protein of the invention (*i.e.*, by mutagenesis of the corresponding gene) such that the overall ability of the cell to grow and divide or to remain viable and productive is increased. The production of fine chemicals from *C. glutamicum* is generally accomplished by the large-scale fermentative culture of these microorganisms, conditions which are frequently suboptimal for growth and cell division. By engineering a protein of the invention (*e.g.*, a stress response protein, a cell wall protein, or proteins involved in the metabolism of compounds necessary for cell growth and division to occur, such as nucleotides and amino acids) such that it is better able to survive, grow, and multiply in such conditions, it may be possible to increase the number and productivity of such engineered *C. glutamicum* cells in large-scale culture, which in turn should result in increased yields and/or efficiency of production of one or more desired fine chemicals. Further, the metabolic pathways of any cell are necessarily interrelated and coregulated. By altering the activity or regulation of any one metabolic pathway in *C. glutamicum* (*i.e.*, by altering the activity of one of the proteins of the invention which participates in such a pathway), it is possible to concomitantly alter the activity or regulation of other metabolic pathways in this microorganism, which may be directly involved in the synthesis or degradation of a fine chemical.

The invention provides novel nucleic acid molecules which encode proteins, referred to herein as MCP proteins, which are capable of, for example, modulating the production or efficiency of production of one or more fine chemicals from *C. glutamicum*, or of serving as identifying markers for *C. glutamicum* or related organisms. Nucleic acid molecules encoding an MCP protein are referred to herein as MCP nucleic acid molecules. In a preferred embodiment, the MCP protein is capable of modulating the production or efficiency of production of one or more fine chemicals from *C. glutamicum*, or of serving as identifying markers for *C. glutamicum* or related

organisms. Examples of such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (e.g., cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an MCP protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of MCP-encoding nucleic acid (e.g., DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth in Appendix A or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth in Appendix A, or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth in Appendix B. The preferred MCP proteins of the present invention also preferably possess at least one of the MCP activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B, e.g., sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains an MCP activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to modulate the production or efficiency of production of one or more fine chemicals from *C. glutamicum*, or of serving as an identifying marker for *C. glutamicum* or related organisms. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an amino acid sequence of Appendix B (e.g., an entire amino acid sequence selected from those sequences set forth in Appendix B). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (e.g., an MCP fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of

the amino acid sequences of Appendix B and is able to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms, and which also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of Appendix A. Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* MCP protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an MCP protein by culturing the host cell in a suitable medium. The MCP protein can then be isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an MCP gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding wild-type or mutated MCP sequence as a transgene. In another embodiment, an endogenous MCP gene within the genome of the microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered MCP gene. In another embodiment, an endogenous or introduced MCP gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional MCP protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an MCP gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the MCP gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

In another aspect, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the

sequences set forth in Appendix A or Appendix B) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated MCP protein or a portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated MCP protein or portion thereof is capable of modulating the production or efficiency of production of one or more fine chemicals from *C. glutamicum*, or of serving as an identifying marker for *C. glutamicum* or related organisms. In another preferred embodiment, the isolated MCP protein or portion thereof is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to, for example, modulate the production or efficiency of production of one or more fine chemicals from *C. glutamicum*, or to serve as identifying markers for *C. glutamicum* or related organisms.

The invention also provides an isolated preparation of an MCP protein. In preferred embodiments, the MCP protein comprises an amino acid sequence of Appendix B. In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of Appendix B (encoded by an open reading frame set forth in Appendix A). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of Appendix B. In other embodiments, the isolated MCP protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of Appendix B and is able to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms.

Alternatively, the isolated MCP protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous, to a nucleotide sequence of Appendix B. It is also preferred that the preferred forms of MCP proteins also have one or more of the MCP bioactivities described herein.

The MCP polypeptide, or a biologically active portion thereof, can be operatively linked to a non-MCP polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the MCP protein alone. In other preferred embodiments, this fusion protein is capable of

modulating the yield, production and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, or of serving as an identifying marker for *C. glutamicum* or related organisms. In particularly preferred embodiments, integration of this fusion protein into a host cell modulates production of a desired compound from the cell.

- 5 In another aspect, the invention provides methods for screening molecules which modulate the activity of an MCP protein, either by interacting with the protein itself or a substrate or binding partner of the MCP protein, or by modulating the transcription or translation of an MCP nucleic acid molecule of the invention.

- Another aspect of the invention pertains to a method for producing a fine
10 chemical. This method involves the culturing of a cell containing a vector directing the expression of an MCP nucleic acid molecule of the invention, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an MCP nucleic acid. In another preferred embodiment, this
15 method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3.

- Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an
20 agent which modulates MCP protein activity or MCP nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum* MCP protein activities, such that the yield, production, and/or efficiency of production of a desired fine chemical by this microorganism is improved. The agent which
25 modulates MCP protein activity can be an agent which stimulates MCP protein activity or MCP nucleic acid expression. Examples of agents which stimulate MCP protein activity or MCP nucleic acid expression include small molecules, active MCP proteins, and nucleic acids encoding MCP proteins that have been introduced into the cell. Examples of agents which inhibit MCP activity or expression include small molecules
30 and antisense MCP nucleic acid molecules.

- Another aspect of the invention pertains to methods for modulating yields, production, and/or efficiency of production of a desired compound from a cell, involving the introduction of a wild-type or mutant MCP gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If
35 integrated into the genome, such integration can be random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a

preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

5 **Detailed Description of the Invention**

The present invention provides MCP nucleic acid and protein molecules. These MCP nucleic acid molecules may be utilized in the identification of *Corynebacterium glutamicum* or related organisms, in the mapping of the *C. glutamicum* genome (or a genome of a closely related organism), or in the identification of microorganisms which
10 may be used to produce fine chemicals, *e.g.*, by fermentation processes. The proteins encoded by these nucleic acids may be utilized in the direct or indirect modulation of the production or efficiency of production of one or more fine chemicals from *C. glutamicum*, as identifying markers for *C. glutamicum* or related organisms, in the oxidation of terpenoids or the degradation of hydrocarbons, or as targets for the
15 development of therapeutic pharmaceutical compounds. Aspects of the invention are further explicated below.

I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by
20 an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in Biotechnology vol. 6, Rehm *et al.*, eds. VCH:
25 Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of
30 Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCs Press, (1995)), enzymes,
35 polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in Gutcho (1983) Chemicals by Fermentation, Noyes Data Corporation, ISBN:

0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

A. Amino Acid Metabolism and Uses

5 Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art-recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in
10 proteins (see Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH: Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins. Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids have been well characterized in both prokaryotic and eukaryotic cells (see, for example,
15 Stryer, L. Biochemistry, 3rd edition, pages 578-590 (1988)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate,
20 cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various
25 applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-
30 methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/ L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino acids – technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6,
35 chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetyl cysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others

described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

- The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E.(1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α -ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transfer of the side-chain β -carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase. Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.
- Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. *Biochemistry* 3rd ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. *Biochemistry*, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although they are readily synthesized by other organisms such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins may encompass cofactors and nutraceutical compounds. The language "cofactor" includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such molecules are vitamins, antioxidants, and also certain lipids (e.g., polyunsaturated fatty acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCs Press: Champaign, IL X, 374 S).

Thiamin (vitamin B₁) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B₂) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B₆' (e.g., pyridoxine, pyridoxamine, pyridoxa-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)-β-alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate

biosynthesis consist of the ATP-driven condensation of β -alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β -alanine and for the condensation to pantothenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5

- 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of pantothenate, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthanol (provitamin B₅), pantotheine (and its derivatives) and coenzyme A.

- Biotin biosynthesis from the precursor molecule pimeloyl-CoA in
10 microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the α -ketoglutarate
15 dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which in turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

- 20 Corrinoids (such as the cobalamines and particularly vitamin B₁₂) and porphyrines belong to a group of chemicals characterized by a tetrapyrrole ring system. The biosynthesis of vitamin B₁₂ is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are
25 also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

- The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B₆, pantothenate, and
30 biotin. Only Vitamin B₁₂ is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

- 35 *C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses*

Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language

“purine” or “pyrimidine” includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term “nucleotide” includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language “nucleoside” includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which may serve as energy stores (e.g., ADP, ATP) or as coenzymes (i.e., FAD and NAD).

Several publications have described the use of these chemicals for these medical indications, by influencing purine and/or pyrimidine metabolism (e.g. Christopherson, R.I. and Lyons, S.D. (1990) “Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents.” *Med. Res. Reviews* 10: 505-548). Studies of enzymes involved in purine and pyrimidine metabolism have been focused on the development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) “Enzymes in nucleotide synthesis.” *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (e.g., thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (e.g., ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (e.g., IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) *Nucleotides and Related Compounds in Biotechnology* vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) “*de novo* purine nucleotide biosynthesis”, in: *Progress in Nucleic Acid Research and Molecular Biology*, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) “Nucleotides and Nucleosides”, Chapter 8 in: *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from

ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell.

5 Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate

10 deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

D. Trehalose Metabolism and Uses

Trehalose consists of two glucose molecules, bound in α , α -1,1 linkage. It is

15 commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S. Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and

20 Shiosaka, M. (1997) *J. Japan* 172: 97-102). Trehalose is produced by enzymes from many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

II. Elements and Methods of the Invention

25 The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as MCP nucleic acid molecules. These MCP nucleic acid molecules are useful not only for the identification of *C. glutamicum* or related bacterial species, but also as markers for the mapping of the *C. glutamicum* genome and in the identification of bacteria useful for the production of fine chemicals by, *e.g.*,

30 fermentative processes. The present invention is also based, at least in part, on the MCP protein molecules encoded by these MCP nucleic acid molecules. These MCP proteins are capable of modulating the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, of serving as identifying markers for *C. glutamicum* or related organisms, of degrading hydrocarbons, and of serving as targets

35 for the development of therapeutic pharmaceutical compounds. In one embodiment, the MCP molecules of the invention directly or indirectly participate in one or more fine chemical metabolic pathways in *C. glutamicum*. In a preferred embodiment, the activity

of the MCP molecules of the invention to indirectly or directly participate in such metabolic pathways has an impact on the production of a desired fine chemical by this microorganism. In a particularly preferred embodiment, the MCP molecules of the invention are modulated in activity, such that the *C. glutamicum* metabolic pathways in which the MCP proteins of the invention participate are modulated in efficiency or output, which either directly or indirectly modulates the production or efficiency of production of a desired fine chemical by *C. glutamicum*.

The language, "MCP protein" or "MCP polypeptide" includes proteins which are able to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target protein for drug screening or design, or to serve as identifying markers for *C. glutamicum* or related organisms. Examples of MCP proteins include those encoded by the MCP genes set forth in Table 1 and Appendix A. The terms "MCP gene" or "MCP nucleic acid sequence" include nucleic acid sequences encoding an MCP protein, which consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of MCP genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (*e.g.*, kg product per hour per liter). The term "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes the efficiency of the conversion of the carbon source into the product (*i.e.*, fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (*e.g.*, the metabolism of an amino acid such as glycine) comprises the overall

biosynthetic, modification, and degradation pathways in the cell related to this compound.

In another embodiment, the MCP molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*, either directly or indirectly. Using recombinant genetic techniques, one or more of the MCP proteins of the invention may be manipulated such that its function is modulated. Such modulation of function may result in the modulation of the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*.

For example, by modifying the activity of a protein involved in the biosynthesis or degradation of a fine chemical (*i.e.*, through mutagenesis of the corresponding gene), one may directly modulate the ability of the cell to synthesize or to degrade this compound, thereby modulating the yield and/or efficiency of production of the fine chemical. Similarly, by modulating the activity of a protein which regulates a fine chemical metabolic pathway, one may directly influence whether the production of the desired compound is up- or down-regulated, either of which will modulate the yield or efficiency of production of the fine chemical from the cell.

Indirect modulation of fine chemical production may also result by modifying the activity of a protein of the invention (*i.e.*, by mutagenesis of the corresponding gene) such that the overall ability of the cell to grow and divide or to remain viable and productive is increased. The production of fine chemicals from *C. glutamicum* is generally accomplished by the large-scale fermentative culture of these microorganisms, conditions which are frequently suboptimal for growth and cell division. By engineering a protein of the invention (*e.g.*, a stress response protein, a cell wall protein, or proteins involved in the metabolism of compounds necessary for cell growth and division to occur, such as nucleotides and amino acids) such that it is better able to survive, grow, and multiply in such conditions, it may be possible to increase the number and productivity of such engineered *C. glutamicum* cells in large-scale culture, which in turn should result in increased yields and/or efficiency of production of one or more desired fine chemicals. Further, the metabolic pathways of any cell are necessarily interrelated and coregulated. By altering the activity or regulation of any one metabolic pathway in *C. glutamicum* (*i.e.*, by altering the activity of one of the proteins of the invention which participates in such a pathway), it is possible to concomitantly alter the activity or regulation of other metabolic pathways in this microorganism, which may be directly involved in the synthesis or degradation of a fine chemical.

The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type

Culture Collection, given designation ATCC 13032. The nucleotide sequences of the isolated *C. glutamicum* MCP nucleic acid molecules and the predicted amino acid sequences of the *C. glutamicum* MCP proteins are shown in Appendices A and B, respectively. Computational analyses were performed which classified and/or identified many of these nucleotide sequences as sequences having homology to *E. coli* or *Bacillus subtilis* genes.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of Appendix B. As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, *e.g.*, the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

The MCP protein or a biologically active portion or fragment thereof of the invention is able to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms.

Various aspects of the invention are described in further detail in the following subsections:

25 A. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules that encode MCP polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of MCP-encoding nucleic acid (*e.g.*, MCP DNA). These nucleic acid molecules may be used to identify *C. glutamicum* or related organisms, to map the genome of *C. glutamicum* or closely related bacteria, or to identify microorganisms useful for the production of fine chemicals, *e.g.*, by fermentative processes. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides of sequence upstream from the 5' end of the coding region and at

least about 20 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of

5 the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated MCP nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide
10 sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (e.g., a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

15 A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having a nucleotide sequence of Appendix A, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* MCP DNA can be isolated from a *C. glutamicum* library using all or portion of one of the sequences of Appendix A as a hybridization probe and
20 standard hybridization techniques (*e.g.*, as described in Sambrook, J., Fritsch, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the sequences of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide
25 primers designed based upon this sequence (*e.g.*, a nucleic acid molecule encompassing all or a portion of one of the sequences of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence of Appendix A). For example, mRNA can be isolated from normal endothelial cells (*e.g.*, by the guanidinium-thiocyanate extraction procedure of Chirgwin *et al.* (1979)
30 *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (*e.g.*, Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL) and random polynucleotide primers or oligonucleotide primers based upon one of the nucleotide sequences shown in Appendix A. Synthetic oligonucleotide primers for
35 polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in Appendix A. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate

oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an MCP nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in Appendix A. The sequences of Appendix A correspond to the *Corynebacterium glutamicum* MCP DNAs of the invention. This cDNA comprises sequences encoding MCP proteins (*i.e.*, the "coding region", indicated in each sequence in Appendix A), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in Appendix A. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the sequences in Appendix A.

For the purposes of this application, it will be understood that each of the sequences set forth in Appendix A has an identifying RXA or RXN number having the designation "RXA" or "RXN" followed by 5 digits (*i.e.*, RXA00003 or RXN00022). Each of these sequences comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA or RXN designation to eliminate confusion. The recitation "one of the sequences in Appendix A", then, refers to any of the sequences in Appendix A, which may be distinguished by their differing RXA or RXN designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is set forth in Appendix B. The sequences of Appendix B are identified by the same RXA or RXN designations as Appendix A, such that they can be readily correlated. For example, the amino acid sequence in Appendix B designated RXA00003 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXA00003 in Appendix A, and the amino acid sequence in Appendix B designated RXN00022 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXN00022 in Appendix A. Each of the RXA and RXN nucleotide and amino acid sequences of the invention has also been assigned a SEQ ID NO, as indicated in Table 1.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA designation. For example, SEQ ID NO:3, designated, as indicated on Table 1, as "F RXA01638", is an F-designated gene, as are SEQ ID NOs: 5, 9, and 11 (designated on Table 1 as "F RXA01639", "F RXA01590", and "F RXA01542", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences shown in Appendix A, or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences shown in

- 5 Appendix A is one which is sufficiently complementary to one of the nucleotide sequences shown in Appendix A such that it can hybridize to one of the nucleotide sequences shown in Appendix A, thereby forming a stable duplex.

- In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%,
10 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence shown
15 in Appendix A, or a portion thereof. Ranges and identity values intermediate to the above-recited ranges, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid
20 molecule of the invention comprises a nucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, to one of the nucleotide sequences shown in Appendix A, or a portion thereof.

- Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of one of the sequences in Appendix A, for example a
25 fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an MCP protein. The nucleotide sequences determined from the cloning of the MCP genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning MCP homologues in other cell types and organisms, as well as MCP homologues from other *Corynebacteria* or related
30 species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the sequences set forth in Appendix A, an anti-sense sequence of one of the sequences set forth in
35 Appendix A, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of Appendix A can be used in PCR reactions to clone MCP homologues. Probes based on the MCP nucleotide sequences can be used to detect transcripts or

genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells

5 which misexpress an MCP protein, such as by measuring a level of an MCP-encoding nucleic acid in a sample of cells, *e.g.*, detecting MCP mRNA levels or determining whether a genomic MCP gene has been mutated or deleted.

In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently

10 homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms. As used herein, the

15 language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in one of the sequences of Appendix B) amino acid residues to an amino acid sequence of Appendix B such that the protein or portion thereof is able to modulate the yield,

20 production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms. Examples of such activities are also described herein. Thus, "the function of an MCP protein" contributes to the overall regulation of one or more fine chemical

25 metabolic pathways, or to the degradation of a hydrocarbon, or to the oxidation of a terpenoid.

In another embodiment, the protein is at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino

30 acid sequence of Appendix B.

Portions of proteins encoded by the MCP nucleic acid molecules of the invention are preferably biologically active portions of one of the MCP proteins. As used herein, the term "biologically active portion of an MCP protein" is intended to include a portion, *e.g.*, a domain/motif, of an MCP protein that modulates the yield, production, and/or

35 efficiency of production of one or more fine chemicals from *C. glutamicum*, that degrades hydrocarbons, that oxidizes terpenoids, that may serve as a target for drug development, or that may serve as an identifying marker for *C. glutamicum* or related

organisms. To determine whether an MCP protein or a biologically active portion thereof can modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, can degrade hydrocarbons, or can oxidize terpenoids, an assay of activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an MCP protein can be prepared by isolating a portion of one of the sequences in Appendix B, expressing the encoded portion of the MCP protein or peptide (e.g., by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the MCP protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences shown in Appendix A (and portions thereof) due to degeneracy of the genetic code and thus encode the same MCP protein as that encoded by the nucleotide sequences shown in Appendix A. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in Appendix B. In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).

It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (e.g., a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 39% identical to the nucleotide sequence designated RXA00008 (SEQ ID NO:1549), a nucleotide sequence which is greater than and/or at least 42% identical to the nucleotide sequence designated RXA00059 (SEQ ID NO:1571), and a nucleotide sequence which is greater than and/or at least 39% identical to the nucleotide sequence designated RXA00096 (SEQ ID NO:93). One of ordinary skill in the art would be able to calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities

greater than the lower threshold so calculated (e.g., at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* MCP nucleotide sequences shown in Appendix A, it will be appreciated by those of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of MCP proteins may exist within a population (e.g., the *C. glutamicum* population). Such genetic polymorphism in the MCP gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an MCP protein, preferably a *C. glutamicum* MCP protein. Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the MCP gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in MCP that are the result of natural variation and that do not alter the functional activity of MCP proteins are intended to be within the scope of the invention.

Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* MCP DNA of the invention can be isolated based on their homology to the *C. glutamicum* MCP nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of Appendix A. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C.

Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a sequence of Appendix A corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* MCP protein.

In addition to naturally-occurring variants of the MCP sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be introduced by mutation into a nucleotide sequence of Appendix A, thereby leading to changes in the amino acid sequence of the encoded MCP protein, without altering the functional ability of the MCP protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a sequence of Appendix A. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the MCP proteins (Appendix B) without altering the activity of said MCP protein, whereas an "essential" amino acid residue is required for MCP protein activity. Other amino acid residues, however, (e.g., those that are not conserved or only semi-conserved in the domain having MCP activity) may not be essential for activity and thus are likely to be amenable to alteration without altering MCP activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding MCP proteins that contain changes in amino acid residues that are not essential for MCP activity. Such MCP proteins differ in amino acid sequence from a sequence contained in Appendix B yet retain at least one of the MCP activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of Appendix B and is able to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to one of the sequences in Appendix B, more preferably at least about 60-70% homologous to one of the sequences in Appendix B, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of the sequences in Appendix B, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the sequences in Appendix B.

To determine the percent homology of two amino acid sequences (e.g., one of the sequences of Appendix B and a mutant form thereof) or of two nucleic acids, the

sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence

5 (*e.g.*, one of the sequences of Appendix B) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the sequence selected from Appendix B), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two

10 sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an MCP protein homologous to a protein sequence of Appendix B can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of Appendix A such that

15 one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the sequences of Appendix A by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is

20 one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine,

25 tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an MCP protein is preferably replaced with another amino acid residue from the same side chain

30 family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an MCP coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an MCP activity described herein to identify mutants that retain MCP activity. Following mutagenesis of one of the sequences of Appendix A, the encoded protein can be expressed recombinantly and the activity of the

35 protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding MCP proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*,

5 complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire MCP coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the

10 coding strand of a nucleotide sequence encoding an MCP protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of SEQ ID NO. 1 (RXN01638) comprises nucleotides 1 to 900). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a

15 nucleotide sequence encoding MCP. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding MCP disclosed herein (*e.g.*, the sequences set forth in Appendix A), antisense nucleic acids of the invention can be

20 designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of MCP mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of MCP mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of MCP mRNA. An

25 antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed by chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified

30 nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil,

35 hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-

methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an MCP protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes

(described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave MCP mRNA transcripts to thereby inhibit translation of MCP mRNA. A ribozyme having specificity for an MCP-encoding nucleic acid can be designed based upon the nucleotide sequence of an MCP DNA disclosed herein (*i.e.*, SEQ ID NO. 1 (RXN01368) in Appendix A). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an MCP-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, MCP mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

Alternatively, MCP gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an MCP nucleotide sequence (*e.g.*, an MCP promoter and/or enhancers) to form triple helical structures that prevent transcription of an MCP gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

B. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an MCP protein (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors,

such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (e.g., in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, repressor binding sites, activator binding sites, enhancer regions and other expression control elements (e.g., terminators, other elements of mRNA secondary structure, or polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as cos-, tac-, trp-, tet-, trp-tet-, lpp-, lac-, lpp-lac-, lacI^q-, T7-, T5-, T3-, gal-, trc-, ara-, SP6-, amy, SPO2, λ -P_R- or λ P_L, which are used preferably in bacteria. Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as ADC1, MFa, AC, P-60, CYC1, GAPDH, TEF, rp28, ADH, promoters from plants such as CaMV35S, SSU, OCS, lib4, usp, STLS1, B33, nos or ubiquitin- or phaseolin-promoters. It is also possible to use artificial promoters. It will be appreciated by those of ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (e.g., MCP proteins, mutant forms of MCP proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of MCP proteins in prokaryotic or eukaryotic cells. For example, MCP genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More

Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge),
 5 algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* -mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants" *Plant Cell Rep.*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the
 10 recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein
 15 encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion
 20 moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly,
 25 MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the MCP protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion
 30 protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant MCP protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315), pLG338, pACYC184, pBR322, pUC18,
 35 pUC19, pKC30, pRep4, pHS1, pHS2, pPLC236, pMBL24, pLG200, pUR290, pIN-III113-B1, λ gt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; and

Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York ISBN 0 444 904018). Target gene expression from the pTrec vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming Streptomyces, while plasmids pUB110, pC194, or pBD214 are suited for transformation of Bacillus species. Several plasmids of use in the transfer of genetic information into Corynebacterium include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York ISBN 0 444 904018).

One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the MCP protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), 2 μ , pAG-1, Yep6, Yep13, pEMBLYe23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York (ISBN 0 444 904018).

Alternatively, the MCP proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.*

(1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In another embodiment, the MCP proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (e.g., the
5 spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHIac+,
10 pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC
15 (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsh, E. F.,
20 and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type
25 (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and
30 Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Patent No. 4,873,316 and
35 European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990)

Science 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to MCP mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.* (1986) "Antisense RNA as a molecular tool for genetic analysis", *Reviews - Trends in Genetics*, Vol. 1(1).

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an MCP protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those of ordinary skill in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation", "transfection", "conjugation" and "transduction" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid,

transposon or other DNA) into a host cell, including using natural competence, chemical mediated transfer, calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an MCP protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by, for example, drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an MCP gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the MCP gene. Preferably, this MCP gene is a *Corynebacterium glutamicum* MCP gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous MCP gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous MCP gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous MCP protein). In the homologous recombination vector, the altered portion of the MCP gene is flanked at its 5' and 3' ends by additional nucleic acid of the MCP gene to allow for homologous recombination to occur between the exogenous MCP gene carried by the vector and an endogenous MCP gene in a microorganism. The additional flanking MCP nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, less than one kilobase of flanking DNA (both at the 5' and 3' ends) is included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and

cells in which the introduced MCP gene has homologously recombined with the endogenous MCP gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene.

- 5 For example, inclusion of an MCP gene on a vector placing it under control of the lac operon permits expression of the MCP gene in the presence of IPTG. Such regulatory systems are well known in the art.

- In another embodiment, an endogenous MCP gene in a host cell is disrupted (e.g., by homologous recombination or other genetic means known in the art) such that
10 expression of its protein product does not occur. In another embodiment, an endogenous or introduced MCP gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional MCP protein. In still another embodiment, one or more of the regulatory regions (e.g., a promoter, repressor, or inducer) of an MCP gene in a microorganism has been altered (e.g., by deletion,
15 truncation, inversion, or point mutation) such that the expression of the MCP gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described MCP gene and protein modifications may be readily produced using the methods of the invention, and are meant to be included in the present invention.

- 20 A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (i.e., express) an MCP protein. Accordingly, the invention further provides methods for producing MCP proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an MCP protein has
25 been introduced, or into which genome has been introduced a gene encoding a wild-type or altered MCP protein) in a suitable medium until MCP protein is produced. In another embodiment, the method further comprises isolating MCP proteins from the medium or the host cell.

30 C. Isolated MCP Proteins

- Another aspect of the invention pertains to isolated MCP proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when
35 chemically synthesized. The language "substantially free of cellular material" includes preparations of MCP protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the

language "substantially free of cellular material" includes preparations of MCP protein having less than about 30% (by dry weight) of non-MCP protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-MCP protein, still more preferably less than about 10% of non-MCP protein, and most preferably less than about 5% non-MCP protein. When the MCP protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of MCP protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of MCP protein having less than about 30% (by dry weight) of chemical precursors or non-MCP chemicals, more preferably less than about 20% chemical precursors or non-MCP chemicals, still more preferably less than about 10% chemical precursors or non-MCP chemicals, and most preferably less than about 5% chemical precursors or non-MCP chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from the same organism from which the MCP protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* MCP protein in a microorganism such as *C. glutamicum*.

An isolated MCP protein or a portion thereof of the invention is able to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an MCP protein of the invention has an amino acid sequence shown in Appendix B. In yet another preferred embodiment, the MCP protein has an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of Appendix A. In still another preferred embodiment, the MCP

protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%,
5 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of Appendix A, or a portion thereof. Ranges and identity values intermediate to the above-recited values, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For
10 example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. The preferred MCP proteins of the present invention also preferably possess at least one of the MCP activities described herein. For example, a preferred MCP protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which
15 hybridizes, e.g., hybridizes under stringent conditions, to a nucleotide sequence of Appendix A, and which is able to modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*, to degrade hydrocarbons, to oxidize terpenoids, to serve as a target for drug development, or to serve as an identifying marker for *C. glutamicum* or related organisms.

20 In other embodiments, the MCP protein is substantially homologous to an amino acid sequence of Appendix B and retains the functional activity of the protein of one of the sequences of Appendix B yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the MCP protein is a protein which comprises an amino acid sequence
25 which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more
30 homologous to an entire amino acid sequence of Appendix B and which has at least one of the MCP activities described herein. Ranges and identity values intermediate to the above-recited values, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended
35 to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of Appendix B.

Biologically active portions of an MCP protein include peptides comprising amino acid sequences derived from the amino acid sequence of an MCP protein, *e.g.*, an amino acid sequence shown in Appendix B or the amino acid sequence of a protein homologous to an MCP protein, which include fewer amino acids than a full length MCP protein or the full length protein which is homologous to an MCP protein, and exhibit at least one activity of an MCP protein. Typically, biologically active portions (peptides, *e.g.*, peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an MCP protein. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an MCP protein include one or more selected domains/motifs or portions thereof having biological activity.

MCP proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the MCP protein is expressed in the host cell. The MCP protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an MCP protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native MCP protein can be isolated from cells (*e.g.*, endothelial cells, bacterial cells, fungal cells or other cells), for example using an anti-MCP antibody, which can be produced by standard techniques utilizing an MCP protein or fragment thereof of this invention.

The invention also provides MCP chimeric or fusion proteins. As used herein, an MCP "chimeric protein" or "fusion protein" comprises an MCP polypeptide operatively linked to a non-MCP polypeptide. An "MCP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an MCP protein, whereas a "non-MCP polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the MCP protein, *e.g.*, a protein which is different from the MCP protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the MCP polypeptide and the non-MCP polypeptide are fused in-frame to each other. The non-MCP polypeptide can be fused to the N-terminus or C-terminus of the MCP polypeptide. For example, in one embodiment the fusion protein is a GST-MCP fusion protein in which the MCP sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of

recombinant MCP proteins. In another embodiment, the fusion protein is an MCP protein containing a heterologous signal sequence at its N-terminus. In certain host cells (e.g., mammalian host cells, bacterial host cells, fungal host cells), expression and/or secretion of an MCP protein can be increased through use of a heterologous signal sequence.

5 Preferably, an MCP chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended
10 termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor
15 primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel et al. John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). An MCP-
20 encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the MCP protein.

Homologues of the MCP protein can be generated by mutagenesis, e.g., discrete point mutation or truncation of the MCP protein. As used herein, the term "homologue" refers to a variant form of the MCP protein which acts as an agonist or antagonist of the
25 activity of the MCP protein. An agonist of the MCP protein can retain substantially the same, or a subset, of the biological activities of the MCP protein. An antagonist of the MCP protein can inhibit one or more of the activities of the naturally occurring form of the MCP protein, by, for example, competitively binding to a downstream or upstream member of a biochemical pathway which includes the MCP protein.

30 In an alternative embodiment, homologues of the MCP protein can be identified by screening combinatorial libraries of mutants, e.g., truncation mutants, of the MCP protein for MCP protein agonist or antagonist activity. In one embodiment, a variegated library of MCP variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of MCP variants
35 can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential MCP sequences is expressible as individual polypeptides, or alternatively, as a set of larger

fusion proteins (e.g., for phage display) containing the set of MCP sequences therein. There are a variety of methods which can be used to produce libraries of potential MCP homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential MCP sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, e.g., Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477).

In addition, libraries of fragments of the MCP protein coding can be used to generate a variegated population of MCP fragments for screening and subsequent selection of homologues of an MCP protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an MCP coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the MCP protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of MCP homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify MCP homologues (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a variegated MCP library, using methods well known in the art.

D. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of MCP protein regions required for function; modulation of an MCP protein activity; modulation of the activity of one or more metabolic pathways; and modulation of cellular production of a desired compound, such as a fine chemical.

- 10 The MCP nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes, and probes based
- 15 thereon; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to pathogenic species, such as *Corynebacterium diphtheriae*.
- 20 *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli secrete toxin which is disseminated through this lesion to distal susceptible tissues of the body. Degenerative changes brought about by the
- 25 inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at
- 30 least 5,000 deaths since 1990.

- In one embodiment, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (e.g., the sequences set forth in Appendix A or Appendix B) in a subject, thereby detecting the
- 35 presence or activity of *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules

in *C. glutamicum* are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

To detect the presence of *C. glutamicum* in a sample, techniques well known in the art may be employed. Specifically, the cells in the sample may optionally first be
5 cultured in a suitable liquid or on a suitable solid culture medium to increase the number of cells in the sample. These cells are lysed, and the total DNA content extracted and optionally purified to remove debris and protein material which may interfere with subsequent analysis. The polymerase chain reaction or a similar technique known in the art is performed (for general reference on methodologies commonly used for the
10 amplification of nucleic acid sequences, see Mullis *et al.*, U.S. Patent No. 4,683,195, Mullis *et al.*, U.S. Patent No. 4,965,188, and Innis, M.A., and Gelfand, D. H., (1989) PCR Protocols, A guide to Methods and Applications, Academic Press, p. 3-12, and (1988) Biotechnology 6:1197, and International Patent Application No. WO89/01050) in which primers specific to an MCP nucleic acid molecule of the invention are
15 incubated with the nucleic acid sample such that, if present in the sample, that particular MCP nucleic acid sequence will be amplified. The particular MCP nucleic acid to be amplified is selected based on its uniqueness to the *C. glutamicum* genome, or to the genomes of *C. glutamicum* and only a few closely related bacteria. The presence of the desired amplified product is thus indicative of the presence of *C. glutamicum*, or an
20 organism closely related to *C. glutamicum*.

Further, the nucleic acid and protein molecules of the invention may serve as markers for specific regions of the genome. It is possible, using techniques well known in the art, to ascertain the physical location on the *C. glutamicum* genome of the MCP
nucleic acid molecules of the invention, which in turn provides markers on the genome
25 which can be used to aid in the placement of other nucleic acid molecules and genes on the genome map. Also, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related bacterial species that these nucleic acid molecules may similarly permit the construction of a genomic map in such bacteria
(*e.g.*, *Brevibacterium lactofermentum*).

30 The nucleic acid molecules of the invention have utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed
35 with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed

multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds.

The MCP nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The metabolic processes in which the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

The MCP protein molecules of the invention may also be utilized as markers for the classification of an unknown bacterium as *C. glutamicum*, or for the identification of *C. glutamicum* or closely related bacteria in a sample. For example, using techniques well known in the art, cells in a sample may optionally be amplified (e.g., by culturing in an appropriate medium) to increase the sample size, and then may be lysed to release proteins contained therein. This sample may optionally be purified to remove debris and nucleic acid molecules which may interfere with subsequent analysis. Antibodies specific for a selected MCP protein of the invention may be incubated with the protein sample in a typical Western assay format (see, e.g., Ausubel *et al.*, (1988) Current Protocols in Molecular Biology, Wiley: New York) in which the antibody will bind to its target protein if this protein is present in the sample. An MCP protein is selected for this type of assay if it is unique or nearly unique to *C. glutamicum* or *C. glutamicum* and bacteria very closely related to *C. glutamicum*. Proteins in the sample are then separated by gel electrophoresis, and transferred to a suitable matrix, such as nitrocellulose. An appropriate secondary antibody having a detectable label (e.g., chemiluminescent or colorimetric) is incubated with this matrix, followed by stringent washing. The presence or absence of the label is indicative of the presence or absence of the target protein in the sample. If the protein is present, then this is indicative of the presence of *C. glutamicum*. A similar process enables the classification of an unknown bacterium as *C. glutamicum*; if a panel of proteins specific to *C. glutamicum* are not detected in protein samples prepared from the unknown bacterium, then that bacterium is not likely to be *C. glutamicum*.

The invention provides methods for screening molecules which modulate the activity of an MCP protein, either by interacting with the protein itself or a substrate or

binding partner of the MCP protein, or by modulating the transcription or translation of an MCP nucleic acid molecule of the invention. In such methods, a microorganism expressing one or more MCP proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression

5 of the MCP protein is assessed.

Genetic manipulation of the MCP nucleic acid molecules of the invention may result in the production of MCP proteins having functional differences from the wild-type MCP proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or

10 activity.

Such changes in activity may directly modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*. For example, by modifying the activity of a protein involved in the biosynthesis or degradation of a fine chemical (*i.e.*, through mutagenesis of the corresponding gene),

15 one may directly modulate the ability of the cell to synthesize or to degrade this compound, thereby modulating the yield and/or efficiency of production of the fine chemical. Similarly, by modulating the activity of a protein which regulates a fine chemical metabolic pathway, one may directly influence whether the production of the desired compound is up- or down-regulated, either of which will modulate the yield or efficiency of production of the fine chemical from the cell.

Indirect modulation of fine chemical production may also result by modifying the activity of a protein of the invention (*i.e.*, by mutagenesis of the corresponding gene) such that the overall ability of the cell to grow and divide or to remain viable and productive is increased. The production of fine chemicals from *C. glutamicum* is
25 generally accomplished by the large-scale fermentative culture of these microorganisms, conditions which are frequently suboptimal for growth and cell division. By engineering a protein of the invention (*e.g.*, a stress response protein, a cell wall protein, or proteins involved in the metabolism of compounds necessary for cell growth and division to occur, such as nucleotides and amino acids) such that it is better able to
30 survive, grow, and multiply in such conditions, it may be possible to increase the number and productivity of such engineered *C. glutamicum* cells in large-scale culture, which in turn should result in increased yields and/or efficiency of production of one or more desired fine chemicals. Further, the metabolic pathways of any cell are necessarily interrelated and coregulated. By altering the activity or regulation of any one metabolic
35 pathway in *C. glutamicum* (*i.e.*, by altering the activity of one of the proteins of the invention which participates in such a pathway), it is possible to concomitantly alter the

activity or regulation of other metabolic pathways in this microorganism, which may be directly involved in the synthesis or degradation of a fine chemical.

The aforementioned mutagenesis strategies for MCP proteins to result in increased yields of a fine chemical from *C. glutamicum* are not meant to be limiting; variations on these strategies will be readily apparent to one of ordinary skill in the art. Using such strategies, and incorporating the mechanisms disclosed herein, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated MCP nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any natural product of *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, Appendices, and the sequence listing cited throughout this application are hereby incorporated by reference.

Exemplification

Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032

A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose, 2.46 g/l MgSO₄ x 7H₂O, 10 ml/l KH₂PO₄ solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l (NH₄)₂SO₄, 1 g/l NaCl, 2 g/l MgSO₄ x 7H₂O, 0.2 g/l CaCl₂, 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l FeSO₄ x H₂O, 10 mg/l ZnSO₄ x 7 H₂O, 3 mg/l MnCl₂ x 4 H₂O, 30 mg/l H₃BO₃, 20 mg/l CoCl₂ x 6 H₂O, 1 mg/l NiCl₂ x 6 H₂O, 3 mg/l Na₂MoO₄ x 2 H₂O, 500 mg/l complexing agent (EDTA or citric acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-pantothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme

was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca.18 h at 37°C. The DNA was purified by extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30 min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (see e.g., Sambrook, J. *et al.* (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCosI (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Example 3: DNA Sequencing and Computational Functional Analysis

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using

- 5 ABI377 sequencing machines (see *e.g.*, Fleischman, R.D. *et al.* (1995) "Whole-genome Random Sequencing and Assembly of *Haemophilus Influenzae* Rd., *Science*, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAACGACGGCCAGT-3'.

10 **Example 4: *In vivo* Mutagenesis**

In vivo mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (*e.g.* *Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain the integrity of their genetic information. Typical mutator strains have mutations in the genes

15 for the DNA repair system (*e.g.*, mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

20 **Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum***

- Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as *e.g.*, pHM1519 or pBL1) which replicate autonomously (for review see, *e.g.*, Martin, J.F. *et al.* (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli*
- 25 and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. *et al.* (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication
- 30 are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the
- 35 literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli* and *C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see *e.g.*, Yoshihama, M. *et al.* (1985) *J. Bacteriol.* 162:591-597,

Martin J.F. et al. (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. et al. (1991) *Gene*, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastumata, R. et al. (1984) *J. Bacteriol.* 159:306-311), electroporation (Liebl, E. et al. (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described e.g. in Schäfer, A et al. (1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an Mcr-deficient *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other *Corynebacterium* or *Brevibacterium* species may be accomplished by well-known methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, e.g., DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (e.g., a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) *From Genes to Clones – Introduction to Gene Technology*. VCH: Weinheim.

35 **Example 6: Assessment of the Expression of the Mutant Protein**

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity

to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.* (1988) *Current Protocols in Molecular Biology*, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.

To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) *Current Protocols in Molecular Biology*, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for *Corynebacteria* are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: *The Prokaryotes*, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be advantageous to supply mixtures of different carbon sources. Other possible carbon

sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or ammonia salts, such as NH_4Cl or $(\text{NH}_4)_2\text{SO}_4$, NH_4OH , nitrates, urea, amino acids or
5 complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt, molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be
10 added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently
15 originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0
20 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if
25 necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media.
30 An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It is also possible to maintain a constant culture pH through the addition of NaOH or NH_4OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex
35 compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes.

- 5 For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance
10 of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

- If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD₆₀₀ of 0.5 – 1.5 using cells grown on agar plates, such as CM plates
15 (10 g/l glucose, 2.5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.
20

Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

- The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well
25 within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) *Enzymes*. Longmans: London; Fersht, (1985) *Enzyme Structure and Mechanism*.
30 Freeman: New York; Walsh, (1979) *Enzymatic Reaction Mechanisms*. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) *Fundamentals of Enzymology*. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) *The Enzymes*, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) *Enzymkinetik*, 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) *Methods of*
35 *Enzymatic Analysis*, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's *Encyclopedia of Industrial Chemistry* (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

- The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

- The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in *Biomembranes, Molecular Structure and Function*, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product

- The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical chromatography such as high performance liquid chromatography (see, for example, Ullman, *Encyclopedia of Industrial Chemistry*, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in: *Laboratory Techniques in Biochemistry and Molecular Biology*, vol. 17; Rehm *et al.* (1993) *Biotechnology*, vol. 3, Chapter III: "Product recovery and purification", page 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) *Bioseparations: downstream processing for biotechnology*, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) *Recovery processes for biological materials*, John Wiley and Sons; Shaiwitz, J.A. and Henry, J.D. (1988) *Biochemical separations*, in: *Ullmann's Encyclopedia of Industrial Chemistry*, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J. (1989) *Separation and purification techniques in biotechnology*, Noyes Publications.)

- In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to determine the overall efficiency of production of the compound. Analysis methods

- include measurements of nutrient levels in the medium (e.g., sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these
- 5 measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

Example 10: Purification of the Desired Product from *C. glutamicum* Culture

- 10 Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and
- 15 the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum* cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

- The supernatant fraction from either purification method is subjected to
- 20 chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate
- 25 chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

- There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification
- 30 techniques are described, for example, in Bailey, J.E. & Ollis, D.F. Biochemical Engineering Fundamentals, McGraw-Hill: New York (1986).

- The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic
- 35 assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotechnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia

of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, John Wiley and Sons; Fallon, A. *et al.* (1987) *Applications of HPLC in Biochemistry in: Laboratory Techniques in*

- 5 *Biochemistry and Molecular Biology*, vol. 17.

Example 11: Analysis of the Gene Sequences of the Invention

- The comparison of sequences and determination of percent homology between two sequences are art-known techniques, and can be accomplished using a mathematical
- 10 algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100,
 - 15 wordlength = 12 to obtain nucleotide sequences homologous to MCP nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to MCP protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*,
 - 20 (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

- Another example of a mathematical algorithm utilized for the comparison of
- 25 sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for
 - 30 sequence analysis are known in the art, and include ADVANCE and ADAM. described in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

- The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at
- 35 <http://www.gcg.com>), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the

GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins*. John Wiley and Sons: New York). The gene sequences of the invention were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For example, a value of "40,345" in this column represents "40.345%".

Example 12: Construction and Operation of DNA Microarrays

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose, nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic

acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998), *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as described in Schena, M. *et al.* (1995) *supra* and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations

based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

Example 13: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (e.g., in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (e.g., during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18: 1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (e.g., ^{35}S -methionine, ^{35}S -cysteine, ^{14}C -labelled amino acids, ^{15}N -amino acids, $^{15}\text{NO}_3$ or $^{15}\text{NH}_4^+$ or ^{13}C -labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly,

fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined

- 5 quantitatively using, for example, optical methods and can be compared to the amount of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

- 10 To determine the identity of any given protein, direct sequencing or other standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, *e.g.*, Langen.*et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification
- 15 of *C. glutamicum* proteins by these techniques.

- The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (*e.g.*, different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments
- 20 alone, or in combination with other techniques, can be used for various applications, such as to compare the behavior of various organisms in a given (*e.g.*, metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

25 **Equivalents**

Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding an MCP protein, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
2. The isolated nucleic acid molecule of claim 1, wherein said nucleic acid molecule encodes an MCP protein involved in fine chemical production.
3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the group consisting of those sequences set forth in Appendix A, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide selected from the group of amino acid sequences consisting of those sequences set forth in Appendix B, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth in Appendix A, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth in Appendix A, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.
9. An isolated nucleic acid molecule comprising the nucleic acid molecule of claim 1 or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.
10. A vector comprising the nucleic acid molecule of any one of claims 1-9.
11. The vector of claim 10, which is an expression vector.
12. A host cell transfected with the expression vector of claim 11.
13. The host cell of claim 12, wherein said cell is a microorganism.
14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.
16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.
17. A method of producing a polypeptide comprising culturing the host cell of claim 12 in an appropriate culture medium to, thereby, produce the polypeptide.
18. An isolated MCP polypeptide from *Corynebacterium glutamicum*, or a portion thereof.
19. The polypeptide of claim 18, wherein said polypeptide is involved in fine chemical production.

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 5 21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, or a portion thereof, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 10 22. The isolated polypeptide of claim 18, further comprising heterologous amino acid sequences.
- 15 23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth in Appendix A, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.
- 20 24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 25 25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.
26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.
- 30 27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.
- 35 28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.

29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetophilum*, *Corynebacterium ammoniagenes*, *Corynebacterium fujiokense*, *Corynebacterium nitrilophilus*, *Brevibacterium ammoniagenes*, *Brevibacterium butanicum*, *Brevibacterium divaricatum*, *Brevibacterium flavum*, *Brevibacterium healtii*, *Brevibacterium ketoglutamicum*, *Brevibacterium ketosoreductum*, *Brevibacterium lactofermentum*, *Brevibacterium linens*, *Brevibacterium paraffinolyticum*, and those strains set forth in Table 3.
30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.
31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.
32. The method of claim 25, wherein said fine chemical is an amino acid.
33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, and tryptophan.
34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.
35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in a subject, comprising detecting the presence of one or more of the sequences set forth in Appendix A or Appendix B in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1, thereby diagnosing the presence or activity of *Corynebacterium diphtheriae* in the subject.

36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the nucleic acid molecule is disrupted.

5 37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the nucleic acid molecule comprises one or more nucleic acid modifications from the sequence set forth in Appendix A.

10 38. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule.

15

Customer Number: 000959

Attorney's
Docket No. BGI-129CP

DECLARATION, PETITION AND POWER OF ATTORNEY FOR PATENT APPLICATION

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL PROTEINS

the specification of which:

 X is attached hereto.

 was filed on as Application Serial No.

and was amended on
(if applicable)

I do not know and do not believe that the subject matter of this application was known or used by others in the United States or patented or described in a printed publication in any country before my invention thereof, or patented or described in a printed publication in any country or in public use or on sale in the United States more than one year prior to the date of this application, or first patented or caused to be patented or made the subject of an inventor's certificate by me or my legal representatives or assigns in a country foreign to the United States prior to the date of this application on an application filed more than twelve months (six months if this application is for a design) before the filing of this application; and I acknowledge my duty to disclose information of which I am aware which is material to the examination of this application, that no application for patent or inventor's certificate on the subject matter of this application has been filed by me or my representatives or assigns in any country foreign to the United States, except those identified below, and that I have reviewed and understand the contents of the specification, including the claims as amended by any amendment referred to herein.

I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56.

CLAIM OF BENEFIT OF EARLIER FOREIGN APPLICATION(S)

I hereby claim priority benefits under Title 35, United States Code, §119 of any foreign application(s) for patent or inventor's certificate listed below, and have also identified below any foreign application(s) for patent or inventor's certificate filed by me on the same subject matter having a filing date before that of the application(s) from which priority is claimed.

Check one:

☒ no such applications have been filed.

☐ such applications have been filed as follows

**EARLIEST FOREIGN APPLICATION(S), IF ANY, FILED WITHIN 12 MONTHS
(6 MONTHS FOR DESIGN) PRIOR TO THIS U.S. APPLICATION**

Country	Application Number	Date of Filing (month,day,year)	Priority Claimed Under 35 USC 119
			<input type="checkbox"/> Yes <input type="checkbox"/> No <input type="checkbox"/>
			<input type="checkbox"/> Yes <input type="checkbox"/> No <input type="checkbox"/>
			<input type="checkbox"/> Yes <input type="checkbox"/> No <input type="checkbox"/>
			<input type="checkbox"/> Yes <input type="checkbox"/> No <input type="checkbox"/>
			<input type="checkbox"/> Yes <input type="checkbox"/> No <input type="checkbox"/>

**ALL FOREIGN APPLICATION(S), IF ANY FILED MORE THAN 12 MONTHS
(6 MONTHS FOR DESIGN) PRIOR TO THIS U.S. APPLICATION**

CLAIM FOR BENEFIT OF U.S. PROVISIONAL APPLICATION(S)

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

60/142,764
(Application Serial No.)

July 8, 1999
(Filing Date)

60/152,318
(Application Serial No.)

September 3, 1999
(Filing Date)

CLAIM FOR BENEFIT OF EARLIER U.S./PCT APPLICATION(S)

I hereby claim the benefit under Title 35, United States Code, §120 of any earlier United States application(s) or PCT international application(s) designating the United States listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the earlier application(s) in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56 which became available between the filing date(s) of the earlier application(s) and the national or PCT international filing date of this application. As to subject matter of this application which is common to my earlier application(s), if any, described below, I do not know and do not believe that the same was known or used by others in the United States or patented or described in a printed publication in any country before my invention thereof, or patented or described in a printed publication in any country or in public use or on sale in the United States more than one year prior to the date(s) of said earlier application(s), or first patented or caused to be patented or made the subject of an inventor's certificate by me or my legal representatives or assigns in a country foreign to the United States prior to the date(s) of said earlier application(s) on an application filed more than twelve months (six months if this application is for a design) before the filing of said earlier application(s); and I acknowledge that no application for patent or inventor's certificate on said subject matter has been filed by me or my representatives or assigns in any country foreign to the United States except those identified herein.

(Application Serial No.)

(Filing Date)

(Status)
(patented,pending,aband.)

(Application Serial No.)

(Filing Date)

(Status)
(patented,pending,aband.)

POWER OF ATTORNEY: As a named inventor, I hereby appoint the following attorneys and/or agents to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

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Jane E. Remillard	Reg. No. 38,872		Under 37 C.F.R. § 10.9(b)
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Giulio A. DeConti, Jr., Esq., (617) 227-7400

Wherefore I petition that letters patent be granted to me for the invention or discovery described and claimed in the attached specification and claims, and hereby subscribe my name to said specification and claims and to the foregoing declaration, power of attorney, and this petition.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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TABLE 1: GENES IN THE APPLICATION

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig</u>	<u>NT Start</u>	<u>NT Stop</u>
1	2	RXN01638	VV0005	54646	55545
3	4	F RXA01638	GR00456	825	436
5	6	F RXA01639	GR00456	1334	897
7	8	RXN01590	VV0015	66740	60294
9	10	F RXA01590	GR00445	1710	427
11	12	F RXA01542	GR00429	3	5063
13	14	RXN01539	VV0015	60006	57841
15	16	F RXA01539	GR00428	120	2042
17	18	RXN01422	VV0122	17001	16030
19	20	F RXA01422	GR00416	2003	1221
21	22	RXN01403	VV0126	4644	3997
23	24	F RXA01403	GR00409	4410	3997
25	26	RXN01326	VV0102	23923	24288
27	28	F RXA01326	GR00386	45	338
29	30	RXN01301	VV0068	8224	8748
31	32	F RXA01301	GR00375	1993	1589
33	34	RXN01276	VV0009	31190	31633
35	36	F RXA01276	GR00367	29993	30538
37	38	RXN01231	VV0020	30144	29902
39	40	F RXA01231	GR00356	1384	1887
41	42	RXN01210	VV0169	4230	5060
43	44	F RXA01210	GR00349	3	695
45	46	RXN01206	VV0268	303	4
47	48	F RXA01206	GR00346	593	853
49	50	RXN01121	VV0182	5808	6893
51	52	F RXA01121	GR00310	2479	3156
53	54	RXN01085	VV0093	16599	15721
55	56	F RXA01085	GR00303	960	4
57	58	RXN00022	VV0015	27262	28962
59	60	F RXA00022	GR00002	20563	21297
61	62	F RXA01921	GR00551	943	5
63	64	RXN00027	VV0127	60015	59650
65	66	F RXA00027	GR00003	5142	5507
67	68	RXN00028	VV0127	57099	59045
69	70	F RXA00028	GR00003	8058	6112
71	72	RXN00033	VV0127	51753	53087
73	74	RXN00056	VV0044	11980	12729
75	76	F RXA00056	GR00009	1463	714
77	78	RXN00067	VV0019	29740	29255
79	80	F RXA00067	GR00011	708	223
81	82	RXN00077	VV0154	4222	5583
83	84	F RXA00077	GR00012	4228	5589
85	86	RXN00080	VV0154	8446	6917
87	88	F RXA00080	GR00012	7342	6923
89	90	RXN00087	VV0048	204	731
91	92	F RXA00087	GR00013	3983	3456
93	94	RXN00096	VV0129	22302	22000
95	96	F RXA00096	GR00014	4746	5048
97	98	RXN00097	VV0129	21841	20666
99	100	F RXA00097	GR00014	5222	6382
101	102	RXN00114	VV0129	5849	6337
103	104	F RXA00114	GR00017	3420	3908

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105	106	RXN00120	VV0142	2612	3451
107	108	F RXA00120	GR00019	2798	3451
109	110	RXN00128	VV0124	7960	9663
111	112	F RXA00128	GR00020	4709	3006
113	114	RXN00154	VV0167	3283	4125
115	116	F RXA00154	GR00023	8568	7726
117	118	RXN00162	VV0084	9489	9842
119	120	F RXA00162	GR00024	5438	5791
121	122	RXN00167	VV0232	4324	4821
123	124	F RXA00167	GR00025	4324	4584
125	126	RXN00171	VV0031	5311	5054
127	128	F RXA00171	GR00026	10316	10086
129	130	RXN00194	VV0115	4174	4614
131	132	F RXA00194	GR00030	290	6
133	134	RXN00197	VV0115	2733	1522
135	136	F RXA00197	GR00030	1731	2741
137	138	RXN00216	VV0096	16292	15303
139	140	RXN00222	VV0096	21079	22224
141	142	F RXA00222	GR00032	21073	22218
143	144	RXN00232	VV0214	601	92
145	146	F RXA00232	GR00035	527	18
147	148	RXN00236	VV0133	3300	2575
149	150	F RXA00236	GR00036	3300	2575
151	152	RXN00242	VV0133	7031	8308
153	154	F RXA00242	GR00036	7031	8233
155	156	RXN00247	VV0057	35082	34156
157	158	F RXA00247	GR00037	7097	6171
159	160	RXN00256	VV0015	3794	4564
161	162	F RXA00256	GR00039	968	1738
163	164	RXN00264	VV0123	14046	13669
165	166	F RXA00264	GR00040	2459	2836
167	168	RXN00267	VV0123	12366	12683
169	170	F RXA00267	GR00040	4091	3822
171	172	RXN00271	VV0019	4975	3986
173	174	F RXA00271	GR00041	3709	2720
175	176	RXN00272	VV0019	5686	6057
177	178	F RXA00272	GR00041	4420	4791
179	180	RXN00283	VV0127	33097	32066
181	182	F RXA00283	GR00045	142	1269
183	184	RXN00334	VV0197	3581	3246
185	186	F RXA00334	GR00057	16762	17097
187	188	RXN00338	VV0197	26797	25658
189	190	F RXA00338	GR00059	1	783
191	192	F RXA00318	GR00055	426	635
193	194	RXN00342	VV0049	1576	1148
195	196	F RXA00342	GR00061	73	501
197	198	RXN00344	VV0135	42719	43597
199	200	F RXA00344	GR00063	6	584
201	202	RXN00353	VV0135	32107	32799
203	204	F RXA00353	GR00068	988	1680
205	206	RXN00354	VV0135	33604	32792
207	208	RXN00362	VV0176	33334	34680
209	210	F RXA00362	GR00073	2	961
211	212	RXN00373	VV0226	6002	6340
213	214	F RXA00373	GR00079	342	4
215	216	RXN00390	VV0025	9834	9430
217	218	F RXA00390	GR00086	1437	1841

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219	220	RXN00399	VV0025	13735	13421
221	222	F RXA00399	GR00087	830	1144
223	224	RXN00416	VV0181	1	
225	226	F RXA00416	GR00093	1	327
227	228	F RXA00418	GR00094	1	1065
229	230	RXN00422	VV0112	3820	4713
231	232	F RXA00422	GR00097	428	6
233	234	RXN00447	VV0112	23325	22906
235	236	F RXA00447	GR00108	518	817
237	238	RXN00455	VV0076	5523	4774
239	240	F RXA00455	GR00113	2	619
241	242	RXN00473	VV0086	31493	32281
243	244	F RXA00473	GR00119	5799	6563
245	246	RXN00485	VV0086	51200	48906
247	248	F RXA00485	GR00119	25230	23188
249	250	RXN00496	VV0086	17452	18477
251	252	F RXA00496	GR00123	1776	2177
253	254	RXN00503	VV0086	11688	13409
255	256	RXN00504	VV0086	13486	13905
257	258	F RXA00504	GR00125	5007	5252
259	260	RXN00505	VV0086	5810	6304
261	262	F RXA00505	GR00126	1	252
263	264	RXN00507	VV0086	4606	3752
265	266	F RXA00507	GR00127	1098	244
267	268	RXN00510	VV0086	1924	3432
269	270	F RXA00509	GR00128	316	140
271	272	F RXA00510	GR00128	384	914
273	274	RXN00515	VV0144	3289	2588
275	276	F RXA00515	GR00131	3	482
277	278	F RXA00520	GR00132	599	796
279	280	RXN00527	VV0079	23845	25608
281	282	F RXA00527	GR00136	3123	1360
283	284	RXN00547	VV0079	33886	35283
285	286	F RXA00547	GR00142	641	1054
287	288	F RXA00546	GR00142	1	690
289	290	RXN00552	VV0079	27617	28552
291	292	F RXA00552	GR00145	2	718
293	294	RXN00555	VV0079	30437	29499
295	296	F RXA00555	GR00145	2555	1665
297	298	RXN00560	VV0103	7606	7980
299	300	F RXA00560	GR00149	256	492
301	302	RXN00574	VV0323	16133	15255
303	304	F RXA00574	GR00156	767	1645
305	306	RXN00589	VV0323	2680	2231
307	308	F RXA00589	GR00156	14220	14582
309	310	RXN00616	VV0054	5670	5326
311	312	F RXA00616	GR00162	3574	3918
313	314	RXN00647	VV0109	12861	12229
315	316	F RXA00647	GR00169	641	1273
317	318	RXN00653	VV0109	6578	7342
319	320	F RXA00653	GR00169	6924	6160
321	322	RXN00662	VV0142	7711	8979
323	324	F RXA00662	GR00172	2671	1403
325	326	RXN00666	VV0109	1566	2480
327	328	F RXA00666	GR00175	390	4
329	330	RXN00704	VV0005	9240	9866
331	332	F RXA00704	GR00183	2972	3484

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333	334	RXN00712	VV0005	1195	500
335	336	F RXA00712	GR00187	1048	500
337	338	RXN00720	VV0232	4899	5564
339	340	F RXA00720	GR00188	7665	7000
341	342	RXN00722	VV0052	2	
343	344	F RXA00722	GR00189	1015	512
345	346	RXN00729	VV0024	3903	2926
347	348	F RXA00729	GR00194	1	642
349	350	F RXA02867	GR10008	610	5
351	352	RXN00730	VV0024	2031	2837
353	354	F RXA00730	GR00194	1063	731
355	356	RXN00731	VV0133	8314	10809
357	358	F RXA00731	GR00195	2613	142
359	360	RXN00738	VV0254	3	
361	362	F RXA00738	GR00201	78	365
363	364	RXN00750	VV0010	30086	30523
365	366	F RXA00750	GR00202	18937	19374
367	368	RXN00762	VV0103	16953	17828
369	370	RXN00768	VV0103	12997	11879
371	372	F RXA00768	GR00204	5956	6399
373	374	F RXA00767	GR00204	5280	5993
375	376	RXN00769	VV0103	11654	11442
377	378	F RXA00769	GR00204	6624	6836
379	380	RXN00771	VV0103	26639	27457
381	382	F RXA00771	GR00205	857	180
383	384	RXN00785	VV0321	2	658
385	386	F RXA00785	GR00207	625	5
387	388	RXN00795	VV0321	6259	5732
389	390	F RXA00795	GR00211	4228	4755
391	392	RXN00831	VV0180	4205	4906
393	394	F RXA00831	GR00224	1662	961
395	396	RXN00835	VV0138	12068	13021
397	398	F RXA00835	GR00226	3	692
399	400	RXN00836	VV0138	13126	14841
401	402	F RXA00836	GR00226	797	2467
403	404	RXN00840	VV0138	6220	6933
405	406	F RXA00840	GR00228	742	1455
407	408	RXN00841	VV0138	6944	7480
409	410	F RXA00841	GR00228	1466	2002
411	412	RXN00846	VV0138	2367	1498
413	414	F RXA00846	GR00230	391	5
415	416	RXN00850	VV0067	4148	3321
417	418	RXN00854	VV0067	371	159
419	420	F RXA00854	GR00231	4708	4920
421	422	RXN00855	VV0255	735	1019
423	424	F RXA00855	GR00232	526	242
425	426	RXN00869	VV0127	5599	4679
427	428	F RXA00869	GR00239	1	792
429	430	RXN00915	VV0238	886	257
431	432	F RXA00915	GR00251	514	5
433	434	RXN00917	VV0238	7202	4524
435	436	F RXA00917	GR00251	5534	4152
437	438	RXN00921	VV0373	1	513
439	440	F RXA00921	GR00252	4750	2852
441	442	RXN00943	VV0116	11376	12287
443	444	F RXA00943	GR00258	3	509
445	446	F RXA02423	GR00706	221	6

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447	448	RXN00945	VV0107	1876	2847
449	450	RXN00946	VV0107	3034	3807
451	452	F RXA00946	GR00259	3034	3807
453	454	RXN00953	VV0260	1834	1082
455	456	RXN00959	VV0208	402	857
457	458	F RXA00959	GR00265	402	728
459	460	RXN00963	VV0249	1816	2652
461	462	F RXA00963	GR00269	442	5
463	464	RXN00971	VV0149	14706	14389
465	466	F RXA00971	GR00273	1421	1149
467	468	RXN00991	VV0210	4424	3045
469	470	RXN01004	VV0210	3045	1984
471	472	RXN01016	VV0209	14476	15123
473	474	F RXA01016	GR00290	1141	494
475	476	RXN01023	VV0143	2343	3320
477	478	F RXA01023	GR00292	1817	867
479	480	RXN01028	VV0015	29000	31048
481	482	F RXA01028	GR00295	3	626
483	484	F RXA01812	GR00514	3	1232
485	486	RXN01069	VV0030	986	273
487	488	F RXA01069	GR00299	606	4
489	490	RXN01071	VV0030	4879	2816
491	492	F RXA02898	GR10040	1631	6
493	494	F RXA01071	GR00299	2822	2436
495	496	RXN01075	VV0084	42045	41635
497	498	F RXA01075	GR00300	3269	2859
499	500	RXN01128	VV0157	2427	3440
501	502	F RXA01128	GR00314	1325	312
503	504	RXN01134	VV0077	774	4
505	506	F RXA01134	GR00317	2	460
507	508	RXN01140	VV0077	1642	710
509	510	F RXA01140	GR00318	3272	4057
511	512	RXN01148	VV0136	3147	3746
513	514	F RXA01148	GR00323	1452	2051
515	516	RXN01153	VV0265	546	4
517	518	F RXA01153	GR00325	546	4
519	520	RXN01154	VV0266	644	6
521	522	F RXA01154	GR00326	608	6
523	524	RXN01155	VV0225	252	1721
525	526	F RXA01155	GR00327	1370	6
527	528	RXN01167	VV0117	12777	13172
529	530	F RXA01167	GR00333	3	323
531	532	RXN01169	VV0117	5804	6799
533	534	F RXA01169	GR00334	1	567
535	536	RXN01173	VV0117	11085	10471
537	538	F RXA01173	GR00334	4853	4239
539	540	RXN01174	VV0117	12236	11487
541	542	F RXA01174	GR00334	6004	5255
543	544	RXN01229	VV0020	32482	31205
545	546	F RXA01229	GR00355	2806	3498
547	548	RXN01246	VV0104	2815	3321
549	550	F RXA01246	GR00360	1824	2462
551	552	RXN01249	VV0271	1	
553	554	F RXA01249	GR00363	303	4
555	556	RXN01251	VV0219	13143	12835
557	558	F RXA01251	GR00365	228	536
559	560	RXN01263	VV0009	11816	12727

561	562	F RXA01263	GR00367	10720	11631
563	564	RXN01266	VV0009	15553	14519
565	566	F RXA01266	GR00367	14457	13423
567	568	RXN01275	VV0009	29514	30431
569	570	F RXA01275	GR00367	28418	29335
571	572	RXN01281	VV0212	4506	5267
573	574	F RXA01281	GR00369	3869	4630
575	576	RXN01296	VV0209	10462	9380
577	578	F RXA01296	GR00373	5836	4754
579	580	RXN01306	VV0148	8158	7151
581	582	F RXA01306	GR00376	5691	4684
583	584	RXN01324	VV0082	6588	6887
585	586	RXN01331	VV0005	39816	42212
587	588	F RXA01331	GR00387	1606	1031
589	590	F RXA00668	GR00176	797	6
591	592	F RXA00674	GR00177	755	6
593	594	RXN01337	VV0032	1925	3337
595	596	F RXA01337	GR00389	5065	3653
597	598	RXN01351	VV0123	2841	3425
599	600	RXN01362	VV0051	27040	23387
601	602	F RXA01362	GR00395	3	1397
603	604	F RXA01364	GR00396	1869	4
605	606	RXN01379	VV0091	10518	11459
607	608	F RXA01379	GR00402	926	6
609	610	RXN01390	VV0277	6654	7310
611	612	F RXA01390	GR00408	992	336
613	614	RXN01391	VV0277	5568	6257
615	616	F RXA01391	GR00408	2078	1389
617	618	RXN01400	VV0126	2988	1489
619	620	F RXA01400	GR00409	2988	1489
621	622	RXN01409	VV0278	5304	4483
623	624	F RXA01409	GR00410	5296	4481
625	626	RXN01434	VV0050	13792	10841
627	628	F RXA01434	GR00417	10228	9863
629	630	RXN01448	VV0089	9602	10768
631	632	F RXA01448	GR00418	19796	19017
633	634	RXN01459	VV0233	3311	4120
635	636	F RXA01459	GR00420	3311	4120
637	638	RXN01460	VV0233	4066	4359
639	640	F RXA01460	GR00420	4066	4359
641	642	RXN01471	VV0019	11467	10661
643	644	F RXA01471	GR00422	5243	4437
645	646	RXN01479	VV0019	18635	18874
647	648	F RXA01479	GR00422	12423	12650
649	650	RXN01484	VV0019	26292	25747
651	652	F RXA01484	GR00422	20068	19523
653	654	RXN01485	VV0019	26454	28505
655	656	F RXA01485	GR00422	20230	22281
657	658	RXN01492	VV0139	36004	36807
659	660	F RXA01492	GR00423	6133	5330
661	662	RXN01518	VV0008	23238	23711
663	664	F RXA01518	GR00424	23238	23711
665	666	RXN01549	VV0080	46	1704
667	668	F RXA01549	GR00430	8426	7566
669	670	F RXA02011	GR00603	46	363
671	672	RXN01557	VV0323	959	1774
673	674	F RXA01557	GR00433	959	1774

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675	676	RXN01574	VV0009	48980	47946
677	678	F RXA01574	GR00438	6963	5929
679	680	RXN01589	VV0227	1216	197
681	682	RXN01592	VV0229	14706	13405
683	684	F RXA01592	GR00447	3	1295
685	686	RXN01597	VV0229	8480	7299
687	688	F RXA01597	GR00447	6220	7401
689	690	RXN01598	VV0229	7286	6324
691	692	F RXA01598	GR00447	7414	8376
693	694	RXN01618	VV0050	23629	23246
695	696	F RXA01618	GR00451	1387	1004
697	698	RXN01634	VV0050	43466	42915
699	700	F RXA01634	GR00454	4988	5539
701	702	RXN01635	VV0050	42879	42139
703	704	F RXA01635	GR00454	5575	6315
705	706	RXN01647	VV0005	43276	44445
707	708	F RXA01647	GR00456	12422	11535
709	710	RXN01658	VV0010	44183	42351
711	712	F RXA01658	GR00461	5	1489
713	714	RXN01659	VV0089	5059	5604
715	716	F RXA01659	GR00462	3	488
717	718	RXN01663	VV0089	4271	5128
719	720	F RXA01663	GR00463	438	4
721	722	RXN01669	VV0057	4529	5443
723	724	F RXA01669	GR00465	1002	271
725	726	RXN01672	VV0179	7849	8190
727	728	F RXA01672	GR00467	2	310
729	730	RXN01694	VV0139	13054	13953
731	732	F RXA01694	GR00474	3931	3032
733	734	RXN01696	VV0115	1381	203
735	736	F RXA01696	GR00475	799	203
737	738	RXN01697	VV0139	1581	625
739	740	F RXA01697	GR00476	761	1486
741	742	RXN01701	VV0162	375	4
743	744	F RXA01701	GR00478	196	528
745	746	RXN01703	VV0089	7108	8220
747	748	F RXA01703	GR00479	2118	1648
749	750	RXN01709	VV0022	847	416
751	752	F RXA01709	GR00483	745	416
753	754	RXN01711	VV0191	8153	6996
755	756	F RXA01711	GR00484	2007	850
757	758	RXN01721	VV0036	1026	4
759	760	RXN01734	VV0221	1251	1784
761	762	F RXA01734	GR00492	544	1077
763	764	RXN01742	VV0233	5246	4743
765	766	F RXA01742	GR00493	7614	8117
767	768	RXN01754	VV0127	38790	36850
769	770	F RXA01754	GR00497	4082	2142
771	772	RXN01761	VV0010	11968	7505
773	774	F RXA00739	GR00202	819	4
775	776	F RXA01587	GR00442	120	2102
777	778	F RXA01761	GR00499	7001	5484
779	780	RXN01765	VV0054	17190	18131
781	782	F RXA01765	GR00500	3144	4085
783	784	RXN01767	VV0015	55242	55706
785	786	F RXA01767	GR00501	341	6
787	788	RXN01769	VV0015	54296	54736

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789	790	F RXA01769	GR00501	1275	847
791	792	RXN01771	VV0050	35063	35764
793	794	F RXA01771	GR00502	886	185
795	796	RXN01774	VV0015	1794	2519
797	798	F RXA01774	GR00503	634	1416
799	800	RXN01787	VV0039	256	948
801	802	F RXA01787	GR00506	2	355
803	804	RXN01796	VV0137	2070	2843
805	806	F RXA01796	GR00508	2	484
807	808	RXN01803	VV0216	3355	4314
809	810	F RXA01803	GR00509	5671	4712
811	812	RXN01809	VV0081	9171	10346
813	814	F RXA01062	GR00297	490	5
815	816	F RXA01809	GR00510	3	638
817	818	RXN01811	VV0146	1243	1923
819	820	RXN01813	VV0084	46618	45953
821	822	F RXA01813	GR00515	635	6
823	824	RXN01815	VV0084	49277	50068
825	826	F RXA01815	GR00515	3294	4085
827	828	RXN01825	VV0083	2847	2578
829	830	F RXA01825	GR00516	2847	2578
831	832	RXN01831	VV0083	10874	10413
833	834	F RXA01831	GR00516	10874	10413
835	836	RXN01834	VV0143	11244	11945
837	838	F RXA01834	GR00517	2478	1777
839	840	RXN01846	VV0010	287	6
841	842	F RXA01846	GR00523	261	4
843	844	RXN01847	VV0139	19018	18284
845	846	F RXA01847	GR00524	52	786
847	848	RXN01874	VV0248	352	5
849	850	F RXA01874	GR00535	2556	2903
851	852	RXN01875	VV0145	2894	2049
853	854	F RXA01875	GR00536	516	1313
855	856	F RXA02734	GR00762	6514	6897
857	858	RXN01877	VV0105	3493	2423
859	860	F RXA01877	GR00537	135	1199
861	862	RXN01879	VV0105	1505	573
863	864	F RXA01879	GR00537	2117	2704
865	866	F RXA01880	GR00537	2641	3048
867	868	RXN01896	VV0098	75888	76523
869	870	F RXA01896	GR00544	2	580
871	872	RXN01899	VV0098	77817	78602
873	874	F RXA01899	GR00544	1874	2659
875	876	RXN01902	VV0098	84095	83037
877	878	F RXA01902	GR00544	7957	7094
879	880	RXN01908	VV0187	4030	4875
881	882	F RXA01908	GR00545	4030	4512
883	884	RXN01909	VV0218	69	947
885	886	F RXA01909	GR00546	59	937
887	888	RXN01910	VV0218	1040	1885
889	890	F RXA01910	GR00546	1030	1875
891	892	RXN01911	VV0218	2209	3147
893	894	F RXA01911	GR00546	2199	3044
895	896	RXN01930	VV0127	46545	47495
897	898	F RXA01930	GR00555	3817	2867
899	900	RXN01944	VV0050	42128	41157
901	902	F RXA01944	GR00558	2	385

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903	904	F RXA01636	GR00454	6326	6898
905	906	RXN01945	VV0050	41150	39159
907	908	F RXA01945	GR00558	392	1633
909	910	F RXA01627	GR00453	1	495
911	912	RXN01960	VV0200	2259	1942
913	914	F RXA01960	GR00565	187	504
915	916	RXN01985	VV0056	1331	282
917	918	RXN01987	VV0149	167	379
919	920	F RXA01987	GR00576	167	379
921	922	RXN01988	VV0149	887	462
923	924	F RXA01988	GR00576	779	462
925	926	RXN01991	VV0230	926	1798
927	928	F RXA01991	GR00581	926	1720
929	930	RXN01996	VV0174	28434	27898
931	932	F RXA01996	GR00585	88	624
933	934	RXN02007	VV0324	855	223
935	936	F RXA02007	GR00598	651	223
937	938	RXN02014	VV0137	8298	8804
939	940	F RXA02014	GR00607	935	540
941	942	RXN02019	VV0129	44705	44205
943	944	F RXA02019	GR00612	597	106
945	946	RXN02023	VV0160	3234	4001
947	948	F RXA02023	GR00613	3234	4001
949	950	RXN02032	VV0117	5181	5750
951	952	F RXA02032	GR00618	4160	4729
953	954	RXN02039	VV0190	1482	643
955	956	F RXA02039	GR00621	3	812
957	958	RXN02044	VV0025	17208	15826
959	960	RXN02045	VV0025	15823	15563
961	962	F RXA02045	GR00623	1913	2173
963	964	RXN02049	VV0009	35549	36157
965	966	F RXA02049	GR00624	1583	2029
967	968	RXN02050	VV0009	36003	36797
969	970	F RXA02050	GR00624	2462	2833
971	972	RXN02059	VV0222	10306	10800
973	974	F RXA02059	GR00625	4678	4184
975	976	RXN02066	VV0222	6187	6678
977	978	F RXA02066	GR00626	6187	6678
979	980	RXN02067	VV0222	6733	7188
981	982	F RXA02067	GR00626	6733	7188
983	984	RXN02075	VV0318	12990	13778
985	986	RXN02076	VV0318	13879	14412
987	988	F RXA02076	GR00628	6902	7435
989	990	RXN02094	VV0126	18268	18984
991	992	F RXA02094	GR00629	13282	13998
993	994	RXN02104	VV0318	7435	6314
995	996	F RXA02104	GR00631	5327	4908
997	998	F RXA02071	GR00628	458	6
999	1000	RXN02107	VV0123	21585	21244
1001	1002	F RXA02107	GR00632	1536	1877
1003	1004	RXN02108	VV0123	21217	20609
1005	1006	F RXA02108	GR00632	2077	2511
1007	1008	RXN02114	VV0180	3	
1009	1010	F RXA02114	GR00634	615	130
1011	1012	RXN02121	VV0102	12833	12129
1013	1014	F RXA02121	GR00636	5813	5109
1015	1016	RXN02138	VV0300	4409	4750

1017	1018	F RXA02138	GR00639	4409	4750
1019	1020	RXN02151	VV0300	19913	21100
1021	1022	F RXA02151	GR00639	19913	21100
1023	1024	RXN02169	VV0100	3172	4017
1025	1026	F RXA02169	GR00641	3172	4017
1027	1028	RXN02180	VV0100	16813	15356
1029	1030	F RXA02180	GR00641	16813	15356
1031	1032	RXN02185	VV0100	20185	20763
1033	1034	F RXA02185	GR00641	20185	20763
1035	1036	RXN02186	VV0100	21192	20995
1037	1038	F RXA02186	GR00641	21213	20995
1039	1040	RXN02207	VV0302	802	5
1041	1042	F RXA02207	GR00646	10909	11667
1043	1044	RXN02223	VV0308	2732	3232
1045	1046	F RXA02223	GR00652	425	6
1047	1048	RXN02226	VV0068	1059	4
1049	1050	F RXA02226	GR00653	1059	4
1051	1052	RXN02238	VV0204	1345	1629
1053	1054	F RXA02238	GR00654	5241	5525
1055	1056	RXN02254	VV0202	2	
1057	1058	F RXA02254	GR00654	21769	22449
1059	1060	RXN02271	VV0020	14281	14838
1061	1062	F RXA02271	GR00655	5406	5963
1063	1064	RXN02279	VV0020	236	1693
1065	1066	F RXA02279	GR00657	1	1404
1067	1068	RXN02296	VV0127	24138	24626
1069	1070	F RXA02296	GR00662	6978	7466
1071	1072	RXN02300	VV0127	28354	28022
1073	1074	F RXA02300	GR00662	11194	10862
1075	1076	RXN02301	VV0127	29070	28354
1077	1078	F RXA02301	GR00662	11910	11194
1079	1080	RXN02302	VV0127	29196	30074
1081	1082	F RXA02302	GR00662	12036	12800
1083	1084	RXN02303	VV0127	13326	14231
1085	1086	F RXA02303	GR00663	1	720
1087	1088	RXN02307	VV0127	12611	11991
1089	1090	F RXA02307	GR00664	395	6
1091	1092	RXN02314	VV0025	23092	23532
1093	1094	F RXA02314	GR00665	6379	5939
1095	1096	RXN02337	VV0141	4679	3357
1097	1098	F RXA02337	GR00672	2893	3816
1099	1100	RXN02339	VV0195	1	
1101	1102	F RXA02339	GR00674	1	492
1103	1104	RXN02340	VV0195	1640	576
1105	1106	F RXA02338	GR00673	484	5
1107	1108	F RXA02340	GR00674	1214	576
1109	1110	RXN02341	VV0078	4279	4764
1111	1112	F RXA02341	GR00675	415	5
1113	1114	RXN02360	VV0051	14638	12206
1115	1116	F RXA02360	GR00685	3644	6076
1117	1118	RXN02361	VV0051	12122	11472
1119	1120	F RXA02361	GR00685	6160	6810
1121	1122	RXN02367	VV0102	4639	5247
1123	1124	F RXA02367	GR00687	2162	1554
1125	1126	RXN02368	VV0102	3883	4557
1127	1128	F RXA02368	GR00687	2918	2244
1129	1130	RXN02381	VV0213	3765	2743

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1131	1132	F RXA02381	GR00691	1792	770
1133	1134	RXN02383	VV0213	639	4
1135	1136	F RXA02383	GR00692	608	6
1137	1138	RXN02387	VV0176	2729	3490
1139	1140	F RXA02387	GR00694	683	6
1141	1142	RXN02398	VV0176	12750	11149
1143	1144	F RXA02398	GR00698	2841	4370
1145	1146	RXN02406	VV0084	22016	22564
1147	1148	F RXA02406	GR00701	1322	774
1149	1150	RXN02407	VV0084	21758	21387
1151	1152	F RXA02407	GR00701	1580	1885
1153	1154	RXN02408	VV0084	20832	19921
1155	1156	F RXA02408	GR00702	832	5
1157	1158	RXN02409	VV0084	21371	20835
1159	1160	F RXA02409	GR00702	1248	835
1161	1162	RXN02428	VV0110	4585	3452
1163	1164	F RXA02428	GR00707	4585	3452
1165	1166	RXN02454	VV0196	2810	1569
1167	1168	F RXA02454	GR00711	3	815
1169	1170	RXN02457	VV0124	19193	18084
1171	1172	F RXA02457	GR00712	1295	2404
1173	1174	RXN02460	VV0124	14649	15152
1175	1176	F RXA02460	GR00712	5839	5336
1177	1178	RXN02464	VV0211	1990	3189
1179	1180	F RXA02464	GR00713	1107	1613
1181	1182	RXN02465	VV0211	3590	3192
1183	1184	F RXA02465	GR00713	2014	1616
1185	1186	RXN02466	VV0211	92	6
1187	1188	F RXA02466	GR00714	92	6
1189	1190	RXN02505	VV0007	23969	24139
1191	1192	F RXA02505	GR00720	18423	18593
1193	1194	RXN02510	VV0171	17467	16832
1195	1196	F RXA02510	GR00721	1983	2618
1197	1198	RXN02519	VV0183	2709	4337
1199	1200	F RXA02519	GR00724	1933	128
1201	1202	RXN02520	VV0183	2243	1560
1203	1204	F RXA02520	GR00724	2222	2905
1205	1206	RXN02534	VV0057	11192	11995
1207	1208	F RXA02534	GR00726	5536	6339
1209	1210	RXN02537	VV0057	14617	15078
1211	1212	F RXA02537	GR00726	8961	9422
1213	1214	RXN02538	VV0057	15078	15749
1215	1216	F RXA02538	GR00726	9422	10093
1217	1218	RXN02555	VV0101	5340	4738
1219	1220	F RXA02555	GR00731	1757	1155
1221	1222	RXN02564	VV0154	10016	9015
1223	1224	F RXA02564	GR00732	2543	3217
1225	1226	RXN02568	VV0245	1657	5
1227	1228	F RXA02568	GR00735	1363	5
1229	1230	RXN02593	VV0098	11073	11669
1231	1232	F RXA02593	GR00741	18693	18481
1233	1234	F RXA02594	GR00741	19077	18754
1235	1236	RXN02606	VV0098	34557	35927
1237	1238	F RXA02606	GR00742	13514	12144
1239	1240	RXN02610	VV0098	31620	30694
1241	1242	F RXA02610	GR00742	16452	17378
1243	1244	RXN02624	VV0129	29202	30497

1245	1246	F RXA02624	GR00746	5602	4889
1247	1248	RXN02626	VV0314	2012	1008
1249	1250	RXN02656	VV0090	15756	14917
1251	1252	RXN02673	VV0315	14030	13398
1253	1254	F RXA02673	GR00753	14030	13398
1255	1256	RXN02680	VV0098	64917	66200
1257	1258	F RXA02680	GR00754	6392	5109
1259	1260	F RXA02679	GR00754	5268	5693
1261	1262	F RXA02681	GR00754	5751	6194
1263	1264	RXN02693	VV0098	74100	75875
1265	1266	F RXA02693	GR00755	1650	4
1267	1268	RXN02696	VV0017	7946	7491
1269	1270	F RXA02696	GR00756	742	287
1271	1272	RXN02697	VV0017	31257	32783
1273	1274	F RXA02697	GR00757	1	699
1275	1276	F RXA02719	GR00758	19598	20245
1277	1278	RXN02720	VV0017	8727	8026
1279	1280	F RXA02720	GR00759	631	5
1281	1282	RXN02744	VV0074	893	1696
1283	1284	F RXA02744	GR00763	14460	13657
1285	1286	RXN02770	VV0171	4202	2637
1287	1288	F RXA02770	GR00772	3	1322
1289	1290	RXN02781	VV0084	14566	13376
1291	1292	F RXA02781	GR00774	1345	155
1293	1294	RXN02782	VV0093	7148	8446
1295	1296	F RXA02782	GR00775	204	875
1297	1298	RXN02812	VV0210	342	4
1299	1300	F RXA02812	GR00793	2	568
1301	1302	RXN02817	VV0346	403	5
1303	1304	F RXA02817	GR00798	403	5
1305	1306	RXN02818	VV0347	611	6
1307	1308	F RXA02818	GR00799	611	6
1309	1310	RXN02825	VV0082	3589	1751
1311	1312	F RXA01322	GR00385	443	6
1313	1314	F RXA02824	GR00805	531	4
1315	1316	F RXA02825	GR00806	565	182
1317	1318	RXN02838	VV0161	1	
1319	1320	F RXA02838	GR00831	1	462
1321	1322	RXN02840	VV0365	488	339
1323	1324	F RXA02840	GR00835	488	339
1325	1326	RXN02841	VV0055	11788	12222
1327	1328	F RXA02841	GR00840	283	5
1329	1330	RXN02846	VV0127	30861	30112
1331	1332	F RXA02846	GR00845	578	6
1333	1334	RXN02847	VV0113	47	1135
1335	1336	F RXA02847	GR00847	598	5
1337	1338	RXN02849	VV0237	2	
1339	1340	F RXA02849	GR00849	2	283
1341	1342	RXN02911	VV0135	24643	25101
1343	1344	RXN02914	VV0127	17305	16763
1345	1346	RXN02921	VV0213	1871	1401
1347	1348	RXN02924	VV0088	4557	5105
1349	1350	RXN02927	VV0082	18836	19303
1351	1352	RXN02928	VV0082	19511	20203
1353	1354	RXN02931	VV0090	25420	25644
1355	1356	RXN02932	VV0176	23391	24362
1357	1358	RXN02934	VV0103	14533	14838

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1359	1360	RXN02936	VV0197	24360	24557
1361	1362	RXN02939	VV0008	33988	32387
1363	1364	F RXA01383	GR00406	1147	5
1365	1366	RXN02950	VV0224	7629	7306
1367	1368	RXN02951	VV0176	5739	5131
1369	1370	RXN02957	VV0020	30448	30158
1371	1372	RXN02967	VV0318	6614	6931
1373	1374	RXN02971	VV0210	951	640
1375	1376	RXN02978	VV0010	2191	683
1377	1378	RXN02995	VV0069	348	1913
1379	1380	RXN02997	VV0069	3709	2981
1381	1382	RXN03001	VV0170	422	874
1383	1384	RXN03005	VV0237	1101	334
1385	1386	RXN03009	VV0238	353	6
1387	1388	RXN03010	VV0238	7435	7199
1389	1390	RXN03011	VV0098	2984	3184
1391	1392	RXN03012	VV0241	2	571
1393	1394	RXN03017	VV0218	5720	7258
1395	1396	F RXA02753	GR00765	2630	138
1397	1398	RXN03018	VV0218	7221	8213
1399	1400	RXN03024	VV0003	6315	7730
1401	1402	RXN03025	VV0003	8668	7796
1403	1404	RXN03027	VV0008	17	151
1405	1406	RXN03029	VV0009	95	607
1407	1408	RXN03031	VV0011	1	789
1409	1410	RXN03032	VV0012	3652	3936
1411	1412	RXN03034	VV0013	2	661
1413	1414	F RXA00063	GR00010	1658	1374
1415	1416	RXN03037	VV0015	5364	5549
1417	1418	RXN03041	VV0018	1770	1273
1419	1420	F RXA02892	GR10035	1171	668
1421	1422	RXN03045	VV0019	33044	34039
1423	1424	RXN03046	VV0020	1	336
1425	1426	RXN03047	VV0020	25070	26485
1427	1428	F RXA00036	GR00004	7204	8619
1429	1430	RXN03048	VV0020	27423	26551
1431	1432	F RXA00037	GR00004	9557	8685
1433	1434	RXN03050	VV0021	6368	7333
1435	1436	RXN03053	VV0026	12	1535
1437	1438	F RXA02885	GR10021	1	1536
1439	1440	RXN03055	VV0026	3519	3947
1441	1442	F RXA00261	GR00039	11693	11265
1443	1444	F RXA02888	GR10024	326	754
1445	1446	RXN03059	VV0030	5373	4894
1447	1448	F RXA02899	GR10040	2125	1646
1449	1450	RXN03062	VV0035	525	4
1451	1452	RXN03066	VV0038	7298	6636
1453	1454	F RXA02876	GR10016	405	1067
1455	1456	RXN03067	VV0038	7493	7323
1457	1458	RXN03068	VV0038	7648	7529
1459	1460	RXN03073	VV0042	1573	944
1461	1462	F RXA02905	GR10044	477	4
1463	1464	RXN03085	VV0048	4511	4161
1465	1466	RXN03089	VV0053	1183	26
1467	1468	F RXA00071	GR00011	4013	5464
1469	1470	RXN03098	VV0064	2100	2723
1471	1472	RXN03099	VV0064	5576	6250

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1473	1474	RXN03104	VV0071	401	577
1475	1476	RXN03106	VV0074	15930	16121
1477	1478	RXN03107	VV0076	232	432
1479	1480	RXN03113	VV0086	6541	8139
1481	1482	F RXA00506	GR00126	489	1829
1483	1484	RXN03115	VV0089	148	546
1485	1486	RXN03122	VV0104	3329	3475
1487	1488	RXN03134	VV0127	65312	65662
1489	1490	RXN03135	VV0127	66674	67402
1491	1492	F RXA02285	GR00660	1544	2272
1493	1494	RXN03138	VV0129	21194	21664
1495	1496	RXN03140	VV0131	4550	4302
1497	1498	RXN03141	VV0135	31144	31473
1499	1500	RXN03146	VV0143	25998	26468
1501	1502	RXN03147	VV0144	2726	2977
1503	1504	RXN03149	VV0146	969	1235
1505	1506	RXN03152	VV0166	264	536
1507	1508	RXN03153	VV0176	46481	47044
1509	1510	RXN03154	VV0179	1328	2239
1511	1512	RXN03156	VV0187	4908	5087
1513	1514	F RXA00176	GR00027	3475	3317
1515	1516	RXN03162	VV0195	909	1304
1517	1518	RXN03167	VV0327	633	4
1519	1520	F RXA02862	GR10006	1695	2330
1521	1522	RXN03170	VV0328	457	209
1523	1524	F RXA02856	GR10003	459	211
1525	1526	RXN03172	VV0329	1392	367
1527	1528	F RXA02858	GR10004	1392	367
1529	1530	RXN03173	VV0330	1340	243
1531	1532	F RXA02874	GR10015	1348	869
1533	1534	RXN03174	VV0331	461	6
1535	1536	F RXA02884	GR10020	1695	2156
1537	1538	RXN03177	VV0333	816	151
1539	1540	F RXA02881	GR10019	94	759
1541	1542	RXN03182	VV0339	276	4
1543	1544	RXN03184	VV0374	517	20
1545	1546	RXN03185	VV0375	311	123
1547	1548	RXA00003	GR00001	2279	3019
1549	1550	RXA00008	GR00002	606	115
1551	1552	RXA00015	GR00002	5999	6307
1553	1554	RXA00018	GR00002	12979	14277
1555	1556	RXA00020	GR00002	17142	16363
1557	1558	RXA00021	GR00002	18766	20538
1559	1560	RXA00025	GR00003	2211	3647
1561	1562	RXA00031	GR00003	10383	9982
1563	1564	RXA00049	GR00008	2270	2956
1565	1566	RXA00052	GR00008	7957	7247
1567	1568	RXA00054	GR00008	8557	11469
1569	1570	RXA00058	GR00009	7394	6831
1571	1572	RXA00059	GR00009	8301	8020
1573	1574	RXA00065	GR00010	4140	4412
1575	1576	RXA00068	GR00011	1305	724
1577	1578	RXA00079	GR00012	6599	6820
1579	1580	RXA00082	GR00012	9019	8456
1581	1582	RXA00083	GR00013	771	1070
1583	1584	RXA00093	GR00014	204	2426
1585	1586	RXA00101	GR00014	10514	10107

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1587	1588	RXA00108	GR00015	546	4
1589	1590	RXA00110	GR00016	364	912
1591	1592	RXA00117	GR00019	791	201
1593	1594	RXA00118	GR00019	918	1172
1595	1596	RXA00119	GR00019	1704	2462
1597	1598	RXA00121	GR00019	3473	4183
1599	1600	RXA00122	GR00019	4220	5842
1601	1602	RXA00127	GR00020	2871	2416
1603	1604	RXA00134	GR00021	1648	1079
1605	1606	RXA00140	GR00022	3841	3656
1607	1608	RXA00141	GR00022	4307	3846
1609	1610	RXA00142	GR00022	4776	4300
1611	1612	RXA00150	GR00023	4085	4858
1613	1614	RXA00151	GR00023	4956	5552
1615	1616	RXA00153	GR00023	7656	7231
1617	1618	RXA00155	GR00023	8615	9397
1619	1620	RXA00159	GR00024	3868	2687
1621	1622	RXA00161	GR00024	4893	5354
1623	1624	RXA00169	GR00026	5222	3150
1625	1626	RXA00170	GR00026	9914	8061
1627	1628	RXA00173	GR00027	1716	1384
1629	1630	RXA00174	GR00027	2079	1795
1631	1632	RXA00175	GR00027	2732	2103
1633	1634	RXA00179	GR00028	1714	1256
1635	1636	RXA00180	GR00028	2334	1795
1637	1638	RXA00183	GR00028	7344	8195
1639	1640	RXA00185	GR00028	9418	12045
1641	1642	RXA00199	GR00031	2172	754
1643	1644	RXA00200	GR00031	2837	2535
1645	1646	RXA00207	GR00032	6430	6747
1647	1648	RXA00211	GR00032	10120	10782
1649	1650	RXA00218	GR00032	18104	19243
1651	1652	RXA00220	GR00032	20666	20163
1653	1654	RXA00230	GR00034	746	27
1655	1656	RXA00233	GR00036	420	4
1657	1658	RXA00234	GR00036	998	459
1659	1660	RXA00237	GR00036	3668	4045
1661	1662	RXA00238	GR00036	4186	4554
1663	1664	RXA00239	GR00036	5118	4534
1665	1666	RXA00240	GR00036	5342	5133
1667	1668	RXA00244	GR00037	1565	930
1669	1670	RXA00245	GR00037	3049	1565
1671	1672	RXA00248	GR00037	7843	7121
1673	1674	RXA00250	GR00038	6	221
1675	1676	RXA00252	GR00038	485	727
1677	1678	RXA00257	GR00039	1760	2215
1679	1680	RXA00258	GR00039	3219	3890
1681	1682	RXA00260	GR00039	9234	10409
1683	1684	RXA00273	GR00042	185	1297
1685	1686	RXA00274	GR00042	1556	4165
1687	1688	RXA00275	GR00042	4696	4238
1689	1690	RXA00276	GR00042	5016	4675
1691	1692	RXA00279	GR00043	4001	2616
1693	1694	RXA00282	GR00044	793	5
1695	1696	RXA00285	GR00046	3	515
1697	1698	RXA00286	GR00046	579	1142
1699	1700	RXA00294	GR00047	2761	3189

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1701	1702	RXA00297	GR00048	2861	3772
1703	1704	RXA00320	GR00057	358	537
1705	1706	RXA00321	GR00057	2411	597
1707	1708	RXA00322	GR00057	3658	2555
1709	1710	RXA00325	GR00057	8594	9238
1711	1712	RXA00326	GR00057	9378	9857
1713	1714	RXA00336	GR00057	19461	19931
1715	1716	RXA00337	GR00058	530	6
1717	1718	RXA00339	GR00059	817	1533
1719	1720	RXA00349	GR00066	3	1061
1721	1722	RXA00355	GR00069	635	510
1723	1724	RXA00375	GR00080	549	49
1725	1726	RXA00380	GR00082	836	216
1727	1728	RXA00387	GR00084	1403	591
1729	1730	RXA00392	GR00086	3890	3027
1731	1732	RXA00394	GR00086	5322	4990
1733	1734	RXA00395	GR00086	5417	5716
1735	1736	RXA00396	GR00086	6653	6183
1737	1738	RXA00397	GR00086	7206	6667
1739	1740	RXA00398	GR00087	1	681
1741	1742	RXA00408	GR00091	642	1088
1743	1744	RXA00409	GR00091	1088	2500
1745	1746	RXA00411	GR00092	1685	1011
1747	1748	RXA00423	GR00097	909	457
1749	1750	RXA00424	GR00097	1379	909
1751	1752	RXA00425	GR00097	1433	1657
1753	1754	RXA00428	GR00098	2657	2025
1755	1756	RXA00429	GR00098	3063	2662
1757	1758	RXA00430	GR00098	3473	3063
1759	1760	RXA00433	GR00100	1446	1970
1761	1762	RXA00451	GR00110	816	325
1763	1764	RXA00457	GR00114	1451	372
1765	1766	RXA00462	GR00116	3023	1644
1767	1768	RXA00463	GR00116	4209	3388
1769	1770	RXA00468	GR00118	1282	464
1771	1772	RXA00469	GR00119	1647	472
1773	1774	RXA00472	GR00119	5449	4589
1775	1776	RXA00474	GR00119	6575	8152
1777	1778	RXA00475	GR00119	8822	8163
1779	1780	RXA00476	GR00119	8961	9821
1781	1782	RXA00481	GR00119	17636	18220
1783	1784	RXA00486	GR00120	1	702
1785	1786	RXA00490	GR00121	2676	1774
1787	1788	RXA00491	GR00122	1057	638
1789	1790	RXA00493	GR00123	3	326
1791	1792	RXA00519	GR00132	4	516
1793	1794	RXA00528	GR00136	3562	4650
1795	1796	RXA00529	GR00136	5274	4732
1797	1798	RXA00530	GR00136	6837	5557
1799	1800	RXA00535	GR00137	5155	5871
1801	1802	RXA00540	GR00139	2027	2269
1803	1804	RXA00549	GR00143	502	897
1805	1806	RXA00550	GR00143	935	1255
1807	1808	RXA00553	GR00145	742	1062
1809	1810	RXA00554	GR00145	1606	1136
1811	1812	RXA00563	GR00151	1	2739
1813	1814	RXA00564	GR00151	3744	4148

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1815	1816	RXA00573	GR00156	117	767
1817	1818	RXA00576	GR00156	2916	2245
1819	1820	RXA00577	GR00156	2980	3327
1821	1822	RXA00578	GR00156	4087	3365
1823	1824	RXA00582	GR00156	9442	8924
1825	1826	RXA00585	GR00156	11894	11577
1827	1828	RXA00586	GR00156	12818	11937
1829	1830	RXA00587	GR00156	13008	13490
1831	1832	RXA00595	GR00159	3	332
1833	1834	RXA00597	GR00159	797	1066
1835	1836	RXA00598	GR00159	1070	1387
1837	1838	RXA00601	GR00159	3459	3749
1839	1840	RXA00602	GR00159	4907	4155
1841	1842	RXA00604	GR00159	5489	5779
1843	1844	RXA00610	GR00161	1193	2056
1845	1846	RXA00611	GR00161	3640	2165
1847	1848	RXA00613	GR00162	1652	1200
1849	1850	RXA00614	GR00162	1680	2594
1851	1852	RXA00617	GR00162	4002	5084
1853	1854	RXA00628	GR00165	1284	877
1855	1856	RXA00631	GR00166	172	1626
1857	1858	RXA00637	GR00167	2002	2754
1859	1860	RXA00646	GR00169	446	6
1861	1862	RXA00649	GR00169	2823	3278
1863	1864	RXA00652	GR00169	5449	5997
1865	1866	RXA00654	GR00169	7213	8478
1867	1868	RXA00656	GR00169	9495	9235
1869	1870	RXA00657	GR00169	10882	9980
1871	1872	RXA00661	GR00172	664	1353
1873	1874	RXA00667	GR00175	593	1177
1875	1876	RXA00676	GR00178	647	1393
1877	1878	RXA00678	GR00179	1037	303
1879	1880	RXA00691	GR00181	2152	1223
1881	1882	RXA00692	GR00181	3450	2317
1883	1884	RXA00693	GR00181	4303	3821
1885	1886	RXA00701	GR00182	427	801
1887	1888	RXA00707	GR00185	377	1348
1889	1890	RXA00713	GR00188	71	1033
1891	1892	RXA00714	GR00188	1809	1249
1893	1894	RXA00716	GR00188	3002	3514
1895	1896	RXA00719	GR00188	5283	6911
1897	1898	RXA00724	GR00191	811	164
1899	1900	RXA00726	GR00192	841	701
1901	1902	RXA00740	GR00202	1646	1068
1903	1904	RXA00741	GR00202	2986	2054
1905	1906	RXA00742	GR00202	5517	3868
1907	1908	RXA00743	GR00202	6652	6230
1909	1910	RXA00745	GR00202	13874	13341
1911	1912	RXA00746	GR00202	13755	14945
1913	1914	RXA00747	GR00202	15067	15654
1915	1916	RXA00748	GR00202	15917	16360
1917	1918	RXA00749	GR00202	17240	16542
1919	1920	RXA00751	GR00202	20245	19418
1921	1922	RXA00752	GR00202	21847	21419
1923	1924	RXA00757	GR00203	3119	4372
1925	1926	RXA00763	GR00204	1384	2166
1927	1928	RXA00765	GR00204	3283	3969

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1929	1930	RXA00781	GR00206	2682	2395
1931	1932	RXA00788	GR00209	910	686
1933	1934	RXA00804	GR00215	438	881
1935	1936	RXA00805	GR00215	2057	2938
1937	1938	RXA00808	GR00217	1029	352
1939	1940	RXA00812	GR00219	287	1345
1941	1942	RXA00814	GR00219	2463	3236
1943	1944	RXA00815	GR00219	3236	3808
1945	1946	RXA00816	GR00219	4382	4678
1947	1948	RXA00826	GR00223	567	37
1949	1950	RXA00830	GR00224	266	988
1951	1952	RXA00853	GR00231	3775	3173
1953	1954	RXA00861	GR00235	6	431
1955	1956	RXA00862	GR00236	580	17
1957	1958	RXA00874	GR00241	758	1846
1959	1960	RXA00876	GR00241	4208	2454
1961	1962	RXA00881	GR00242	8057	8434
1963	1964	RXA00882	GR00242	8788	9465
1965	1966	RXA00883	GR00242	10060	9542
1967	1968	RXA00887	GR00242	13544	14266
1969	1970	RXA00889	GR00242	15341	15928
1971	1972	RXA00893	GR00244	789	193
1973	1974	RXA00895	GR00244	2578	1988
1975	1976	RXA00904	GR00246	1457	702
1977	1978	RXA00908	GR00247	1611	2168
1979	1980	RXA00916	GR00251	4108	518
1981	1982	RXA00926	GR00253	466	104
1983	1984	RXA00930	GR00253	3841	3089
1985	1986	RXA00932	GR00253	5068	5541
1987	1988	RXA00933	GR00253	6047	5586
1989	1990	RXA00940	GR00257	129	524
1991	1992	RXA00949	GR00259	5400	6047
1993	1994	RXA00969	GR00273	1	147
1995	1996	RXA00973	GR00274	2272	1670
1997	1998	RXA00978	GR00276	217	831
1999	2000	RXA00986	GR00280	60	401
2001	2002	RXA00987	GR00280	875	411
2003	2004	RXA00988	GR00280	1371	949
2005	2006	RXA01005	GR00286	520	1365
2007	2008	RXA01007	GR00287	2572	866
2009	2010	RXA01008	GR00287	2719	4659
2011	2012	RXA01011	GR00288	2089	857
2013	2014	RXA01017	GR00290	2175	1567
2015	2016	RXA01021	GR00291	1759	2280
2017	2018	RXA01029	GR00295	1338	1826
2019	2020	RXA01031	GR00295	3182	3847
2021	2022	RXA01032	GR00295	3974	4348
2023	2024	RXA01033	GR00295	4363	4698
2025	2026	RXA01034	GR00295	5177	4824
2027	2028	RXA01035	GR00295	5818	6423
2029	2030	RXA01036	GR00295	6513	6965
2031	2032	RXA01037	GR00295	7000	7527
2033	2034	RXA01038	GR00295	7530	8276
2035	2036	RXA01039	GR00295	9540	8965
2037	2038	RXA01040	GR00295	9711	10613
2039	2040	RXA01041	GR00295	10780	10932
2041	2042	RXA01042	GR00295	11088	12365

2043	2044	RXA01043	GR00295	12774	13346
2045	2046	RXA01044	GR00295	14024	15280
2047	2048	RXA01045	GR00295	15407	17230
2049	2050	RXA01046	GR00295	17441	19219
2051	2052	RXA01047	GR00295	19244	19717
2053	2054	RXA01058	GR00296	8566	8246
2055	2056	RXA01063	GR00297	828	499
2057	2058	RXA01066	GR00298	605	1330
2059	2060	RXA01068	GR00298	2184	3254
2061	2062	RXA01074	GR00300	2811	2107
2063	2064	RXA01076	GR00300	4374	3355
2065	2066	RXA01078	GR00300	6043	6876
2067	2068	RXA01083	GR00302	1777	1502
2069	2070	RXA01088	GR00304	3083	1902
2071	2072	RXA01091	GR00305	546	76
2073	2074	RXA01092	GR00305	702	881
2075	2076	RXA01092	GR00305	702	881
2077	2078	RXA01096	GR00306	4341	3643
2079	2080	RXA01102	GR00306	10018	8774
2081	2082	RXA01103	GR00306	10316	10092
2083	2084	RXA01107	GR00306	13612	14811
2085	2086	RXA01108	GR00306	15562	14912
2087	2088	RXA01109	GR00306	16281	15640
2089	2090	RXA01119	GR00310	1068	139
2091	2092	RXA01122	GR00311	557	36
2093	2094	RXA01123	GR00311	1090	644
2095	2096	RXA01127	GR00314	2	280
2097	2098	RXA01129	GR00314	1461	3326
2099	2100	RXA01131	GR00315	445	1311
2101	2102	RXA01137	GR00318	1101	1460
2103	2104	RXA01156	GR00327	1588	1388
2105	2106	RXA01158	GR00328	2580	1639
2107	2108	RXA01159	GR00328	3089	2775
2109	2110	RXA01160	GR00328	4187	3213
2111	2112	RXA01163	GR00331	710	6
2113	2114	RXA01165	GR00332	2155	1583
2115	2116	RXA01166	GR00332	3005	2523
2117	2118	RXA01170	GR00334	638	1120
2119	2120	RXA01171	GR00334	1714	2406
2121	2122	RXA01176	GR00335	1980	1477
2123	2124	RXA01177	GR00335	2121	4106
2125	2126	RXA01178	GR00335	4106	4555
2127	2128	RXA01184	GR00338	1489	17
2129	2130	RXA01186	GR00338	3742	2645
2131	2132	RXA01186	GR00338	3742	2645
2133	2134	RXA01187	GR00338	3850	4308
2135	2136	RXA01195	GR00343	1413	1859
2137	2138	RXA01196	GR00343	1889	2578
2139	2140	RXA01197	GR00343	3333	2881
2141	2142	RXA01198	GR00343	3422	3724
2143	2144	RXA01207	GR00347	126	773
2145	2146	RXA01213	GR00351	1508	282
2147	2148	RXA01218	GR00353	1078	1506
2149	2150	RXA01234	GR00357	633	250
2151	2152	RXA01237	GR00358	2751	2311
2153	2154	RXA01267	GR00367	16799	15486
2155	2156	RXA01268	GR00367	19365	18526

2157	2158	RXA01271	GR00367	23467	21656
2159	2160	RXA01273	GR00367	26475	25042
2161	2162	RXA01282	GR00369	5444	4665
2163	2164	RXA01294	GR00373	3537	2872
2165	2166	RXA01295	GR00373	3764	4738
2167	2168	RXA01304	GR00376	1982	2467
2169	2170	RXA01310	GR00380	803	477
2171	2172	RXA01313	GR00381	1116	172
2173	2174	RXA01315	GR00382	1394	744
2175	2176	RXA01316	GR00382	1855	1553
2177	2178	RXA01317	GR00382	2296	1877
2179	2180	RXA01318	GR00382	3616	2315
2181	2182	RXA01330	GR00387	569	1024
2183	2184	RXA01333	GR00389	1231	227
2185	2186	RXA01336	GR00389	3640	3038
2187	2188	RXA01342	GR00389	11296	12807
2189	2190	RXA01348	GR00392	261	752
2191	2192	RXA01349	GR00392	1531	755
2193	2194	RXA01357	GR00393	4357	4659
2195	2196	RXA01359	GR00393	6857	8038
2197	2198	RXA01366	GR00397	1369	980
2199	2200	RXA01367	GR00397	1518	1919
2201	2202	RXA01370	GR00398	1875	2225
2203	2204	RXA01372	GR00399	1	591
2205	2206	RXA01378	GR00401	1281	4
2207	2208	RXA01380	GR00403	2	2017
2209	2210	RXA01384	GR00406	3238	1523
2211	2212	RXA01396	GR00408	6475	6218
2213	2214	RXA01397	GR00408	6894	6475
2215	2216	RXA01401	GR00409	3193	3453
2217	2218	RXA01402	GR00409	3508	3981
2219	2220	RXA01405	GR00410	1844	1389
2221	2222	RXA01413	GR00412	854	1453
2223	2224	RXA01414	GR00412	1628	2134
2225	2226	RXA01417	GR00414	645	49
2227	2228	RXA01421	GR00416	1215	829
2229	2230	RXA01425	GR00417	1701	2585
2231	2232	RXA01429	GR00417	5651	6268
2233	2234	RXA01439	GR00418	5949	6494
2235	2236	RXA01440	GR00418	7496	6489
2237	2238	RXA01441	GR00418	8542	7514
2239	2240	RXA01445	GR00418	15083	14091
2241	2242	RXA01447	GR00418	17885	18733
2243	2244	RXA01452	GR00419	2363	2641
2245	2246	RXA01456	GR00420	898	1419
2247	2248	RXA01457	GR00420	1499	2173
2249	2250	RXA01463	GR00421	2493	1330
2251	2252	RXA01469	GR00422	2091	3122
2253	2254	RXA01470	GR00422	4112	3687
2255	2256	RXA01472	GR00422	5783	5328
2257	2258	RXA01473	GR00422	6596	5832
2259	2260	RXA01474	GR00422	6678	7223
2261	2262	RXA01475	GR00422	7651	7226
2263	2264	RXA01476	GR00422	7847	8188
2265	2266	RXA01488	GR00423	2179	1349
2267	2268	RXA01494	GR00423	8515	7520
2269	2270	RXA01497	GR00424	262	1179

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2271	2272	RXA01501	GR00424	8130	7843
2273	2274	RXA01504	GR00424	10710	11318
2275	2276	RXA01505	GR00424	11318	11815
2277	2278	RXA01506	GR00424	11815	12225
2279	2280	RXA01507	GR00424	12239	12661
2281	2282	RXA01519	GR00424	23725	24471
2283	2284	RXA01520	GR00424	24784	25167
2285	2286	RXA01523	GR00424	27951	28901
2287	2288	RXA01525	GR00424	32301	30580
2289	2290	RXA01527	GR00425	5126	2616
2291	2292	RXA01536	GR00427	4066	2825
2293	2294	RXA01540	GR00428	3083	2382
2295	2296	RXA01543	GR00430	2802	37
2297	2298	RXA01544	GR00430	3496	2897
2299	2300	RXA01545	GR00430	4838	3588
2301	2302	RXA01546	GR00430	5584	4889
2303	2304	RXA01547	GR00430	6371	5709
2305	2306	RXA01548	GR00430	7432	6425
2307	2308	RXA01552	GR00431	6122	5145
2309	2310	RXA01554	GR00432	3719	1578
2311	2312	RXA01560	GR00435	767	438
2313	2314	RXA01575	GR00438	8024	7005
2315	2316	RXA01577	GR00438	8811	9185
2317	2318	RXA01579	GR00439	671	1054
2319	2320	RXA01585	GR00441	1226	600
2321	2322	RXA01586	GR00441	1597	1229
2323	2324	RXA01595	GR00447	3326	4285
2325	2326	RXA01600	GR00447	10460	11128
2327	2328	RXA01602	GR00447	13591	12062
2329	2330	RXA01605	GR00448	960	2474
2331	2332	RXA01610	GR00449	4343	3615
2333	2334	RXA01611	GR00449	4832	4476
2335	2336	RXA01612	GR00449	5235	4891
2337	2338	RXA01619	GR00451	2407	1433
2339	2340	RXA01622	GR00452	1908	2510
2341	2342	RXA01623	GR00452	2514	3224
2343	2344	RXA01624	GR00452	3220	3564
2345	2346	RXA01628	GR00453	866	1879
2347	2348	RXA01630	GR00454	341	1417
2349	2350	RXA01641	GR00456	5182	6552
2351	2352	RXA01642	GR00456	6557	7798
2353	2354	RXA01643	GR00456	8374	7949
2355	2356	RXA01645	GR00456	10574	9969
2357	2358	RXA01646	GR00456	11513	10695
2359	2360	RXA01656	GR00460	1548	2444
2361	2362	RXA01665	GR00463	2152	1433
2363	2364	RXA01671	GR00466	854	1468
2365	2366	RXA01673	GR00467	1807	773
2367	2368	RXA01675	GR00467	2824	3234
2369	2370	RXA01676	GR00467	4179	3424
2371	2372	RXA01677	GR00467	5043	4300
2373	2374	RXA01681	GR00467	10681	11313
2375	2376	RXA01685	GR00470	1488	910
2377	2378	RXA01686	GR00470	2026	1586
2379	2380	RXA01693	GR00474	1553	2974
2381	2382	RXA01714	GR00485	985	371
2383	2384	RXA01715	GR00485	1267	1962

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2385	2386	RXA01729	GR00489	2636	3154
2387	2388	RXA01731	GR00491	109	807
2389	2390	RXA01738	GR00493	3971	4684
2391	2392	RXA01741	GR00493	7535	6738
2393	2394	RXA01748	GR00495	3681	4460
2395	2396	RXA01749	GR00495	4633	6249
2397	2398	RXA01750	GR00496	1878	3518
2399	2400	RXA01752	GR00497	557	6
2401	2402	RXA01753	GR00497	2095	557
2403	2404	RXA01760	GR00498	5095	5376
2405	2406	RXA01768	GR00501	827	450
2407	2408	RXA01770	GR00501	5134	1370
2409	2410	RXA01773	GR00503	34	444
2411	2412	RXA01775	GR00504	178	741
2413	2414	RXA01776	GR00504	838	2289
2415	2416	RXA01777	GR00504	2319	2777
2417	2418	RXA01778	GR00504	2912	4048
2419	2420	RXA01779	GR00504	4246	5664
2421	2422	RXA01780	GR00504	5721	6095
2423	2424	RXA01781	GR00504	6052	6312
2425	2426	RXA01782	GR00504	6384	6779
2427	2428	RXA01783	GR00504	6842	7078
2429	2430	RXA01785	GR00505	729	1304
2431	2432	RXA01788	GR00506	361	801
2433	2434	RXA01789	GR00506	875	1516
2435	2436	RXA01790	GR00506	1672	1731
2437	2438	RXA01791	GR00506	1885	2247
2439	2440	RXA01792	GR00506	2310	2582
2441	2442	RXA01793	GR00506	2916	3149
2443	2444	RXA01794	GR00506	3194	3477
2445	2446	RXA01799	GR00509	377	1570
2447	2448	RXA01800	GR00509	2292	1573
2449	2450	RXA01804	GR00509	6117	5797
2451	2452	RXA01805	GR00509	6515	6186
2453	2454	RXA01806	GR00509	6595	7074
2455	2456	RXA01816	GR00515	4210	4941
2457	2458	RXA01817	GR00515	4941	5573
2459	2460	RXA01820	GR00515	8360	9733
2461	2462	RXA01842	GR00522	1397	480
2463	2464	RXA01844	GR00522	1950	1771
2465	2466	RXA01845	GR00522	1919	2326
2467	2468	RXA01856	GR00527	225	770
2469	2470	RXA01857	GR00527	939	1589
2471	2472	RXA01858	GR00529	578	6
2473	2474	RXA01870	GR00534	2123	2797
2475	2476	RXA01871	GR00534	2797	3759
2477	2478	RXA01903	GR00545	3	281
2479	2480	RXA01904	GR00545	762	340
2481	2482	RXA01905	GR00545	1074	1604
2483	2484	RXA01906	GR00545	2322	2786
2485	2486	RXA01907	GR00545	3176	3787
2487	2488	RXA01923	GR00552	1311	1739
2489	2490	RXA01931	GR00555	4913	5566
2491	2492	RXA01941	GR00557	995	1429
2493	2494	RXA01942	GR00557	3526	2927
2495	2496	RXA01957	GR00564	389	850
2497	2498	RXA01958	GR00564	910	1416

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2499	2500	RXA01959	GR00564	1639	2019
2501	2502	RXA01961	GR00565	521	1000
2503	2504	RXA01962	GR00565	1022	1591
2505	2506	RXA01963	GR00565	1757	2440
2507	2508	RXA01964	GR00566	1329	4
2509	2510	RXA01965	GR00566	1935	1375
2511	2512	RXA01966	GR00567	47	703
2513	2514	RXA01968	GR00567	3295	2138
2515	2516	RXA01969	GR00567	5689	5216
2517	2518	RXA01973	GR00570	2	583
2519	2520	RXA01974	GR00570	658	2109
2521	2522	RXA01976	GR00571	3742	2222
2523	2524	RXA01977	GR00571	4547	3972
2525	2526	RXA01982	GR00573	3001	1844
2527	2528	RXA01990	GR00581	1	999
2529	2530	RXA01992	GR00583	709	260
2531	2532	RXA01999	GR00589	2384	2854
2533	2534	RXA02001	GR00590	700	152
2535	2536	RXA02004	GR00594	3	209
2537	2538	RXA02006	GR00597	498	4
2539	2540	RXA02009	GR00601	127	5
2541	2542	RXA02013	GR00607	553	5
2543	2544	RXA02021	GR00613	2008	1061
2545	2546	RXA02036	GR00619	3441	3821
2547	2548	RXA02040	GR00621	1452	925
2549	2550	RXA02046	GR00623	2680	2943
2551	2552	RXA02051	GR00624	3186	3683
2553	2554	RXA02053	GR00624	5484	6062
2555	2556	RXA02057	GR00625	2972	3502
2557	2558	RXA02058	GR00625	4051	3500
2559	2560	RXA02069	GR00627	1116	1694
2561	2562	RXA02070	GR00627	1733	2830
2563	2564	RXA02080	GR00628	11017	10211
2565	2566	RXA02081	GR00628	12307	13935
2567	2568	RXA02084	GR00629	2920	2576
2569	2570	RXA02089	GR00629	8431	8901
2571	2572	RXA02090	GR00629	9764	8964
2573	2574	RXA02091	GR00629	10512	9862
2575	2576	RXA02097	GR00630	184	3555
2577	2578	RXA02102	GR00631	4479	3322
2579	2580	RXA02103	GR00631	4510	4905
2581	2582	RXA02109	GR00632	3460	2540
2583	2584	RXA02117	GR00636	1056	1529
2585	2586	RXA02123	GR00636	6558	7928
2587	2588	RXA02124	GR00636	7956	9911
2589	2590	RXA02125	GR00637	739	1539
2591	2592	RXA02129	GR00637	5906	6139
2593	2594	RXA02132	GR00638	737	1375
2595	2596	RXA02137	GR00639	4166	3369
2597	2598	RXA02141	GR00639	8457	8864
2599	2600	RXA02146	GR00639	14742	15368
2601	2602	RXA02152	GR00640	237	638
2603	2604	RXA02163	GR00640	10072	10824
2605	2606	RXA02164	GR00640	10824	12398
2607	2608	RXA02165	GR00640	12388	12999
2609	2610	RXA02166	GR00640	13048	13224
2611	2612	RXA02168	GR00641	2894	81

2613	2614	RXA02170	GR00641	4798	4025
2615	2616	RXA02172	GR00641	6919	6581
2617	2618	RXA02177	GR00641	12683	13615
2619	2620	RXA02178	GR00641	13628	14497
2621	2622	RXA02181	GR00641	17168	17845
2623	2624	RXA02183	GR00641	18663	19187
2625	2626	RXA02187	GR00641	21249	23447
2627	2628	RXA02199	GR00646	2591	3160
2629	2630	RXA02203	GR00646	7469	7092
2631	2632	RXA02206	GR00646	9927	10862
2633	2634	RXA02211	GR00648	2537	2989
2635	2636	RXA02212	GR00649	964	467
2637	2638	RXA02216	GR00651	2	307
2639	2640	RXA02217	GR00651	968	306
2641	2642	RXA02218	GR00651	1299	1565
2643	2644	RXA02219	GR00651	1578	2963
2645	2646	RXA02221	GR00651	6720	8081
2647	2648	RXA02227	GR00653	1236	1853
2649	2650	RXA02230	GR00653	4156	3620
2651	2652	RXA02231	GR00653	5111	4356
2653	2654	RXA02244	GR00654	12058	13590
2655	2656	RXA02255	GR00654	22507	23442
2657	2658	RXA02266	GR00655	653	1165
2659	2660	RXA02267	GR00655	2053	1181
2661	2662	RXA02280	GR00658	2	754
2663	2664	RXA02286	GR00660	3285	3833
2665	2666	RXA02287	GR00660	4071	4622
2667	2668	RXA02294	GR00662	5992	5618
2669	2670	RXA02295	GR00662	6842	6063
2671	2672	RXA02297	GR00662	7502	8638
2673	2674	RXA02298	GR00662	10310	8652
2675	2676	RXA02304	GR00663	1613	723
2677	2678	RXA02308	GR00664	939	511
2679	2680	RXA02324	GR00668	1548	2633
2681	2682	RXA02325	GR00668	4314	3445
2683	2684	RXA02331	GR00671	396	761
2685	2686	RXA02336	GR00672	2731	2552
2687	2688	RXA02347	GR00677	509	189
2689	2690	RXA02349	GR00678	394	5
2691	2692	RXA02352	GR00681	2	556
2693	2694	RXA02356	GR00684	761	1756
2695	2696	RXA02358	GR00685	1239	1529
2697	2698	RXA02362	GR00685	7045	10743
2699	2700	RXA02374	GR00688	1626	2246
2701	2702	RXA02390	GR00695	1500	832
2703	2704	RXA02393	GR00697	168	449
2705	2706	RXA02395	GR00698	2	733
2707	2708	RXA02396	GR00698	1309	1031
2709	2710	RXA02403	GR00700	896	1660
2711	2712	RXA02412	GR00703	2043	2522
2713	2714	RXA02417	GR00705	4755	2632
2715	2716	RXA02421	GR00705	7237	6428
2717	2718	RXA02425	GR00707	1	630
2719	2720	RXA02427	GR00707	3447	3061
2721	2722	RXA02430	GR00707	7498	7683
2723	2724	RXA02433	GR00708	2981	3580
2725	2726	RXA02437	GR00709	1661	2470

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2727	2728	RXA02443	GR00709	6818	7771
2729	2730	RXA02444	GR00709	7836	9113
2731	2732	RXA02452	GR00710	5271	5092
2733	2734	RXA02459	GR00712	4341	5075
2735	2736	RXA02461	GR00712	6252	5845
2737	2738	RXA02467	GR00714	643	419
2739	2740	RXA02472	GR00715	5435	5725
2741	2742	RXA02473	GR00715	6664	5924
2743	2744	RXA02475	GR00715	9595	8441
2745	2746	RXA02478	GR00716	1245	10
2747	2748	RXA02482	GR00718	914	105
2749	2750	RXA02483	GR00718	1813	1001
2751	2752	RXA02484	GR00718	2317	1817
2753	2754	RXA02486	GR00718	3441	4076
2755	2756	RXA02488	GR00719	1	369
2757	2758	RXA02489	GR00719	373	996
2759	2760	RXA02495	GR00720	9002	6435
2761	2762	RXA02496	GR00720	10025	9219
2763	2764	RXA02498	GR00720	11016	11819
2765	2766	RXA02500	GR00720	13460	13558
2767	2768	RXA02506	GR00720	19484	18603
2769	2770	RXA02514	GR00723	1	837
2771	2772	RXA02518	GR00723	3464	3874
2773	2774	RXA02521	GR00724	2924	4366
2775	2776	RXA02524	GR00725	2405	3094
2777	2778	RXA02525	GR00725	3113	3490
2779	2780	RXA02540	GR00726	12438	12001
2781	2782	RXA02544	GR00726	16715	18142
2783	2784	RXA02545	GR00726	18749	18192
2785	2786	RXA02546	GR00726	19927	18824
2787	2788	RXA02549	GR00728	1331	6
2789	2790	RXA02552	GR00730	924	130
2791	2792	RXA02554	GR00731	1050	427
2793	2794	RXA02569	GR00736	82	831
2795	2796	RXA02570	GR00736	837	1478
2797	2798	RXA02573	GR00739	594	151
2799	2800	RXA02575	GR00739	1907	3064
2801	2802	RXA02576	GR00740	1569	148
2803	2804	RXA02577	GR00740	2463	1579
2805	2806	RXA02584	GR00741	8925	8575
2807	2808	RXA02585	GR00741	9917	8937
2809	2810	RXA02588	GR00741	13037	12354
2811	2812	RXA02591	GR00741	15780	17609
2813	2814	RXA02598	GR00742	2576	3166
2815	2816	RXA02600	GR00742	5027	3630
2817	2818	RXA02601	GR00742	5258	7246
2819	2820	RXA02602	GR00742	7239	7742
2821	2822	RXA02604	GR00742	8800	10875
2823	2824	RXA02609	GR00742	16197	16445
2825	2826	RXA02617	GR00745	1404	1910
2827	2828	RXA02619	GR00746	204	1103
2829	2830	RXA02620	GR00746	1192	1845
2831	2832	RXA02639	GR00749	511	1344
2833	2834	RXA02647	GR00751	4155	4616
2835	2836	RXA02649	GR00752	1284	283
2837	2838	RXA02652	GR00752	2973	3551
2839	2840	RXA02655	GR00752	9313	8330

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2841	2842	RXA02662	GR00753	1461	1724
2843	2844	RXA02665	GR00753	6497	6018
2845	2846	RXA02670	GR00753	10199	10780
2847	2848	RXA02672	GR00753	12303	13400
2849	2850	RXA02678	GR00754	3858	4775
2851	2852	RXA02683	GR00754	7742	7065
2853	2854	RXA02685	GR00754	10058	9402
2855	2856	RXA02688	GR00754	12256	12924
2857	2858	RXA02689	GR00754	13405	13064
2859	2860	RXA02690	GR00754	14502	13405
2861	2862	RXA02700	GR00757	3507	4742
2863	2864	RXA02701	GR00757	4838	6145
2865	2866	RXA02712	GR00758	13067	12273
2867	2868	RXA02714	GR00758	14754	14326
2869	2870	RXA02715	GR00758	15847	15458
2871	2872	RXA02721	GR00759	1373	636
2873	2874	RXA02725	GR00760	1478	867
2875	2876	RXA02727	GR00760	6287	5376
2877	2878	RXA02735	GR00763	777	73
2879	2880	RXA02736	GR00763	1753	797
2881	2882	RXA02751	GR00764	6393	5920
2883	2884	RXA02756	GR00766	3851	2961
2885	2886	RXA02757	GR00766	4475	3930
2887	2888	RXA02765	GR00769	3552	2794
2889	2890	RXA02766	GR00770	986	594
2891	2892	RXA02774	GR00773	3	473
2893	2894	RXA02775	GR00773	744	968
2895	2896	RXA02776	GR00773	1713	1372
2897	2898	RXA02777	GR00773	4626	5732
2899	2900	RXA02778	GR00773	10095	10319
2901	2902	RXA02779	GR00773	10617	10895
2903	2904	RXA02780	GR00773	10954	11280
2905	2906	RXA02783	GR00775	845	1393
2907	2908	RXA02784	GR00775	1751	1936
2909	2910	RXA02786	GR00777	2	808
2911	2912	RXA02789	GR00777	5237	5782
2913	2914	RXA02793	GR00777	9385	8684
2915	2916	RXA02796	GR00778	1648	1100
2917	2918	RXA02798	GR00778	2842	4266
2919	2920	RXA02799	GR00780	182	454
2921	2922	RXA02815	GR00796	3	554
2923	2924	RXA02823	GR00804	275	6
2925	2926	RXA02827	GR00812	428	6
2927	2928	RXA02842	GR00841	356	15
2929	2930	RXA02845	GR00844	2	616
2931	2932	RXA02848	GR00848	113	511

TABLE 2: GENES IDENTIFIED FROM GENBANK

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-amino acids using said strains," Patent: EP 0358940-A 3 0321/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moockel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 0720/95
AB003132	murC; fisQ; fisZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the fisZ gene from coryneform bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; fisQ		Wachi, M. et al. "A murC gene from Corynebacterium bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	disR		Kimura, E. et al. "Molecular cloning of a novel gene, disR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	disR1; disR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkl	transketolase	
AB024708	glbB; glbD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aud	Replication protein; aminoglycoside adenylyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	
AF036932	aroD	3-dehydroquinate dehydratase	

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF038548	pyc	Pyruvate carboxylase	
AF038651	dcIAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehner, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamate phosphatase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," <i>Mol. Cells</i> , 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinate synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-phosphoribosylhydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF124518	aroD; aroE	3-dehydroquinate; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinate synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		
AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	fisX; glnB; glnD; srp; ampP	Involved in cell division; pH protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in <i>Corynebacterium glutamicum</i> : Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AJ132968	cat		
AJ224946	mgo	Chloramphenicol acetyl transferase L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from <i>Corynebacterium glutamicum</i> ," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of <i>Corynebacterium glutamicum</i> : The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes, A.A. et al. "Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the <i>Corynebacterium glutamicum</i> (Brevibacterium lactofermentum AJ12036) <i>odhA</i> gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
F01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E01377		Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937		Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040		Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diamionopelargonic acid aminotransferase and deshydrobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
F04041		Deshydrobiotinsynthetase	Kohama, K. et al. "Gene coding diamionopelargonic acid aminotransferase and deshydrobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307		Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376		Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377		Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484		Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108		Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112		Dihydro-dipicolinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93

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GenBank TM Accession No.	Gene Name	Gene Function	Reference
E05776		Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779		Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110		Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111		Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146		Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825		Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
F08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in corynebacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in corynebacterium," Patent: JP 1995031476-A 1 02/03/95

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138(11):167-175 (1992)
M89931	acd; brnQ; ylbw	Beta C-5 lyase; branched-chain amino acid uptake carrier; hypothetical protein ylbw	Rosol, I. et al. "The Corynebacterium glutamicum acd gene encodes a C-5 lyase with alpha, beta-elimination activity that degrades aminothyleysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "isoleucine uptake in Corynebacterium glutamicum ATCC 13032 is directed by the brnQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of Corynebacterium glutamicum: identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	trpD	Anthraniolate phosphoribosyltransferase	O'Garra, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum ATCC 21850 trpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cgIIIM; cgIIR; cglIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schaefer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergeneric conjugation with Escherichia coli," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schaefer, A. et al. "The Corynebacterium glutamicum cglIM gene encoding a 5-cytosine in an McrBC-deficient Escherichia coli strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC	L-proline: NAD(P) ⁺ 5-oxidoreductase	Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?gamma glutamyl kinase-similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
U31281	bioB	Biotin synthase	Serebriskii, I.G. "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thrR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	35S-aminoglycoside phosphotransferase		
U89648	aphA-3	<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the <i>lysA</i> gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> fda gene: structural comparison of <i>C. glutamicum</i> fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i>
X53903	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonmassie, S. et al. "Nucleic sequence of the <i>dapA</i> gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
X54223		attB-related site	Ciancio, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum, and the attP site of lambdacorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the Corynebacterium glutamicum lysA gene," <i>Mol. Microbiol.</i> , 4(11):1819-1830 (1990)
X55994	trpL, trpE	Putative leader peptide; anthranilate synthase component I	Heery, D.M. et al. "Nucleotide sequence of the Corynebacterium glutamicum trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the Corynebacterium glutamicum threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Ciancio, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum, and the attP site of lambdacorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in Corynebacterium glutamicum," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)
X59403	gap/pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmans, B.J. "Identification, sequence analysis, and expression of a Corynebacterium glutamicum gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bornman, E.R. et al. "Molecular analysis of the Corynebacterium glutamicum gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the Corynebacterium glutamicum lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)

002293" 00229360

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X66078	cop1	Psi protein	Iotiff, G. et al. "Cloning and nucleotide sequence of the <i>cop1</i> gene encoding PSI, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i> : The deduced N-terminal region of PSI is similar to the Mycobacterium antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the <i>Corynebacterium glutamicum</i> <i>gltA</i> gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	Peyret, J.L. et al. "Characterization of the <i>espB</i> gene encoding PS2, an ordered surface-layer protein in <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)
X69103	esp2	Surface layer protein PS2	
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a <i>Corynebacterium glutamicum</i> IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)
X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Leucine synthesis in <i>Corynebacterium glutamicum</i> : enzyme activities, structure of <i>leuA</i> , and effect of <i>leuA</i> inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the <i>Corynebacterium glutamicum</i> <i>icd</i> gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X75083, X70584	mirA	5-methyltryptophan resistance	Fitzpatrick, R. et al. "Construction and characterization of <i>recA</i> mutant strains of <i>Corynebacterium glutamicum</i> and <i>Brevibacterium lactofermentum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75085	recA		
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from <i>Corynebacterium glutamicum</i> and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
X06580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahn, H. et al. "D-pantoic acid synthesis in <i>Corynebacterium glutamicum</i> and use of panBC and genes encoding L-valine synthetase for D-pantoic acid overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)
X06962 X09289		Insertion sequence IS1207 and transposase Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer <i>Brevibacterium lactofermentum</i> (<i>Corynebacterium glutamicum</i> ATCC-13869)," <i>Gene</i> , 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00151	dah	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the <i>Corynebacterium glutamicum</i> hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y08904	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from <i>Brevibacterium lactofermentum</i> ," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of <i>Corynebacterium glutamicum</i> and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from <i>Corynebacterium glutamicum</i> : characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from <i>Corynebacterium glutamicum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of coryneophage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)

TABLE 3: *Corynebacterium* and *Brevibacterium* Strains Which May be Used in the Practice of the Invention

Genus	Species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
<i>Brevibacterium</i>	<i>ammonia</i> genes	21054							
<i>Brevibacterium</i>	<i>ammonia</i> genes	19350							
<i>Brevibacterium</i>	<i>ammonia</i> genes	19351							
<i>Brevibacterium</i>	<i>ammonia</i> genes	19352							
<i>Brevibacterium</i>	<i>ammonia</i> genes	19353							
<i>Brevibacterium</i>	<i>ammonia</i> genes	19354							
<i>Brevibacterium</i>	<i>ammonia</i> genes	19355							
<i>Brevibacterium</i>	<i>ammonia</i> genes	19356							
<i>Brevibacterium</i>	<i>ammonia</i> genes	21055							
<i>Brevibacterium</i>	<i>ammonia</i> genes	21077							
<i>Brevibacterium</i>	<i>ammonia</i> genes	21553							
<i>Brevibacterium</i>	<i>ammonia</i> genes	21580							
<i>Brevibacterium</i>	<i>ammonia</i> genes	39101							
<i>Brevibacterium</i>	<i>butanicum</i>	21196							
<i>Brevibacterium</i>	<i>divaricatum</i>	21792	P928						
<i>Brevibacterium</i>	<i>flavum</i>	21474							
<i>Brevibacterium</i>	<i>flavum</i>	21129							
<i>Brevibacterium</i>	<i>flavum</i>	21518							
<i>Brevibacterium</i>	<i>flavum</i>			B11474					
<i>Brevibacterium</i>	<i>flavum</i>			B11472					
<i>Brevibacterium</i>	<i>flavum</i>	21127							
<i>Brevibacterium</i>	<i>flavum</i>	21128							
<i>Brevibacterium</i>	<i>flavum</i>	21427							
<i>Brevibacterium</i>	<i>flavum</i>	21475							
<i>Brevibacterium</i>	<i>flavum</i>	21517							
<i>Brevibacterium</i>	<i>flavum</i>	21528							
<i>Brevibacterium</i>	<i>flavum</i>	21529							

Brevibacterium	flavum				B11477				
Brevibacterium	flavum				B11478				
Brevibacterium	flavum	21127							
Brevibacterium	healii	15527			B11474				
Brevibacterium	ketoglutaricum	21004							
Brevibacterium	ketoglutaricum	21089							
Brevibacterium	ketoreductum	21914							
Brevibacterium	lactofermentum					70			
Brevibacterium	lactofermentum					74			
Brevibacterium	lactofermentum					77			
Brevibacterium	lactofermentum	21798							
Brevibacterium	lactofermentum	21799							
Brevibacterium	lactofermentum	21800							
Brevibacterium	lactofermentum	21801							
Brevibacterium	lactofermentum				B11470				
Brevibacterium	lactofermentum				B11471				
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum					11160			
Brevibacterium	spec.						717.73		
Brevibacterium	spec.						717.73		
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							

Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							

Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum		B8183						
Corynebacterium	glutamicum		B8182						
Corynebacterium	glutamicum		B12416						
Corynebacterium	glutamicum		B12417						
Corynebacterium	glutamicum		B12418						
Corynebacterium	glutamicum		B11476						
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419					11594		
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							

TABLE 4: ALIGNMENT RESULTS

[illegible]

TABLE 4: ALIGNMENT RESULTS

GB_HTTG2-HSJ74H919	253387	AL117390	Homo sapiens chromosome 20 clone RP4_74H919 map q11.1-13.33, *** SEQUENCING IN PROGRESS ***; in unorderd pieces.	Homo sapiens	37,132	03-DEC-1999
GB_HTTG3-AC010137	155817	AC010137	Homo sapiens clone RH016001, *** SEQUENCING IN PROGRESS ***; 4 unorderd pieces	Homo sapiens	40,052	17-OCT-1999
GB_HTTG3-AB92012	342	AB92012	w41460 t1 NCI, GNP, Penta1, *** SEQUENCING IN PROGRESS ***; 3 similar to SWALC2, HUMAN P01717 IG Alpha-2 CHAIN C, HUMAN sequence	Homo sapiens	40,486	20-Aug-99
GB_GS513-AC0454792	450	A0454792	HS_51952_B2_HJ04_SBE1 RPCI-11 Human Male BAC Library Homo sapiens genomic clone P146771 Col1a6 Row-P genomic survey sequence	Homo sapiens	40,991	21-Apr-99
GB_GS513-A0454792	450	A0454792	HS_51952_B2_HJ04_SBE1 RPCI-11 Human Male BAC Library Homo sapiens genomic clone P146771 Col1a6 Row-P genomic survey sequence	Homo sapiens	40,278	21-Apr-99
GB_GS55-A0773786	459	A0773786	HS_2222_A1_E07_MMT_C01 Approved Human Genomic Sperm Library D Homo sapiens genomic clone P1467-2222 Col13 Row11 genomic survey sequence	Homo sapiens	40,087	29-Jul-99
GB_GS55-A0773786	459	A0773786	HS_2222_A1_E07_MMT_C01 Approved Human Genomic Sperm Library D Homo sapiens genomic clone P1467-2222 Col13 Row11 genomic survey sequence	Homo sapiens	40,087	29-Jul-99
GB_INT1-CEF5849	873	Z74473	Ceenorhabditis elegans cosmid F58H9, complete sequence	Ceenorhabditis elegans	35,301	23-Nov-98
GB_INT1-CEF5849	873	Z74473	Ceenorhabditis elegans cosmid F58H9, complete sequence	Ceenorhabditis elegans	38,941	23-Nov-98
GB_HTTG6-AC011647	141830	AC011647	Homo sapiens clone RP1-1-15D18, *** SEQUENCING IN PROGRESS ***; 29 unorderd pieces	Homo sapiens	39,839	04-DEC-1999
GB_HTTG6-AC011647	141830	AC011647	HS_5441_A2_C02_SBE1 RPCI-11 Human Male BAC Library Homo sapiens genomic clone P1467-1071 Col14 Row14 genomic survey sequence	Homo sapiens	37,337	04-DEC-1999
GB_GS556-A0235754	483	A0235754	HS_5441_A2_C02_SBE1 RPCI-11 Human Male BAC Library Homo sapiens genomic clone P1467-1071 Col14 Row14 genomic survey sequence	Homo sapiens	34,444	27-Aug-99
GB_PAT1-932939	30001	I32939	Sequence 1 from patient US598365	Unknown	42,049	6-Feb-97
GB_PAT1-AR031772	30001	AR031772	Sequence 1 from patient US568410	Unknown	42,049	29-Sep-99
GB_PAT1-E16763	2517	E16763	gDNA encoding aspartate transferase (AAT)	Corynebacterium glutamicum	88,765	28-Jul-99
GB_EST32-A050556	813	A050556	AU050556 Paracitrichus oiveaceus library (Aoki T) Paracitrichus oiveaceus cDNA clone W47-19, mRNA sequence.	Paracitrichus oiveaceus	35,638	8-Jun-99
GB_EST32-A0505215	733	A0505215	AU050215 Paracitrichus oiveaceus library (Aoki T) Paracitrichus oiveaceus cDNA clone W61-12, mRNA sequence	Paracitrichus oiveaceus	35,638	8-Jun-99
GB_HTTG3-AC008289	115120	AC008289	Drosophila melanogaster chromosome 2 clone BACR404E6 (01055) RPCI-98 04 E5 map 57B-57B strain Y, cn bw sp, *** SEQUENCING IN PROGRESS ***; 100 unorderd pieces	Drosophila melanogaster	30,397	17-Aug-99
GB_INT2-AC004443	85862	AC004443	Drosophila melanogaster, chromosome 2R, region 57B1-57B6, P1 clone D538359, complete sequence.	Drosophila melanogaster	35,501	01-DEC-1998
GB_HTTG3-AC008289	115120	AC008289	Drosophila melanogaster chromosome 2 clone BACR404E6 (01055) RPCI-98 04 E5 map 57B-57B strain Y, cn bw sp, *** SEQUENCING IN PROGRESS ***; 100 unorderd pieces	Drosophila melanogaster	30,397	17-Aug-99
GB_PL12-ATAC095021	87947	AC009501	Arabidopsis thaliana chromosome 11BAC T27K22 genomic sequencs, complete sequencia	Arabidopsis thaliana	39,099	12-MAR-1999
GB_HTTG3-AC010148	271437	AC010148	Homo sapiens clone RH035513, WORKING DRAFT SEQUENCE, 1 unorderd pieces	Homo sapiens	34,237	12-Nov-99
GB_GS53-B85079	307	B85079	RPCI11-2609 TP RPCI-11 Homo sapiens genomic clone RPCI-11-29009, genomic survey sequence.	Homo sapiens	39,560	9-Apr-99
GB_PRM4-AC007157	123037	AC007157	Homo sapiens, clone IRPK_73_A_1, complete sequencia	Homo sapiens	37,661	27-Apr-98
GB_HTTG1-CE143C5	149571	AL021449	Ceenorhabditis elegans chromosome IV clone Y43C5, *** SEQUENCING IN PROGRESS ***; in unorderd pieces	Ceenorhabditis elegans	25,242	23-Jun-98
GB_HTTG1-CEY4AC5	149571	AL021449	Ceenorhabditis elegans chromosome IV clone Y43C5, *** SEQUENCING IN PROGRESS ***; in unorderd pieces	Ceenorhabditis elegans	38,258	23-Jun-98
GB_INT1-CTA42763	1097	A002973	Chironomus tentans mRNA for P23 protein (23 kDa)	Chironomus tentans	38,176	26-Jan-98
GB_INT1-CTA62763	732	A003820	Chironomus tentans mRNA for mRNP protein, Irp23	Chironomus tentans	32,022	02-DEC-1998
GB_EST11-AM050674	540	A465074	30788 Lambda-PRL2 Arabidopsis thaliana cDNA clone 271G77, mRNA sequence	Arabidopsis thaliana	36,965	31-OCT-1997
GB_EST38-AM039986	594	AM039986	EST228247 tomato mixed elector, BT1 Lycopersicon esculentum cDNA clone cLET19F23, mRNA sequence.	Lycopersicon esculentum	38,078	18-OCT-1999

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TABLE 4: ALIGNMENT RESULTS

GB_EST33.A178332	378	A178332	EST250211 tomato susceptible, Cornell Lycopersicon esculentum cDNA clone cLESSA13, mRNA sequence.	Lycopersicon esculentum	38,298	29-Jun-99
GB_EST38.AW039888	564	AW039888	EST242479 tomato mixed elicitor, BT1 Lycopersicon esculentum cDNA clone cLET19P23, mRNA sequence	Lycopersicon esculentum	38,078	19-OCT-1999
ra000802	687	GB_PR1.HSS171	Human sapiens chromosome 21q22.3, PAC clones 314N7, 2251S, BAC clone 7B7, complete sequence bases 1, 333303	Homo sapiens	38,111	10-Nov-98
		GB_PR1.HSS171	Human sapiens chromosome 21q22.3, PAC clones 314N7, 2251S, BAC clone 7B7, complete sequence bases 1, 333303	Homo sapiens	35,432	10-Nov-98
ra000903	423	GB_PR3.ACO04000	Human PAC clone D404F18 from Xap23, complete sequence	Homo sapiens	38,750	15-Jan-98
		AL109769	Human sapiens chromosome 14 clone R-501E21, *** SEQUENCING IN PROGRESS *** , in ordered pieces	Homo sapiens	33,806	15-OCT-1999
		GB_LFTG1.CNS0180Y	Human sapiens chromosome 14 clone R-501E21, *** SEQUENCING IN PROGRESS *** , in ordered pieces	Homo sapiens	33,806	15-OCT-1999
ra000807	651	GB_PR3.HS16223	Human DNA sequence from clone 516C23 on chromosome 6q12. Contains CA repeat (B6S402) and GSS3, complete sequence	Homo sapiens	36,562	23-Nov-99
		GB_BA1.PSEBPHABC	P Pseudocatalgaines dioxygenase (tpbABC) gene cluster, complete cds	Pseudomonas	39,564	28-Apr-93
		GB_BA1.PSEBPHA	Pseudomonas sp. L5400 (bphE) dioxygenase (bphA), bphE dioxygenase (bphE), bphE (bphE) dioxygenase (bphE) and bphE dioxygenase (bphE), complete cds, and bphE dioxygenase (bphE), partial cds	Burkholderia	39,564	18-Jun-97
ra000903	2346	GB_PAT.E04215	Benzene dioxygenase gene.	Pseudomonas aeruginosa	46,814	29-Sep-97
		GB_HTG2.ACO07381	Human sapiens clone NH0144P23, *** SEQUENCING IN PROGRESS *** , 1 unordered pieces	Homo sapiens	37,779	23-Apr-99
		GB_PR4.ACO06043	Human sapiens BAC clone NH0538D15 from 7q11.23-q21.1, complete sequence	Homo sapiens	37,060	20-Feb-99
		AC007381	Human sapiens clone NH0144P23, *** SEQUENCING IN PROGRESS *** , 1 unordered pieces	Homo sapiens	37,779	23-Apr-99
ra000906	420	GB_EST15.AA533064	np0006.81 NCLCGAP_P19 Homo sapiens cDNA clone IMAGE 98875, mRNA sequence	Homo sapiens	39,024	21-Aug-97
		GB_INT1.CELF01G12	Ctenorhabdus elegans cosmid F01G12.	Ctenorhabdus elegans	38,060	5-Apr-96
		GB_PR3.ACO04511	Human sapiens chromosome 5, P1 clone 792C12 (LBNL H22), complete sequence	Homo sapiens	39,163	31-MAR-1998
ra000907	1299	GB_OM.CF060900	Centa families TTX-resistant sodium channel mRNA, complete cds	Centa families	39,628	8-Jan-98
		GB_GS15.AQ064394	HS_5480_BT_102_SREI RPC1-11 Human Male BAC Library Homo sapiens genomic clone	Homo sapiens	39,668	23-Jun-99
		GB_BA2.RSAF000233	Plat-1050 Col-5 Row-D, genomic survey sequence	Rhodobacter sphaeroides	37,500	6-Jun-97
ra00101			Rhodobacter sphaeroides nitric oxide reductase operon, norC, norD, norE, norF and norH genes, complete cds	Rhodobacter sphaeroides	37,500	
ra00108	643	GB_PR4.ACO07115	Human sapiens chromosome 12 clone 91705, complete sequence	Homo sapiens	35,165	17-Aug-99
		AC000480	Human sapiens chromosome 17 clone 7015421, complete sequence	Homo sapiens	39,460	26-Jun-98
		AC008613	Human sapiens chromosome 17 clone 54515 map p11, *** SEQUENCING IN PROGRESS *** , in unordered pieces	Homo sapiens	39,274	11-Nov-98
ra001010	672	GB_PL1.MA1GENB	A. Italiana mitochondrial genome, part B	Mitochondrion Arabidopsis thaliana	36,391	13-Nov-98
		GB_PL2.ACO10718	Arabidopsis thaliana chromosome I BAC F280.16 genomic sequence, complete sequence	Arabidopsis thaliana	36,622	30-OCT-1999
		AC007729	Arabidopsis thaliana chromosome II BAC T18C8 genomic sequence, complete sequence	Arabidopsis thaliana	35,053	5-Jun-99
ra001014	612	GB_OM.BTMCSD1	B. laurus (cos1E3) microsatellite DNA (382bp)	Bos taurus	37,117	10-Aug-95
		Z27071	B. laurus (cos1E3) microsatellite DNA (382bp)	Bos taurus	36,486	10-Aug-95
ra001017	714	GB_PL2.AFO08249	Arabidopsis thaliana kreen-like heavy chain (KATD), mRNA, complete cds	Arabidopsis thaliana	37,646	14-Apr-99
		AF007270	Arabidopsis thaliana BAC G102P16.	Arabidopsis thaliana	37,710	12-Jun-97
		AF00249	Arabidopsis thaliana kreen-like heavy chain (KATD), mRNA, complete cds	Arabidopsis thaliana	36,508	14-Apr-99
ra001018	378	GB_HTG2.ACO08043	Dioscophila melanogaster chromosome 3 clone B10K0404 (D750) RPO-96 05 A 8 map 94A-94A strain Y, on low copy, *** SEQUENCING IN PROGRESS *** , 86 unordered pieces.	Dioscophila melanogaster	33,780	2-Aug-99

TABLE 4: ALIGNMENT RESULTS

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TABLE 4: ALIGNMENT RESULTS

ra002020	3561	GB_BA2.NSU46844	16951	U46844	Mycobacterium smegmatis catalase-peroxidase (catC), putative arabinosyl transferase (embC, embA, embB), genes complete cds and putative propionyl-coA carboxylase beta chain (pcdB) genes, partial cds	Mycobacterium smegmatis	53,937	12-MAY-1997
		GB_BA2.MAU66560	7853	U66560	Mycobacterium avium EmuR (emuR), EmB (embA) and EmB (embB) genes, complete cds	Mycobacterium avium	52,241	8-Nov-96
		GB_BA1.MTY13D12	37085	Z83043	Mycobacterium tuberculosis H37Rv complete genome, segment 156/162	Mycobacterium tuberculosis	52,812	17-Jun-98
ra002027	441	GB_PR3.HTCRCHRH9	126293	AF029308	Mycobacterium tuberculosis 9 duplication of the T cell receptor beta locus and trypanogen gene families.	Homo sapiens	39,286	13-Apr-98
		GB_PR3.HTCRCHRH9	126293	AF029308	Mycobacterium tuberculosis 9 duplication of the T cell receptor beta locus and trypanogen gene families.	Homo sapiens	37,116	13-Apr-98
ra002011	786	GB_PR2.HSU81831	38674	U81831	Human osmid LL2NCO1-67C6. ETIV gene, intron 1A, partial sequence	Homo sapiens	35,509	3-Jan-97
		GB_RO.MUSKR00552	28845	M28845	Mus musculus zinc finger protein (Knox-24) gene, exon 2	Mus musculus	40,566	21-MAY-1996
		GB_MTG.AG0307440	120642	AC007440	Drosophila melanogaster chromosome 2 gene BACR037.09 (D893) RPCI-98 37.19 map. 40A-108 stain Y, on tw sp, *** SEQUENCING IN PROGRESS ***; 103 unordered pieces.	Drosophila melanogaster	36,753	2-Aug-99
ra002018								
ra002020	827	GB_BA1.ASU04436	4668	U04436	Anabaena sp. PCC 7120 putative polyketide synthase gene, complete cds	Anabaena sp	33,766	21-DEC-1993
		GB_RO.AFO8199	3490	AF08199	Mus musculus D-dopachrome tautomerase gene, complete cds	Mus musculus	38,633	26-Aug-98
		GB_RO.AFO8199	3490	AF08199	Mus musculus D-dopachrome tautomerase gene, complete cds	Mus musculus	34,776	26-Aug-98
ra002022	1269	GB_PL1.AB011477	78181	AB011477	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone. IMH7, complete sequence	Arabidopsis thaliana	38,768	20-Nov-99
		GB_EST17.AA615900	427	AA615900	v09105 r1 Bartshead mouse irradiated colon MPL R87 Mus musculus cDNA clone IMAGE 1066449 5' similar to SW MUC12L RAT P98099 INTESINAL MUCIN-LIKE PROTEIN, mRNA sequence	Mus musculus	39,782	07-OCT-1997
ra002030	843	GB_EST38.AW039188	498	AW039188	EST28123 tomato mixed elicitor. BTL Lycopersicon esculentum cDNA clone cLETDF17, mRNA sequence	Lycopersicon esculentum	41,286	18-OCT-1999
		GB_PR3.AC005255	94343	AC005255	Homo sapiens chromosome 19, CIT-HSP-14668, complete sequence	Homo sapiens	35,990	6-Jul-98
		GB_PR3.AC005255	94343	AC005255	Homo sapiens chromosome 19, CIT-HSP-14668, complete sequence	Homo sapiens	38,775	6-Jul-98
ra002032	633	GB_HTG2.AC007118	20000	AC007118	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***; 45 unordered pieces	Homo sapiens	38,772	19-MAR-1999
		GB_HTG2.AC007118	20000	AC007118	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***; 45 unordered pieces	Homo sapiens	36,772	19-MAR-1999
		GB_GST1.CNS0404WZ	978	AL05537	Drosophila melanogaster genome survey sequence TE19 end of BAC * BAC11002 of RPCL98	Drosophila melanogaster	34,318	3-Jun-99
ra002033	517	GB_BA1.AB002036	7443	AB002036	Streptomyces coelicolor A15 genomic DNA, complete cds	Streptomyces coelicolor	38,690	5-Feb-99
		GB_PR4.AC006999	112878	AC006999	Homo sapiens genes ANR, Anfa, and Anfb genes and 4 ORFs, complete cds	Homo sapiens	40,244	17-Jul-99
		GB_HTG2.AC007042	132400	AC007042	Homo sapiens genes NH0462A19 complete sequence	Homo sapiens	40,244	06-MAR-1999
ra002034	863	GB_PL1.E13059	3480	E13059	gDNA encoding cyclochrome b5	unidentified	40,091	24-Jun-98
		GB_PL1.AB022444	2104	AB022444	Moniella alpina gene for cyclochrome b5, complete cds	Moniella alpina	42,314	14-Jul-98
		GB_GSS9.AB112619	443	AQ112619	CIT-HSP-2371D11 TR CIT-HSP Homo sapiens genomic clone 2371D11, genomic survey sequence.	Homo sapiens	39,623	29-Aug-98
ra002036	849	GB_BA1.GGPR0MF-34	60	X90361	C glutamicum DNA for promoter fragment F34	Corynebacterium glutamicum	98,333	4-Nov-96
		GB_INT.CEF5624	38062	Z81552	Caeonorbis elegans cosmid F56Q4, complete sequence.	Caeonorbis elegans	36,190	08-OCT-1999
		GB_EST16.C51159	370	C51159	C51159 Yuj Kohara unpublished cDNA Stain N2 hermaphrodite embryo Caeonorbis elegans cDNA clone YK49103.5, mRNA sequence	Caeonorbis elegans	41,098	18-OCT-1999
ra002037	501	GB_GSS9.AQ148005	511	AQ148005	HS_3137_B92_A17 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone P1467-3137 Col-22 Row-B, genomic survey sequence	Homo sapiens	37,969	08-OCT-1998
		GB_GSS11.AQ274889	822	AQ274889	RPCI-5-1111N377 RPCI-5 Homo sapiens genomic clone RPCI-5-1111N377, genomic survey sequence	Homo sapiens	44,628	10-Nov-98

TABLE 4: ALIGNMENT RESULTS

23-Nov-99	44,843	Homo sapiens	Human DNA sequence from clone 142F18 on chromosome Xp28.3-2.7. Contains part of a gene similar to melanoma-associated antigen, EST, GSS and an inverted, complete sequence	141672	AL031073	101320	AC007177	Drosophila melanogaster, chromosome 2R, region 56C1-56C5, P1 clones D506821 and D502186, complete sequence	23-MAR-1999	36,721	Drosophila melanogaster
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TABLE 4: ALIGNMENT RESULTS

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TABLE 4: ALIGNMENT RESULTS

na00457	1203	GB_GSS8/AQ000125	38	AQ000125	CIT-HSP-2282P3 TF CIT-HSP Homo sapiens genomic clone 2282P3, genomic survey sequence	25-Nov-98
na00463	945	GB_BA1/SC69	37730	AL049841	Staphylococcus coelicolor strain E9	19-MAY-1999
na00463	945	GB_BA1/SC69	37730	AF1052652	Corynebacterium glutamicum	19-MAR-1998
na00463	945	GB_GSS12/AQ000770	358	AQ007770	HS_5069_B1_F03_7TA RPEC-11 Human Male BAC Library Homo sapiens genomic clone	17-MAR-1999
na00468	942	GB_GSS15/AQ056209	358	AQ056209	HS_5492_A2_H10_SRIPE RPEC11 Human Male BAC Library Homo sapiens genomic clone	6-Jun-99
na00468	942	GB_EST132/AF163196	341	AF163196	W65904 X1 NCI_GCAP_Kc1212 Homo sapiens cDNA clone IMAGE 2394231 3', mRNA sequence	24-Jun-99
na00472	942	GB_EST17/AQ052964	329	AQ052964	ra52c02 s1 NCI_GCAP_P122 Homo sapiens cDNA clone IMAGE 1188218 3', mRNA sequence	11-Jun-97
na00472	942	GB_EST20/AQ084303	411	AQ084303	ra54d02 s1 NCI_GCAP_G4 Homo sapiens cDNA clone IMAGE 1470435 3', mRNA sequence	13-NOV-1998
na00469	1299	GB_PRA/AQ005988	173126	AQ005988	Homo sapiens chromosome 17, clone hRPK_299_G_24, complete sequence	15-Jan-99
na00473	912	GB_HTG3/AQ009116	186232	AC009116	Homo sapiens chromosome 16, clone hRPK_299_G_24, complete sequence	35-Jul-99
na00472	942	GB_HTG3/AQ007882	214882	AC007882	Homo sapiens chromosome 17, clone RPEC-11_477D3_*** SEQUENCING IN PROGRESS ***	8-Sep-99
na00473	912	GB_PRC/HAC002038	161973	AC002038	Homo sapiens chromosome 19, clone CIT-HSPC_246B18_*** SEQUENCING IN PROGRESS ***	8-Sep-99
na00474	1701	GB_GSS1/AQ001145	144370	AC001145	Homo sapiens chromosome 19, clone CIT-HSPC_246B18_*** SEQUENCING IN PROGRESS ***	07-OCT-1999
na00474	1701	GB_GSS1/AQ001145	144370	AC001145	Homo sapiens chromosome 19, clone CIT-HSPC_246B18_*** SEQUENCING IN PROGRESS ***	07-OCT-1999
na00474	1701	GB_GSS1/AQ0023838	543	AQ023838	Mus musculus DNA, 5 flanking region of interleukin 12 receptor beta 1	02-OCT-1999
na00475	783	GB_P12/GMAKSHD42	10355	AF049708	HS_2218_A1_H03_MIR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone P12-2218 Col-5 Row-0, genomic survey sequence	20-Sep-98
na00476	984	GB_GSS12/AQ007769	554	AQ007769	HS_2218_A1_H03_MIR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone P12-2218 Col-5 Row-0, genomic survey sequence	20-Sep-98
na00476	984	GB_GSS12/AQ007769	554	AQ007769	HS_2218_A1_H03_MIR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone P12-2218 Col-5 Row-0, genomic survey sequence	20-Sep-98
na00481	768	GB_PRA/AC005013	185910	AC005013	Gycomax max aspartyltransferase-homomeric dehydrogenase (AK-HSDH) gene, partial cds	7-Jul-99
na00481	768	GB_HTG1/FNAL4P4	224448	AA035477	W65904 X1 NCI_GCAP_Kc1212 Homo sapiens cDNA clone IMAGE 760793 3', mRNA sequence	23-Apr-97
na00481	768	GB_GSS12/AQ007769	554	AQ007769	HS_2218_A1_H03_MIR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone P12-2218 Col-5 Row-0, genomic survey sequence	23-Apr-97
na00481	768	GB_GSS12/AQ007769	554	AQ007769	HS_2218_A1_H03_MIR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone P12-2218 Col-5 Row-0, genomic survey sequence	23-Apr-97
na00481	768	GB_GSS12/AQ007769	554	AQ007769	HS_2218_A1_H03_MIR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone P12-2218 Col-5 Row-0, genomic survey sequence	23-Apr-97
na00481	768	GB_GSS12/AQ007769	554	AQ007769	HS_2218_A1_H03_MIR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone P12-2218 Col-5 Row-0, genomic survey sequence	23-Apr-97
na00481	768	GB_GSS12/AQ007769	554	AQ007769	HS_2218_A1_H03_MIR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone P12-2218 Col-5 Row-0, genomic survey sequence	23-Apr-97
na00481	768	GB_GSS12/AQ007769	554	AQ007769	HS_2218_A1_H03_MIR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone P12-2218 Col-5 Row-0, genomic survey sequence	23-Apr-97
na00481	768	GB_GSS12/AQ007769	554	AQ007769	HS_2218_A1_H03_MIR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone P12-2218 Col-5 Row-0, genomic survey sequence	23-Apr-97
na00481	768	GB_GSS12/AQ007769	554	AQ007769	HS_2218_A1_H03_MIR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone P12-2218 Col-5 Row-0, genomic survey sequence	23-Apr-97
na00481	768	GB_GSS12/AQ007769	554	AQ007769	HS_2218_A1_H03_MIR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone P12-2218 Col-5 Row-0, genomic survey sequence	23-Apr-97
na00481	768	GB_GSS12/AQ007769	554	AQ007769	HS_2218_A1_H03_MIR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone P12-2218 Col-5 Row-0, genomic survey sequence	23-Apr-97
na00481	768	GB_GSS12/AQ007769	554	AQ007769	HS_2218_A1_H03_MIR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone P12-2218 Col-5 Row-0, genomic survey sequence	23-Apr-97
na00481	768	GB_GSS12/AQ007769	554	AQ007769	HS_2218_A1_H03_MIR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone P12-2218 Col-5 Row-0, genomic survey sequence	23-Apr-97
na00481	768	GB_GSS12/AQ007769	554	AQ007769	HS_2218_A1_H03_MIR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone P12-2218 Col-5 Row-0, genomic survey sequence	23-Apr-97
na00481	768	GB_GSS12/AQ007769	554	AQ007769	HS_2218_A1_H03_MIR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone P12-2218 Col-5 Row-0, genomic survey sequence	23-Apr-97
na00481	768	GB_GSS12/AQ007769	554	AQ007769	HS_2218_A1_H03_MIR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone P12-2218 Col-5 Row-0, genomic survey sequence	23-Apr-97
na00481	768	GB_G				

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TABLE 4: ALIGNMENT RESULTS

na000515	825	GB_BA1 CGICD	3595	X71489	C glutamicum tcd gene for monomeric isocitrate dehydrogenase.	Corynebacterium glutamicum	100,000	17-Feb-95
		GB_BA1 CGICD	3595	X71489	C glutamicum tcd gene for monomeric isocitrate dehydrogenase	Corynebacterium glutamicum	38,150	17-Feb-95
		GB_GSS13 AQ41896	509	AQ41896	HS_5184_B1_C03_SP9E RPC1-11 Human Male BAC Library Homo sapiens genomic clone	Homo sapiens	38,638	21-Apr-99
na000519	2337	GB_BA1 CGICD	3595	X71489	C glutamicum tcd gene for monomeric isocitrate dehydrogenase	Corynebacterium glutamicum	100,000	17-Feb-95
		GB_BA2 AF127018	2560	AF127018	Streptomyces coelicolor isocitrate dehydrogenase (idh) gene, rth-B allele, complete cds	Streptomyces coelicolor	66,667	1-Jun-99
		GB_BA1 AVICD	3550	D73443	Acetobacter vinelandii tcd gene for isocitrate dehydrogenase, complete cds	Acetobacter vinelandii	63,652	4-Feb-99
na000527	1887	GB_PAT 92049	2248	I92049	Sequence 19 from patent US 57,262,99	Unknown	39,250	01-DEC-1988
		GB_PAT 92053	2213	I92053	Sequence 20 from patent US 57,262,99	Unknown	70,635	01-DEC-1988
		GB_BA1 MTCY98	31225	Z33860	Mycobacterium tuberculosis H37Rv complete genome, segment 103/162	Mycobacterium tuberculosis	37,141	17-Jun-96
na000528	1212	GB_BA1 MSGY219	38721	AD000013	Mycobacterium tuberculosis sequence from clone y219	Mycobacterium tuberculosis	68,672	10-DEC-1996
		GB_BA1 MTCY21D4	20760	Z80775	Mycobacterium tuberculosis H37Rv complete genome, segment 3/262	Mycobacterium tuberculosis	39,782	24-Jun-99
		GB_BA1 SCH24	41625	AL048298	Streptomyces coelicolor cosmid H24	Streptomyces coelicolor	40,411	11-MAY-1998
na000529	666	GB_PR2 HSAC000109	41122	AC000109	Human Cosmid g07714222 from Tg3.1, complete sequence	Homo sapiens	37,462	11-Sep-97
		GB_PR2 HSAC000110	45008	AC000110	Human Cosmid g07714223, complete sequence	Homo sapiens	37,462	30-Jun-97
		GB_PR2 HSAC000109	41122	AC000109	Human DNA sequence from Tg3.1, complete sequence	Homo sapiens	39,724	11-Sep-97
na000530	1404	GB_PR3 HS435C23	151768	Z02844	Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs	Homo sapiens	36,482	23-Nov-99
		GB_PR3 HS435C23	151768	Z02844	Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs	Homo sapiens	37,018	23-Nov-99
		GB_PL1 YSCADE3	4883	M12678	Saccharomyces cerevisiae C-1-leishydrofolate synthase (ADE3) gene, complete cds.	Saccharomyces cerevisiae	37,034	11-MAY-1995
na000535	840	GB_BA1 CGLEUA	3492	X70959	C glutamicum gene leuA for isopropylmalate synthase	Corynebacterium glutamicum	100,000	10-Feb-99
		GB_BA1 CORASKO	2897	L16848	Corynebacterium flavum aspartokinase (ask), and aspartate-semialdehyde dehydrogenase (asd) genes, complete cds	Corynebacterium flavescens	43,750	11-Jun-93
		GB_GSS10 AQ193141	515	AQ103141	HS_3060_B1_F11_MF-CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3060 Cor-21 Row-L, genomic survey sequence	Homo sapiens	44,773	4-Nov-98
na000540	366	GB_PAT 92052	2115	I92052	Drasophila melanogaster chromosome 2, gene BACR11H12 (D332) RPC1.08 11 H 16 map 52A-52A	Unknown	74,765	01-DEC-1988
		GB_HTTG2 AC008095	126322	AC008095	Sequence 19 from patient US 57,262,99	Unknown	41,889	2-Aug-99
		GB_HTTG2 AC008095	126322	AC008095	Sequence 19 from patient US 57,262,99	Unknown	41,889	2-Aug-99
na000547	1521	GB_BA1 MSGY219	38721	AD000013	Mycobacterium tuberculosis sequence from clone y219	Mycobacterium tuberculosis	36,910	10-DEC-1996
		GB_BA1 MTCY21D4	20760	Z80775	Mycobacterium tuberculosis H37Rv complete genome, segment 3/262	Mycobacterium tuberculosis	51,125	24-Jun-99
		GB_EST27 A15174	292	A1415174	m05002 x1 Soares mouse p3WMF19.5 Mus musculus cDNA clone IMAGE 338018 3' mRNA sequence	Mus musculus	39,384	9-Feb-99
na000549	1797	GB_PL12 ATAC007135	27313	AC007135	Arabidopsis thaliana chromosome II BAC F6C22 genomic sequence, complete sequence	Arabidopsis thaliana	35,364	26-MAY-1999
		GB_PL2 ATAC006921	76042	AC006921	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence	Arabidopsis thaliana	36,581	23-MAR-1999
		GB_PL2 ATAC007135	27313	AC007135	Arabidopsis thaliana chromosome II BAC F6C22 genomic sequence, complete sequence	Arabidopsis thaliana	35,627	25-MAY-1999
na000550								
na000552	1059	GB_BA1 D00742	19201	D90742	Escherichia coli genomic DNA (23.6 - 24.2 min)	Escherichia coli	46,072	7-Feb-99
		GB_BA1 ECHTRB	3129	X61000	E. coli K12 Hfr gene	Escherichia coli	36,164	30-Jun-93

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TABLE 4: ALIGNMENT RESULTS

GB_EST28/A481047	438	A481047	vfr1a05.11 Soares mouse mammary gland NAMING Mus musculus cDNA done	Mus musculus	38,128	05-MAR-1999
GB_HTG2/A008205	131658	A008205	IMAGE 851120.3, mRNA sequence	Drosophila melanogaster	33,307	2-Aug-99
GB_HTG2/A008205	131658	A008205	Drosophila melanogaster chromosome 3 clone BACR33F18 (D764) RPO-98 33 F 18 map 96A-96B	Drosophila melanogaster	33,307	2-Aug-99
GB_HTG2/A008205	131658	A008205	strain y, on bw sp. *** SEQUENCING IN PROGRESS ***; 118 unordered pieces	Drosophila melanogaster	33,307	2-Aug-99
GB_INT1/DMBRTC10	58820	AL121804	Drosophila melanogaster chromosome 3 clone BACR33F18 (D764) RPO-98 33 F 18 map 96A-96B	Drosophila melanogaster	41,367	10-OCT-1999
GB_BA1_SNEZ2575	1403	AJ252575	strain y, on bw sp. *** SEQUENCING IN PROGRESS ***; 118 unordered pieces	Snortizobum meliott	41,760	17-Sep-98
GB_PR3_A004655	134329	A004655	Snortizobum meliott partial owl and dehydrogenase genes, isolate lpu119	Homo sapiens	38,422	23-Nov-99
GB_PR3_HS98F2	98856	AL021579	Homo sapiens Xp22-140-141 BAC GS8B-128G5 (Genome Systems Human BAC library) complete sequence	Homo sapiens	38,351	17-MAR-1999
GB_HTG2/A007108	190000	A007108	Human DNA sequence from clone 598F2 on chromosome 1q23.1-24.1 Contains ESTs, STS and GSS, complete sequence	Homo sapiens	17,451	17-MAR-1999
GB_HTG2/A007108	190000	A007108	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***; 24 unordered pieces	Homo sapiens	17,451	17-MAR-1999
GB_HTG2/A007108	190000	A007108	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***; 24 unordered pieces	Homo sapiens	17,451	17-MAR-1999
GB_HTG2/A007108	190000	A007108	Homo sapiens chromosome unknown clone NH480A20, WORKING DRAFT SEQUENCE, in progress	Homo sapiens	35,519	29-OCT-1999
GB_IN2/A004361	87747	A004361	Drosophila melanogaster DNA sequence (P1 D507851 (D49)), complete sequence	Drosophila melanogaster	35,081	25-MAY-1998
GB_PL2/A000958	105420	A000958	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence	Arabidopsis thaliana	43,882	1-Jan-99
GB_BA1_MLCB96	38426	AL035472	Myobacterium leprae cosmid B596	Myobacterium leprae	35,028	27-Aug-99
GB_BA1_MTV025	121125	AL022121	Myobacterium tuberculosis H37Rv complete genome, segment 155/162	Myobacterium tuberculosis	53,061	24-Jun-99
GB_BA1_SC966	9153	AL046731	Streptomyces coelicolor cosmid H66	Streptomyces coelicolor	52,817	26-Apr-99
GB_EST14/AA446728	411	AA446728	zw6403.r1 Soares, total, felus, NC2HF8, 9w Homo sapiens cDNA clone IMAGE 783677 5', mRNA sequence	Homo sapiens	36,448	3-Jun-97
GB_PL1/AB09030	2589	AB09030	Pinax ginseng OSCPNY1 mRNA for beta-Amyrin Synthase, complete cds	Pinax ginseng	39,448	05-OCT-1998
GB_PR3_HS905G11	122489	AL035045	Human DNA sequence from clone 95G51 on chromosome 20p11.2-12.1 Contains STSs, GSSs and genomic marker D20S162, complete sequence	Homo sapiens	39,255	23-Nov-99
GB_RO_MMTCP5	8147	X15147	Mouse 1a region T1c pseudogene for catals 1 antigen major histocompatibility complex	Mus musculus	36,311	19-Feb-90
GB_HTG2/A0010674	22075	A0010674	Homo sapiens chromosome 15 clone RP11-430B1 map 13p21, *** SEQUENCING IN PROGRESS	Homo sapiens	37,714	5-Nov-99
GB_HTG2/A0010674	22075	A0010674	Homo sapiens chromosome 15 clone RP11-430B1 map 15p21, *** SEQUENCING IN PROGRESS	Homo sapiens	39,283	5-Nov-99
GB_BA1_BRLB10AD	2272	D14093	Brevibacterium flavum genes for 7,5-diaminopropionic acid aminotransferase and dehydrobutyryl synthase, complete cds	Corynebacterium glutamicum	47,368	3-Feb-99
GB_PAT_EW041	675	EW0401	DNA sequence coding for diethylenetriamine synthase	Corynebacterium glutamicum	46,552	25-Sep-97
GB_EST10/AA820386	453	AA820386	LD23968.5 prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone	Drosophila melanogaster	45,079	25-Feb-99
GB_HTG2/A007589	134559	A007589	Drosophila melanogaster chromosome 3 clone BACR2D10 (D667) RPO-98 20 D 10 map 82D-82E	Drosophila melanogaster	32,102	2-Aug-99
GB_HTG2/A007589	134559	A007589	strain y, on bw sp. *** SEQUENCING IN PROGRESS ***; 73 unordered pieces	Drosophila melanogaster	32,102	2-Aug-99
GB_HTG2/A009212	125452	A009212	Drosophila melanogaster chromosome 3 clone BACR2D10 (D667) RPO-98 20 D 10 map 82D-82E	Drosophila melanogaster	37,126	25-Aug-99
GB_HTG2/A009212	125452	A009212	strain y, on bw sp. *** SEQUENCING IN PROGRESS ***; 73 unordered pieces	Drosophila melanogaster	37,126	25-Aug-99
GB_HTG2/A009212	125452	A009212	Drosophila melanogaster chromosome 3 clone BACR01A18 (D669) RPO-98 01 A 18 map 82E-82F	Drosophila melanogaster	38,264	13-Sep-99
GB_HTG2/A009212	125452	A009212	strain y, on bw sp. *** SEQUENCING IN PROGRESS ***; 119 unordered pieces	Drosophila melanogaster	38,264	13-Sep-99
GB_HTG2/A009212	125452	A009212	Homo sapiens chromosome 11 clone B15946 map 11q23, *** SEQUENCING IN PROGRESS ***; 119 unordered pieces	Homo sapiens	38,264	13-Sep-99

TABLE 4: ALIGNMENT RESULTS

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na00751	951	GB_PR4 AC006449	286758	AC006449	17	done H6 56_E_17, complete sequence	38,223	23-OCT-1999
		GB_HTG2 AC002118	170891	AC002118	17	done 303_E_14, *** SEQUENCING IN PROGRESS ***	37,112	13-Feb-98
		GB_HTG2 AC002118	170891	AC002118	17	done 303_E_14, *** SEQUENCING IN PROGRESS ***	37,112	13-Feb-98
na00752	552	GB_PU2 F5K24	109786	AF128395	Arabis alpina	Italy	38,899	03-MAR-1999
		GB_BA1 MBHRD9	6300	Y09870	M. barkeri	hde & hrd genes	40,809	04-DEC-1998
		GB_PU1 SC9820	23498	Z49839	S. maritima	chrXIII cosmid 8920	35,154	11-AUG-97
na00757	1377	GB_PAT E13655	2260	E13655	gDNA encoding glucose-6-phosphate dehydrogenase		48,045	24-Jun-98
		GB_GSS9 AC103710	369	AC103710	HS_3092_B1_C01 ME CTF Approved Human Genomic Sperm Library D	Human sapiens genomic	36,339	27-Aug-98
		GB_HTG3 AC009305	167705	AC009305	one Paderborn clone WH133B1, *** SEQUENCING IN PROGRESS ***	3, unorderd pieces	38,691	13-AUG-98
		GB_BA1 SC7897	13800	AL009199	Streptomyces coelicolor	cosmid 187	39,013	02-DEC-1997
na00763	906	GB_HTG2 HSJ47316	203480	AL109942	Human sapiens chromosome 6	done RP4-7316 map q25.5-26, *** SEQUENCING IN PROGRESS	38,192	03-DEC-1999
		GB_HTG2 HSJ47316	203480	AL109942	Human sapiens chromosome 6	done RP4-7316 map q25.5-26, *** SEQUENCING IN PROGRESS	38,192	03-DEC-1999
na00765	810	GB_BA1 MTY043	68848	AL022004	Mycobacterium tuberculosis	H37Rv complete genome, segment 40/162	38,568	24-Jun-99
		GB_BA2 PAL93274	8008	U83274	Pseudomonas aeruginosa	YafE (yafE), LexA (lexA), FimV (fimV), and HsaT (hsaT) genes, complete cds, TrpF (trpF) gene, partial cds, and unknown gene	37,656	23-Jun-98
		GB_BA1 MTCY31	37630	Z73101	Mycobacterium tuberculosis	H37Rv complete genome, segment 41/162	38,209	17-Jun-98
na00768	1242	GB_HTG5 AC008194	194555	AC008194	Drosophila melanogaster chromosome X	done BACH48A05 (D745) RFP-98 48 A 5 map 18A-18A strain y, on bw sp, *** SEQUENCING IN PROGRESS ***	34,078	15-Nov-99
		GB_HTG5 AC008194	194555	AC008194	Drosophila melanogaster chromosome X	done BACH48A05 (D745) RFP-98 48 A 5 map 18A-18A strain y, on bw sp, *** SEQUENCING IN PROGRESS ***	31,164	15-Nov-99
		GB_BA2 AF044495	9999	AF044495	Agrobacterium tumefaciens	chemists operon, complete sequence	40,165	2-Jul-98
na00769	336	GB_PPR3 AC030968	42184	AC030968	Human Cosmid g5126c059 from Tcd3.3	complete sequence	35,152	6-Nov-97
		GB_PPR2 HSJ47314	41885	AC030974	Human Cosmid g5126c059 from Tcd3.3	complete sequence	37,309	6-Nov-97
		GB_PPR3 AC030968	42184	AC030968	Human DNA sequence from PAC 122K on chromosome 6	contains HLA CLASS II DRA pseudogene, DRB3*01:02 genes, DRB9 pseudogene	34,719	23-Nov-99
na00771	942	GB_PPR2 HSJ7262	131254	Z64814	Human sapiens chromosome 20	done RP11-555E18, *** SEQUENCING IN PROGRESS ***	41,450	23-Nov-99
		GB-HTG1 HSA555E18	1177	AL121780	Human sapiens chromosome 20	done RP11-555E18, *** SEQUENCING IN PROGRESS ***	41,450	23-Nov-99
		GB-HTG1 HSA555E18	1177	AL121780	Human sapiens chromosome 20	done 48A11 on chromosome 20p12 Contains EST, STS, GSS, complete sequence	37,274	23-Nov-99
na00781	411	GB_PRR3 HS48A11	129294	AL031132	Human DNA sequence from cosmid C03B1		38,187	23-Nov-99
		GB_INT CEL03B1	42287	UA0652	Caenorhabditis elegans	cosmid C03B1	35,162	25-Nov-99
		GB_PRR3 HS48A11	129294	AL031132	Human DNA sequence from cosmid 48A11	Contains EST, STS, GSS, complete sequence	38,682	23-Nov-99
na00785	680	GB_EST11 AA223451	349	AA223451	zrb001.r1 Stragelene NT2 neuronal precursor	697200 Homo sapiens cDNA clone IMAGE 65689	40,271	19-Feb-97
		GB_EST5 A081255	448	A081255	zrb003.r1 Stragelene endothelial cell	697223 Homo sapiens cDNA clone IMAGE 549231 5', mRNA sequence		21-OCT-1996

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TABLE 4: ALIGNMENT RESULTS

GB_HTG3 AC008329	114408	AC008329	Drosophila melanogaster chromosome 2 clone BACR31D05 (D891) PPO-98.31 D.5 map 26C-28D strain Y, on bw sp. ** SEQUENCING IN PROGRESS **	Drosophila melanogaster	34,317	17-Aug-99
GB_HTG3 AC008329	114408	AC008329	Drosophila melanogaster chromosome 2 clone BACR31D05 (D891) PPO-98.31 D.5 map 26C-28D strain Y, on bw sp. ** SEQUENCING IN PROGRESS **	Drosophila melanogaster	34,317	17-Aug-99
GB_BA1 MTU008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome, segment 108/102	Mycobacterium tuberculosis	36,045	17-Jun-98
GB_GSS14 AQ257766	520	AQ571785	HS_2094_A2_B09_MR_CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone P146-2094 Col18 Roy-C, genomic survey sequence.	Homo sapiens	38,021	1-Jun-99
GB_LO RRF65G	2464	X60468	R rat1a FEG5 gene for adaptor protein interacting with the beta-amyloid precursor protein intracellular domain	Rattus rattus	38,177	1-Feb-96
GB_VIHPXG	5366	M26281	Hamster papovavirus complete genome	Hamster papovavirus	36,579	22-MAY-1995
GB_BA2 AE000878	15432	AE000878	Hamster papovavirus (HapV) genome	Hamster papovavirus	36,579	22-OCT-1999
GB_BA1 CGMTAR	961	X75083	Methanococcus thermolithotrophicum from bases 978001 to 992232 (section 84 of 148) of the complete genome	Methanococcus thermolithotrophicum	36,566	15-Nov-97
GB_BA1 CGMTAR	961	X75083	C. glutamicum mtrA gene locus with 5-methyltyrosine resistance	Corynebacterium	99,133	18-Aug-94
GB_BA1 CGMTAR	587	X75084	C. glutamicum complete corresponding to mtrA locus	Corynebacterium	99,216	18-Aug-94
GB_BA1 BLTRP	7725	X04690	Brevibacterium lactofermentum tyrosophan operon	glutamicum	96,800	10-Feb-99
GB_EST15 A4484511	504	AA444511	nB807 s1 NCL CGAP_L1 Homo sapiens cDNA clone IMAGE 913189 similar to gb Y00784	glutamicum	43,750	18-Aug-97
GB_EST20 A894481	544	AA894481	UBIQUINOL-CYTOCHROME C REDUCTASE 11 KD PROTEIN (HUMAN), mRNA sequence	Homo sapiens	37,500	6-Aug-98
GB_EST15 A4528497	582	AA528497	nB7610 s1 NCL CGAP_P12 Homo sapiens cDNA clone IMAGE 1252507 similar to gb Y00784	Homo sapiens	38,564	5-Aug-97
GB_BA1 CGHOMTHR	3685	Y00546	UBIQUINOL-CYTOCHROME C REDUCTASE 11 KD PROTEIN (HUMAN), mRNA sequence	Corynebacterium	99,988	12-Sep-93
GB_PAT 09077	3685	I09077	Corynebacterium glutamicum hom-hrb genes for homoserine dehydrogenase and homoserine kinase	glutamicum	99,246	02-DEC-1994
GB_BA1 BLTHRA	1483	Y00476	Sequence 1 from Patent WO 8809819	Unknown	99,278	05-MAY-1993
GB_BA1 CGHOMTHR	3685	Y00546	B. lactofermentum thr A gene	Corynebacterium	35,435	12-Sep-93
GB_PAT 09077	3685	I09077	Corynebacterium glutamicum hom-hrb genes for homoserine dehydrogenase and homoserine kinase	glutamicum	35,435	12-DEC-1994
GB_BA1 BLTHRB	1139	Y00140	Sequence 1 from Patent WO 8808819	Unknown	40,964	12-Sep-93
GB_BA1 CGHOMTHR	3685	Y00546	Brevibacterium lactofermentum thrB gene for homoserine kinase	glutamicum	41,797	12-Sep-93
GB_PAT 09077	3685	I09077	Corynebacterium glutamicum hom-hrb genes for homoserine dehydrogenase and homoserine kinase	glutamicum	41,797	02-DEC-1994
GB_IN2 AC006574	127035	AC006574	Sequence 1 from Patent WO 8808819	Unknown	41,797	16-Feb-99
GB_PR2 HSA000372	41730	AC000372	Drosophila melanogaster, chromosome 2R, region 39A3-39B1, P1: clones DS02919 and DS045130, complete sequence	Drosophila melanogaster	37,355	12-MAR-1997
GB_PR3 AC005503	40998	AC005503	Human cosmid g19b01186, complete sequence	Homo sapiens	34,674	20-Aug-98
GB_PR2 HSA000372	41730	AC000372	Human sapiens clone UWC5 g5129a003 from 7q31, complete sequence	Homo sapiens	38,881	12-MAR-1997
GB_GSS10 AQ258013	761	AQ258013	Human cosmid g19b01186, complete sequence	Homo sapiens	31,533	23-OCT-1998
GB_PR3 HSB3L6	61187	Z99130	ribA00119H05f CUGI Rice BAC Library Oryza sativa genomic clone ribA00119H05f, genomic survey sequence	Oryza sativa	38,395	23-Nov-99
GB_PR3 HSB9A24	96558	AL031115	Human DNA sequence from PAC 83L6 on chromosome Xp11.1-11.22 Contains ZKDA (ZFPA) zinc finger gene, ESTs and STS, complete sequence	Homo sapiens	37,333	23-Nov-99
			Human DNA sequence from clone 599A24 on chromosome Xp11.1-11.23 Contains zinc finger X- human proteins ZKDA, ZKDB, ESTs and STS, complete sequence	Homo sapiens		

TABLE 4: ALIGNMENT RESULTS

na01029 612	GB_PR3:HS46P17	149963	AL023806	Human DNA sequence from clone 468P17 on chromosome 9q24. Contains a putative novel gene, the 5' part of the EPMA2 (Lafurin) gene, ESTs, STSs, GSSs, genomic marker D6S1703 and D6S1443, a putative CpG island and a ca repeat polymorphism, complete sequence	Human sapiens	38,330	23-Nov-99
na01031 789	GB_PR4:AC006948	108558	AC006948	Mouse DNA sequence from clone 468P17 on chromosome 9q24. Contains a putative novel gene, the 5' part of the EPMA2 (Lafurin) gene, ESTs, STSs, GSSs, genomic marker D6S1703 and D6S1443, a putative CpG island and a ca repeat polymorphism, complete sequence	Mouse musculus	35,472	5-Feb-99
na01032 408	GB_PR5:AA116349	576	AA116349	Human sapiens chromosome 17, clone HPRK3_M34_M10, complete sequence	Human sapiens	44,005	27-Apr-99
na01033 459	GB_GSS1:AC043468	520	AC043468	Arabidopsis thaliana chromosome 1, BAC T6L1, genomic sequence, complete sequence	Arabidopsis thaliana	38,170	11-Nov-99
na01034 477	GB_PL2:ATT28H11	87011	AL046559	Mus musculus MMTV integration locus, aromatase gene, 3' UTR	Mus musculus	32,586	17-Feb-96
na01035 729	GB_PL2:ATT28H11	87011	AL046559	mouse36 r1 Stragelene mouse testis (#937506) Mus musculus cDNA clone IMAGE 515897 5 similar to go L06852 Mouse (MOUSE), mRNA sequence	Mus musculus	43,058	19-Nov-96
na01036 578	GB_HTG2:HS000408	143577	AC004846	mouse36 r1 Stragelene mouse testis (#937506) Mus musculus cDNA clone IMAGE 515897 5 similar to go L06852 Mouse (MOUSE), mRNA sequence	Mus musculus	42,273	19-Nov-96
na01037 651	GB_HTG2:HS000408	143577	AC004846	Human sapiens chromosome 20 clone RP4-794I6, *** SEQUENCING IN PROGRESS *** in unordered pieces	Human sapiens	38,608	31-MAR-1999
na01038	GB_HTG2:HS000408	143577	AC004846	Human sapiens chromosome 20 clone RP4-794I6, *** SEQUENCING IN PROGRESS *** in unordered pieces	Human sapiens	28,920	27-Nov-99
na01039 699	GB_HTG2:HS000408	143577	AC004846	Human sapiens chromosome 20 clone RP4-794I6, *** SEQUENCING IN PROGRESS *** in unordered pieces	Human sapiens	28,929	27-Nov-99
na01040 1026	GB_HTG2:HS000408	143577	AC004846	Human sapiens chromosome 20 clone RP4-794I6, *** SEQUENCING IN PROGRESS *** in unordered pieces	Human sapiens	32,495	9-Jun-99
na01041 1026	GB_HTG2:HS000408	143577	AC004846	Human sapiens chromosome 20 clone RP4-794I6, *** SEQUENCING IN PROGRESS *** in unordered pieces	Human sapiens	40,042	9-Jun-99
na01042 1026	GB_HTG2:HS000408	143577	AC004846	Human sapiens chromosome 20 clone RP4-794I6, *** SEQUENCING IN PROGRESS *** in unordered pieces	Human sapiens	35,435	09-DEC-1998
na01043 1026	GB_HTG2:HS000408	143577	AC004846	Human sapiens chromosome 20 clone RP4-794I6, *** SEQUENCING IN PROGRESS *** in unordered pieces	Human sapiens	38,406	28-Jun-99
na01044 1026	GB_HTG2:HS000408	143577	AC004846	Human sapiens chromosome 20 clone RP4-794I6, *** SEQUENCING IN PROGRESS *** in unordered pieces	Human sapiens	45,833	8-Apr-99
na01045 1026	GB_HTG2:HS000408	143577	AC004846	Human sapiens chromosome 20 clone RP4-794I6, *** SEQUENCING IN PROGRESS *** in unordered pieces	Human sapiens	37,500	28-Jun-99
na01046 1026	GB_HTG2:HS000408	143577	AC004846	Human sapiens chromosome 20 clone RP4-794I6, *** SEQUENCING IN PROGRESS *** in unordered pieces	Human sapiens	38,137	12-Jun-98
na01047 1026	GB_HTG2:HS000408	143577	AC004846	Human sapiens chromosome 20 clone RP4-794I6, *** SEQUENCING IN PROGRESS *** in unordered pieces	Human sapiens	33,582	18-FEB-96
na01048 1026	GB_HTG2:HS000408	143577	AC004846	Human sapiens chromosome 20 clone RP4-794I6, *** SEQUENCING IN PROGRESS *** in unordered pieces	Human sapiens	38,137	11-Jan-99
na01049 1026	GB_HTG2:HS000408	143577	AC004846	Human sapiens chromosome 20 clone RP4-794I6, *** SEQUENCING IN PROGRESS *** in unordered pieces	Human sapiens	39,750	05-DEC-1998
na01050 1026	GB_HTG2:HS000408	143577	AC004846	Human sapiens chromosome 20 clone RP4-794I6, *** SEQUENCING IN PROGRESS *** in unordered pieces	Human sapiens	41,214	11-Jan-99
na01051 1026	GB_HTG2:HS000408	143577	AC004846	Human sapiens chromosome 20 clone RP4-794I6, *** SEQUENCING IN PROGRESS *** in unordered pieces	Human sapiens	41,214	12-Jun-98
na01052 1026	GB_HTG2:HS000408	143577	AC004846	Human sapiens chromosome 20 clone RP4-794I6, *** SEQUENCING IN PROGRESS *** in unordered pieces	Human sapiens	36,192	23-Nov-99
na01053 1026	GB_HTG2:HS000408	143577	AC004846	Human sapiens chromosome 20 clone RP4-794I6, *** SEQUENCING IN PROGRESS *** in unordered pieces	Human sapiens	34,632	30-Nov-99
na01054 1026	GB_HTG2:HS000408	143577	AC004846	Human sapiens chromosome 20 clone RP4-794I6, *** SEQUENCING IN PROGRESS *** in unordered pieces	Human sapiens	34,632	30-Nov-99
na01055 1026	GB_HTG2:HS000408	143577	AC004846	Human sapiens chromosome 20 clone RP4-794I6, *** SEQUENCING IN PROGRESS *** in unordered pieces	Human sapiens	40,126	29-OCT-1998
na01056 1026	GB_HTG2:HS000408	143577	AC004846	Human sapiens chromosome 20 clone RP4-794I6, *** SEQUENCING IN PROGRESS *** in unordered pieces	Human sapiens	38,652	10-MAR-1997
na01057 1026	GB_HTG2:HS000408	143577	AC004846	Human sapiens chromosome 20 clone RP4-794I6, *** SEQUENCING IN PROGRESS *** in unordered pieces	Human sapiens	39,643	21-Aug-97

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TABLE 4: ALIGNMENT RESULTS

GB_RO AB032899	1914	AB032899	Rattus norvegicus PPK2 alpha mRNA for phosphatidylinositol 5-phosphate 4-kinase alpha, complete cds	38,480	07-OCT-1999
rs001068 1194	GB_HTG4 AC006091	178678	Drosophila melanogaster chromosome 3 clone BACR48G05 (D478) RPCI-96 48 G 5 map 91F1-91F13 strain Y, cn bw sp, *** SEQUENCING IN PROGRESS ***	35,539	27-OCT-1999
	GB_HTG4 AC006091	178678	Drosophila melanogaster chromosome 3 clone BACR48G05 (D478) RPCI-96 48 G 5 map 91F1-91F13 strain Y, cn bw sp, *** SEQUENCING IN PROGRESS ***	35,539	27-OCT-1999
	GB_HTG2 AC008141	100729	Drosophila melanogaster chromosome 3 clone BACR117F04 (D968) RPCI-96 17 F 4 map 91F-91F13 strain Y, cn bw sp, *** SEQUENCING IN PROGRESS ***	34,415	2-Aug-99
rs001069 837	GB_EST15 AA51901	524	TgE223230919.1 TgME49 mvno Bradyzote cDNA size selected Toxoplasma gondii cDNA clone tg232309.1 r1.5, mRNA sequence	43,005	22-Jun-97
	GB_EST15 AA520183	527	Tg233901.01 s1.3, mRNA sequence	40,864	16-Jun-97
	GB_HTG6 AC010846	187611	Drosophila melanogaster chromosome X clone BACR13G15 (D984) RPCI-66 13 G 13 map 14B-14C strain Y, cn bw sp, *** SEQUENCING IN PROGRESS ***	36,679	03-DEC-1999
rs001071 2167	GB_EST24 AA80319	450	NS38001.11 Staglepine mouse lung 351332 Mus musculus cDNA clone IMAGE 1271617.5, mRNA	40,724	26-MAR-1998
	GB_GSS14 AQ558382	435	HS_2068.B1.F06, T7G COT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Phage2068.Cen111 Rowel, genomic survey sequence	36,882	29-MAY-1999
	GB_GSS15 AQ600385	483	HS_3587.B2.C05, SPARE RPCI-11 Human Male BAC Library Homo sapiens genomic clone Phae933.Cot10 RowF, genomic survey sequence	40,476	10-Jun-93
rs001074 828	GB_BA1 FSEHDDH	3060	M74256 Pseudomonas aeruginosa 6-phosphogluconate dehydratase (edd) gene, and glyceraldehyde-3-phosphate dehydrogenase (gap) gene, complete cds	39,168	30-Nov-93
	GB_BA1 GGLU07732	4400	AJ007732 Corynebacterium glutamicum 3 ppc gene, secG gene, secE gene, secY gene, secZ gene, secV gene	43,382	7-Jan-99
	GB_EST9 AA068016	406	mS2712.11 Staglepine mouse testis (4637300) Mus musculus cDNA clone IMAGE 515683.5, mRNA sequence	31,236	3-Feb-97
rs001075 534	GB_EST9 AA068543	445	ue1408.x1 Sigano mouse embryo mewa Mus musculus cDNA clone IMAGE 1480359.3, mRNA sequence	42,264	28-MAY-1998
	GB_EST22 A035794	509	ue17001.Y1 Sigano mouse embryo mewa Mus musculus cDNA clone IMAGE 1480609.5, mRNA sequence	46,637	26-Jun-96
	GB_EST22 A005606	384	ue15708.Y1 Sigano mouse embryo mewa Mus musculus cDNA clone IMAGE 1480359.5, mRNA sequence	38,209	12-Jun-96
rs001076 1143	GB_HTG2 AC007741	182450	Hom0 sapiens clone NH340F16, *** SEQUENCING IN PROGRESS ***	38,209	5-Jun-99
	GB_HTG2 AC007741	182450	Hom0 sapiens clone NH340F16, *** SEQUENCING IN PROGRESS ***	38,209	5-Jun-99
	GB_EST13 A072325	317	A072325 Mus musculus stomach C57BL/6J adult Mus musculus cDNA clone Z20003.EC01, mRNA	46,465	24-Jun-96
rs001078 967	GB_BA2 RCPHSYNG	45959	R capsulatus complete photophysynthesis gene cluster	38,003	2-Sep-99
	GB_BA2 RCPHSYNG	45959	R capsulatus complete photophysynthesis gene cluster	37,989	2-Sep-99
	GB_PR4 AF073931	7988	Hom0 sapiens low-voltage activated calcium channel alpha 1H mRNA, complete cds	37,953	04-MAR-1999
rs001083 399	GB_BA2 AF12335	4363	AF12355 Corynebacterium glutamicum putative glutaredoxin NrdH (nrdH), (nrdI), and ribonucleotide reductase alpha-chain (nrdE) genes, complete cds	99,469	5-Aug-99
	GB_PR3 HS18032	1789	AF053138 Homo sapiens histone deacetylase 3 gene, exons 11, 12, 13 and partial cds	33,512	28-MAR-1998
	GB_PR4 AF059650	18015	AF059650 Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds	38,814	Hom0 sapiens
rs001085 902	GB_EST14 HE5032	951	HHUS4 Sorghum bicolor cv. TX430 Sorghum bicolor cDNA clone HHUS4.9 similar to transferase, chloroplast (TALC1), mRNA sequence	41,111	27-Sep-99
	GB_HTG2 HSB427F12	123489	AL109914 Hom0 sapiens chromosome 6 clone RP11-27F.12 map p22.3-24, *** SEQUENCING IN PROGRESS ***	35,156	30-Nov-99
	GB_HTG2 HSB427F12	123489	AL109914 Hom0 sapiens chromosome 6 clone RP11-27F.12 map p22.3-24, *** SEQUENCING IN PROGRESS ***	35,156	30-Nov-99
rs001088 1305	GB_HTG5 AC010202	170004	AC010202 Hom0 sapiens chromosome 12q seeds clone RP11-210L, *** SEQUENCING IN PROGRESS ***	37,313	6-Nov-99

TABLE 4: ALIGNMENT RESULTS

na01166	813	GB_BA1 MSCY151	37036	AD000018	Myobacterium tuberculosis sequence from clone y151	Myobacterium tuberculosis	36,634	10-DEC-1996
na01168	426	GB_BA1 MTCY130	32514	Z73802	Myobacterium tuberculosis H37Rv complete genome, segment 58162	Myobacterium tuberculosis	59,596	17-Jun-98
na01169	576	GB_BA1 MSCY151	37036	AD000018	Myobacterium tuberculosis sequence from clone y151	Myobacterium tuberculosis	39,567	10-DEC-1996
na01170	524	GB_EST18 AAF78822	524	AA576822	g68c11 s1 Soares_fetal_liver_spleen_1NFUS_S1 Homo sapiens cDNA clone IMAGE:455156 3'	Myobacterium tuberculosis	40,741	19-DEC-1997
na01171	524	GB_EST16 AAF76822	524	AA576822	g68c11 s1 Soares_fetal_liver_spleen_1NFUS_S1 Homo sapiens cDNA clone IMAGE:455156 3'	Myobacterium tuberculosis	40,331	19-DEC-1997
na01172	426	GB_HTG4 AC010195	164035	AC010195	Homo sapiens chromosome 10 clone RPCH11-587C2 *** SEQUENCING IN PROGRESS *** 81	Homo sapiens	36,058	21-OCT-1989
na01173	426	GB_HTG4 AC010195	164035	AC010195	Homo sapiens chromosome 10 clone RPCH11-587C2 *** SEQUENCING IN PROGRESS *** 81	Homo sapiens	36,058	21-OCT-1989
na01174	426	GB_HTG1 CEY44A6	326074	Z98863	Caenorhabditis elegans chromosome V clone Y44A6 *** SEQUENCING IN PROGRESS *** in	Caenorhabditis elegans	39,151	03-DEC-1998
na01175	426	GB_HTG1 CER08A5	51920	Z82281	Caenorhabditis elegans chromosome V clone R08A5 *** SEQUENCING IN PROGRESS *** in	Caenorhabditis elegans	43,557	14-OCT-1998
na01176	426	GB_HTG1 CER08A5	51920	Z82281	Caenorhabditis elegans chromosome V clone R08A5 *** SEQUENCING IN PROGRESS *** in	Caenorhabditis elegans	43,557	14-OCT-1998
na01177	426	GB_HTG1 CER08A5	51920	Z82281	Caenorhabditis elegans chromosome V clone R08A5 *** SEQUENCING IN PROGRESS *** in	Caenorhabditis elegans	34,987	14-OCT-1998
na01178	426	GB_PL2 SPBC802	43757	AL022072	S.pombe chromosome II cosmid c802	Schizosaccharomyces pombe	35,566	24-Nov-99
na01179	426	GB_PL1 AB004538	38911	AB004538	Schizosaccharomyces pombe 39 kb genomic DNA, clone c568	Schizosaccharomyces pombe	35,148	15-Jul-97
na01180	426	GB_HTG8 AC009220	110000	AC009220	Homo sapiens chromosome 7 *** SEQUENCING IN PROGRESS *** 197 unoriented pieces	Homo sapiens	33,940	15-Sep-99
na01181	426	GB_GSS4 AG694235	530	AG694235	HS_5466_A1_D03_17A RPCH11 Human Male BAC Library Homo sapiens genomic clone	Homo sapiens	37,259	6-Jul-98
na01182	426	GB_GSS11 A0322059	519	A0322059	RPCH11-100510 TV RPCH11 Homo sapiens genomic clone RPCH11-100510 genomic survey	Homo sapiens	37,229	06-MAY-1999
na01183	1350	GB_BA1 SCH24	41925	AL049826	Schizosaccharomyces pombe cosmid H24	Schizosaccharomyces pombe	38,126	11-MAY-1999
na01184	1350	GB_PR3 HS35687	20733	AL031714	Human DNA sequence from clone 35687 on chromosome 16. Contains the LBE21 gene for ubiquitin-conjugating enzyme E2 (homologous to yeast UBC9), and an RPS20 (40S Ribosomal protein S20) pseudogene. Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.	Homo sapiens	36,684	23-Nov-99
na01185	1350	GB_PR3 HS35687	20733	AL031714	Human DNA sequence from clone 35687 on chromosome 16. Contains the LBE21 gene for ubiquitin-conjugating enzyme E2 (homologous to yeast UBC9), and an RPS20 (40S Ribosomal protein S20) pseudogene. Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.	Homo sapiens	36,621	23-Nov-99
na01186	552	GB_PR1 HSEF/AL1	1815	X16870	Human DNA sequence from clone 25719 on chromosome 6p25-1:26. Contains gene similar to Cyp19bome B, CA repeat, GSS, complete sequence	Homo sapiens	37,462	12-Jun-90
na01187	552	GB_PR3 HS25719	90866	AL031773	Cyp19bome B, CA repeat, GSS, complete sequence	Homo sapiens	35,887	23-Nov-99
na01188	552	GB_PR3 HS25719	112831	Z85325	Human DNA sequence from clone 25719 on chromosome Xq21.1-21.33. Contains STSs and GSSs, complete sequence	Homo sapiens	37,778	23-Nov-99

TABLE 4: ALIGNMENT RESULTS

10 MAY - 1999	rs2430015	Scorae2_pigpant1.1a.10	NIHPU1 Homo sapiens cDNA, clone IMAGE-471377.3, mRNA	Homo sapiens	40,191
23-Nov-99	rs23999	Human Chromosome 16 BAC clone C19orf38/SKA-2.1.TC6	Human Chromosome 16 BAC clone C19orf38/SKA-2.1.TC6	Homo sapiens	33,933
4-Sep-99	rs23999	Gallus gallus NC class hms308end	Gallus gallus NC class hms308end	Gallus gallus	30,556
28-Sep-99	rs23999	Unknown	Unknown	Unknown	34,304
01-DEC-1998	rs23999	Drosophila melanogaster	Drosophila melanogaster	Drosophila melanogaster	38,279
01-DEC-1998	rs23999	Drosophila melanogaster	Drosophila melanogaster	Drosophila melanogaster	36,893
24-Nov-98	rs23999	Drosophila melanogaster	Drosophila melanogaster	Drosophila melanogaster	44,167
3-Feb-99	rs23999	Oryza sativa	Oryza sativa	Oryza sativa	34,577
29-OCT-1999	rs23999	Homo sapiens Human 12p11-37.2.5.4 BAC RPOC111-12D.5 (Rowell Park Cancer Institute Human BAC Library) complete sequence	Homo sapiens Human 12p11-37.2.5.4 BAC RPOC111-12D.5 (Rowell Park Cancer Institute Human BAC Library) complete sequence	Homo sapiens	34,350
29-OCT-1999	rs23999	Homo sapiens Human 12p11-37.2.5.4 BAC RPOC111-12D.5 (Rowell Park Cancer Institute Human BAC Library) complete sequence	Homo sapiens Human 12p11-37.2.5.4 BAC RPOC111-12D.5 (Rowell Park Cancer Institute Human BAC Library) complete sequence	Homo sapiens	37,998
14-Apr-99	rs23999	Homo sapiens	Homo sapiens	Homo sapiens	36,328
14-Apr-99	rs23999	Homo sapiens	Homo sapiens	Homo sapiens	37,391
2-Aug-99	rs23999	Drosophila melanogaster	Drosophila melanogaster	Drosophila melanogaster	38,188
2-Aug-99	rs23999	Drosophila melanogaster	Drosophila melanogaster	Drosophila melanogaster	38,188
29-OCT-1999	rs23999	Homo sapiens	Homo sapiens	Homo sapiens	38,762
12-Aug-98	rs23999	Typanosoma cruzi rhodesiense	Typanosoma cruzi rhodesiense	Typanosoma cruzi rhodesiense	38,281
12-Aug-98	rs23999	Typanosoma cruzi rhodesiense	Typanosoma cruzi rhodesiense	Typanosoma cruzi rhodesiense	33,894
8-Jul-98	rs23999	Mus musculus	Mus musculus	Mus musculus	41,463
2-Feb-98	rs23999	Mus musculus	Mus musculus	Mus musculus	41,463
2-Sep-99	rs23999	Homo sapiens	Homo sapiens	Homo sapiens	36,131
18-Nov-98	rs23999	Homo sapiens	Homo sapiens	Homo sapiens	39,622
18-Nov-98	rs23999	Homo sapiens	Homo sapiens	Homo sapiens	38,319
15-Sep-99	rs23999	Caenorhabditis elegans	Caenorhabditis elegans	Caenorhabditis elegans	36,884
20-OCT-1999	rs23999	Homo sapiens	Homo sapiens	Homo sapiens	38,070
20-OCT-1999	rs23999	Homo sapiens	Homo sapiens	Homo sapiens	35,131
25-Sep-99	rs23999	Homo sapiens	Homo sapiens	Homo sapiens	38,303
25-Sep-99	rs23999	Myosinoma pulmonis	Myosinoma pulmonis	Myosinoma pulmonis	37,982
30-MAY - 1998	rs23999	Onchocerca volvulus	Onchocerca volvulus	Onchocerca volvulus	40,566
22-DEC-1998	rs23999	Onchocerca volvulus	Onchocerca volvulus	Onchocerca volvulus	36,498
25-Sep-99	rs23999	Homo sapiens	Homo sapiens	Homo sapiens	36,498
25-Sep-99	rs23999	Homo sapiens	Homo sapiens	Homo sapiens	36,554

TABLE 4: ALIGNMENT RESULTS

rs01379	1042	GB_IN2:AC005639	188288	AC005639	sequence	Drosophila melanogaster, chromosome 2R, region 59E3-59F4, BAC clone BAC948M01, complete	Drosophila melanogaster	36,275	6-Jan-99
rs01380	2322	GB_BTGA:AC010031	132108	AC010031	PROGRESS ***, 69 unordered pieces	Drosophila melanogaster, chromosome 3L/70C1 clone RPC198-2M20, *** SEQUENCING IN	Drosophila melanogaster	35,368	16-OCT-1999
rs01381	813	GB_BTGA:AC010031	132108	AC010031	PROGRESS ***, 69 unordered pieces	Drosophila melanogaster, chromosome 3L/70C1 clone RPC198-2M20, *** SEQUENCING IN	Drosophila melanogaster	35,368	16-OCT-1999
rs01382	1639	GB_BTGA:AC010031	68745	AC009932	Homo sapiens clone 114_O_12, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	38,337	05-OCT-1999	
rs01383	1639	GB_BTGA:AC010031	40105	AL049587	Streptomyces coelicolor cosmid SF2A	Streptomyces coelicolor	39,699	24-MAY-1999	
rs01384	1639	GB_BTGA:AC010031	40105	AL049587	B. pertussis tax gene	Bordetella pertussis	59,687	31-Jul-98	
rs01385	1639	GB_BTGA:AC010031	40105	AL049587	Streptomyces coelicolor cosmid SF2A	Streptomyces coelicolor	41,024	24-MAY-1999	
rs01386	1639	GB_GSS15:AC0613816	598	AD013816	Hs_5112_b1_170_LTA, RPC11 Human Male BAC Library	Homo sapiens	39,300	15-Jun-99	
rs01387	1639	GB_GSS15:AC0613816	598	AD013816	Hs_5112_b1_170_LTA, RPC11 Human Male BAC Library	Homo sapiens	39,300	15-Jun-99	
rs01388	1639	GB_GSS15:AC0613816	598	AD013816	Hs_5112_b1_170_LTA, RPC11 Human Male BAC Library	Homo sapiens	39,300	15-Jun-99	
rs01389	780	GB_BTGA:CG101293	2952	AD012293	Corynebacterium glutamicum iM0 gene	Corynebacterium glutamicum	40,413	01-OCT-1999	
rs01390	780	GB_BTGA:AC008213	180754	AC008213	Homo sapiens, clone HRPK_15_A_1, complete sequence	Homo sapiens	33,724	16-Jan-99	
rs01391	813	GB_BTGA:AC008213	98956	AL049488	Anabropsis thaliana DNA chromosome 4, BAC clone F24C24 (ESSA project)	Anabropsis thaliana	33,925	27-Aug-99	
rs01392	813	GB_BTGA:AC008671	44733	AC008671	Homo sapiens chromosome 10 clone UA10NC01_15_E_11 map 10q26.3, *** SEQUENCING IN	Homo sapiens	35,031	09-DEC-1998	
rs01393	813	GB_BTGA:AC008671	44733	AC008671	PROGRESS ***, 3 unordered pieces	Homo sapiens	35,031	09-DEC-1998	
rs01394	813	GB_BTGA:AC008671	44733	AC008671	PROGRESS ***, 3 unordered pieces	Homo sapiens	35,031	09-DEC-1998	
rs01395	381	GB_BTGA:AE000775	14358	AE000775	Aquifex aeolicus section 107 of 109 of the complete genome	Aquifex aeolicus	43,085	25-MAR-1998	
rs01397	543	GB_BTGA:AE000775	401	AB320043	addictin H1 Neurospora crassa everted cDNA library	Neurospora crassa	44,484	28-DEC-1998	
rs01398	543	GB_BTGA:AE000775	14358	AE000775	Aquifex aeolicus section 107 of 109 of the complete genome	Aquifex aeolicus	41,121	25-MAR-1998	
rs01400	1623	GB_GSS11:AC0264714	353	AQ264714	B. subtilis p_xlma and cdc (partial) genes for PHPP synthetase and two undefined gene products	Bacillus subtilis	41,255	30-Sep-93	
rs01401	384	GB_BTGA:AC005653	110000	AC005653	v29001.11 Spores breast SNH181 Homo sapiens cDNA clone IMAGE 15625.5 similar to SP_XPEC_CERAE_P33184 POSSIBLE DNA-REPAIR PROTEIN XPLE mRNA sequence	Homo sapiens	35,407	6-Jul-95	
rs01402	597	GB_BTGA:AC010319	5398	AD010319	90 unordered pieces	Homo sapiens	40,227	27-OCT-1998	
rs01403	597	GB_BTGA:AC010319	5398	AD010319	90 unordered pieces	Homo sapiens	40,227	27-OCT-1998	
rs01404	384	GB_BTGA:CAJ10319	5398	AD010319	90 unordered pieces	Homo sapiens	40,227	27-OCT-1998	
rs01405	597	GB_BTGA:AC010086	187240	AC010086	Thiodiacetic ferrioxalins nitrogen metabolism regulator (ntrA) gene, complete cds	Thiodiacetic ferrioxalins	39,900	26-Apr-93	
rs01406	597	GB_BTGA:AC010086	187240	AC010086	N. pharaonis sHMC, sHMC and sHCA genes	Natronomonas pharaonis	32,718	2-Sep-96	
rs01407	597	GB_BTGA:AC010086	187240	AC010086	Homo sapiens chromosome 3p21.3 clone RPC11-149.D8, *** SEQUENCING IN PROGRESS ***,	Homo sapiens	38,003	21-OCT-1999	
rs01408	597	GB_BTGA:AC010086	187240	AC010086	90 unordered pieces	Homo sapiens	32,718	21-OCT-1999	
rs01409	597	GB_BTGA:AC010086	187240	AC010086	Homo sapiens chromosome 3p21.3 clone RPC11-149.D8, *** SEQUENCING IN PROGRESS ***,	Homo sapiens	32,718	21-OCT-1999	
rs01410	597	GB_BTGA:AC010086	187240	AC010086	90 unordered pieces	Homo sapiens	32,718	21-OCT-1999	
rs01411	597	GB_BTGA:AC010086	187240	AC010086	Homo sapiens chromosome unknown clone NH0607007, WORKING DRAFT SEQUENCE, in	Homo sapiens	33,596	29-OCT-1999	
rs01412	597	GB_BTGA:CAJ10319	5398	AD010319	Corynebacterium glutamicum amP, glnB, glnD genes and partial llyx and spp genes	Corynebacterium glutamicum	39,399	14-MAY-1999	
rs01413	597	GB_BTGA:AC010086	187240	AC010086	Drosophila melanogaster, chromosome 3L/7244 clone RPC198-2501, *** SEQUENCING IN	Drosophila melanogaster	33,881	16-OCT-1999	
rs01414	597	GB_BTGA:AC010086	187240	AC010086	PROGRESS ***, 70 unordered pieces	Drosophila melanogaster	33,881	16-OCT-1999	
rs01415	597	GB_BTGA:AC010086	187240	AC010086	Drosophila melanogaster, chromosome 3L/7244 clone RPC198-2501, *** SEQUENCING IN	Drosophila melanogaster	33,881	16-OCT-1999	
rs01416	597	GB_BTGA:AC010086	187240	AC010086	PROGRESS ***, 70 unordered pieces	Drosophila melanogaster	33,881	16-OCT-1999	

TABLE 4: ALIGNMENT RESULTS

na01403_771	GB_BA1/SC8E10	23990	AL106661	Streptomyces coelicolor cosmid BE10.	Streptomyces coelicolor A3(2)	39,136	5-Aug-99
na01403_771	GB_GS512/AC096728	608	AQ366728	mpy00002E022 CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mpy00002E022, genomic survey sequence	Magnaporthe grisea	39,626	06-MAR-1999
na01403_771	GB_BA1/SC8E10	23990	AL106661	Streptomyces coelicolor cosmid BE10	Streptomyces coelicolor A3(2)	41,403	5-Aug-99
na01405_579	GB_PL2/AF11709	52894	AF117109	Oryza sativa subsp. indica Retrosat 1 retrotransposon and Ty3-Gypsy type Retrosat 2 retrotransposon, complete sequences, and uncloned genes	Oryza sativa subsp. indica A3(2)	34,888	26-Apr-99
na01405_579	GB_GS3/BB9780	696	BB9780	RPC11-24L19 TPC RPC1-11 Homo sapiens genomic clone RPC11-24L19, genomic survey sequence	Homo sapiens	37,204	9-Apr-99
na01409_845	GB_STS/G52436	696	G52436	SHGC-85004 Human Homo sapiens STS genomic, sequence tagged site	Homo sapiens	37,204	25-Jun-99
na01409_845	GB_STS/AC008019	190459	AC008019	Mus musculus, *** SEQUENCING IN PROGRESS ***; 16 unoriented pieces	Mus musculus	39,924	16-Nov-99
na01409_845	GB_PRR/AC006238	127993	AC006238	Homo sapiens chromosome 17, clone HCT1162.E.12, complete sequence	Homo sapiens	33,807	29-DEC-1998
na01413_723	GB_HTG5/AC006819	190459	AC006819	Mus musculus, *** SEQUENCING IN PROGRESS ***; 16 unoriented pieces	Mus musculus	39,924	16-Nov-99
na01413_723	GB_OV2/AC008477	1617	AC008477	Anykatorina ligumini vel cone virus pigment mRNA, complete cds	Anykatorina ligumini	39,819	19-DEC-1998
na01413_723	GB_OV2/AC008477	1617	AC008477	Anykatorina ligumini vel cone virus pigment mRNA, complete cds	Anykatorina ligumini	39,819	19-DEC-1998
na01413_723	GB_PRR/AC002658	102084	AC002658	Homo sapiens chromosome 17, clone RPCHS7C24, complete sequence	Homo sapiens	38,820	14-Jun-98
na01414_630	GB_PL1/SC2610	37730	Z36860	S. cerevisiae chromosome IX sequence derived from lambda clones 5610-5004	Saccharomyces cerevisiae	38,782	20-Aug-97
na01414_630	GB_PL1/VSCDIN1	2669	MS8012	S. cerevisiae rbcuonucleotide reductase DNA damage-inducible regulatory subunit (DIN1) gene, 5' end	Saccharomyces cerevisiae	35,877	27-Apr-93
na01417_720	GB_EST18/AA689161	624	AA689161	ET1200 Trypanosoma brucei rhodesiense ZAP II library Trypanosoma brucei rhodesiense cDNA 5', mRNA sequence	Trypanosoma brucei rhodesiense	37,150	15-DEC-1997
na01417_720	GB_PL1/SC8419	30507	Z48701	S. cerevisiae chromosome IV cosmid 8419	Saccharomyces cerevisiae	36,248	11-Aug-97
na01417_720	GB_PL1/SCPR2863	2452	X56934	S. cerevisiae PRP29 gene	Saccharomyces cerevisiae	45,036	9-Feb-95
na01421	GB_BA1/BACPEFFA	4654	M20035	B. subtilis bacillopeptidase F (bpf) gene, complete cds	Bacillus subtilis	37,324	06-MAR-1995
na01422_1095	GB_EST74/AA03392	344	AU03392	AU03392 Dicyostelium discoideum SL (H1 Unisthara) Dicyostelium discoideum cDNA, clone SL4715, mRNA sequence	Dicyostelium discoideum	38,953	28-Apr-99
na01422_1095	GB_EST14/AA399243	301	AA399243	28Y002.01 Staphylococcus aureus T1T Homo sapiens cDNA clone IMAGE 726455.3 similar to HMO1000, P14-43 NIDOCEN PRECURSOR, mRNA sequence	Homo sapiens	45,183	12-Aug-97
na01425_1008	GB_PRR/AC002037	53957	AC002037	Homo sapiens chromosome 11 Oncodysplasia Corneal cDNA Library, complete sequence	Homo sapiens	37,500	6-Aug-97
na01425_1008	GB_PRR/AC005008	18501	AC005008	Homo sapiens 12n13.3 BAC RPC11-476M19 (Roswell Park Cancer Institute Human BAC Library) complete sequence	Homo sapiens	34,410	20-Jan-99
na01425_1008	GB_PRR/AF11169	183016	AF11169	Homo sapiens chromosome 14 BAC containing gene for KIAA0759 and other possible new transcripts, complete sequence	Homo sapiens	40,635	19-Jul-99
na01429_741	GB_HTG5/AC008284	146797	AC008284	Drosophila melanogaster chromosome 3 clone BACR03M22 (D1000) RPC148.03 M22 map 96C-96D strain Y, c1 bw, s, *** SEQUENCING IN PROGRESS ***; 137 unoriented pieces	Drosophila melanogaster	35,822	2-Aug-99
na01429_741	GB_EST75/AA300084	635	A1000084	qf59002.x1 NCL CGAP, Kld6 Homo sapiens cDNA clone IMAGE 190255.3, mRNA sequence	Homo sapiens	37,353	1-Feb-99
na01429_741	GB_EST18/AF106612	949	AF106612	atb2602.x1 Soares_papillom, tumor, NHPA Homo sapiens cDNA clone 1239938.3, mRNA sequence	Homo sapiens	37,361	12-Jan-99
na01434_3075	GB_STS/AB187084	598	AB187084	wf7907.x1 NCL CGAP, Lnt8 Homo sapiens cDNA clone IMAGE 2408796.3, mRNA sequence	Homo sapiens	38,627	24-Aug-99
na01434_3075	GB_PL1/CAC46C10	37825	AL033467	Calbicans cosmid CAC46C10	Candida albicans	34,724	10-Nov-98
na01434_3075	GB_GS3/B10423	1217	B10423	F19F22-77 GF Arabidopsis thaliana genomic clone F19F22, genomic survey sequence	Arabidopsis thaliana	36,003	14-MAY-1997
na01434_3075	GB_PL1/CAC46C10	37825	AL033467	Calbicans cosmid CAC46C10	Candida albicans	33,794	10-Nov-98

Caenorhabditis elegans chromosome I clone Y47H9, *** SEQUENCING IN PROGRESS ***, in

[illegible]

TABLE 4: ALIGNMENT RESULTS

na01686_584	GE_EST35:AV156415_240	AV156415	Mus musculus head C57BL/6J 12-day embryo Mus musculus cDNA clone 300005G04, mRNA sequence	Mus musculus	40,417	7-Jul-99
	GE_GSS15:AQ11516_597	AQ11518	HS_584_B2_H01_17A RPKC-11 Human Male BAC Library	Homo sapiens	41,148	15-Jun-99
	GE_BA1:PDORAB	Z4818	Pile-660 Col-2 Row-P genomic survey sequence	Brevimontia dimidiata	36,709	15-Aug-95
na01693_1545	GE_INT:CEP4686	Z70780	P. ommidua iOA and iOB genes for inositoline 1-oxidoeductase	Caenorhabditis elegans	38,556	04-DEC-1988
	GE_EST5:L43364	L44364	Caenorhabditis elegans cosmid F4686, complete sequence	Homo sapiens	38,135	17-Jan-96
	GE_PR2:AF009262	AJ229494	HUMEST1G5 Human Tlymua NSTH II Homo sapiens cDNA, mRNA sequence	Homo sapiens	46,809	17-Aug-97
na01694_1023	GE_BA1:GSA224948	AJ229494	Homo sapiens clone FBF3 Cn-du-clat human mRNA	Corynebacterium	100,000	11-Aug-98
	GE_EST7:W22650	W22650	Corynebacterium glutamicum DNA for L-Malate quinone oxidoreductase	glutamicum	37,538	06-MAY-1986
	GE_PRR4:AC005343	AC005343	7182 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional, mRNA sequence	Homo sapiens	38,048	2-Apr-99
na01696_1302	GE_BA1:MSCB1280C3_38985	L78824	BAC library complete sequence 12p13.3 BAC RPKC11.2/K20 (Roswell Park Cancer Institute Human BAC library) complete sequence	Mycobacterium leprae	67,442	15-Jun-96
	GE_BA1:SCA46	42832	Mycobacterium leprae H37Rv DNA sequence	Streptomyces coelicolor	68,021	24-MAR-1989
	GE_BA1:MTU003	13246	Streptomyces coelicolor cosmid B45	Myxobolus	38,602	17-Jun-96
na01697_1080	GE_PL2:HNHNAHR	2559	Mycobacterium tuberculosis H37Rv, complete genome, segment 125/162	Helianthus annuus	38,257	02-OCT-1997
	GE_PL2:HNHNAHR	2559	Helianthus annuus homeodomain protein 1, mRNA, complete cds	Helianthus annuus	37,198	02-OCT-1997
na01701_472	GE_BA2:AF069748	2103	Helianthus annuus homeodomain protein 1, mRNA, complete cds	Pseudomonas chlororaphis	38,130	4-Apr-99
	GE_BA2:AF069748	2103	Pseudomonas chlororaphis polyurethanase esterase A (pueA) gene, complete cds	Pseudomonas chlororaphis	40,271	4-Apr-99
na01703_1268	GE_BA1:CGFDA	3371	Pseudomonas chlororaphis polyurethanase esterase A (pueA) gene, complete cds	Corynebacterium	100,000	12-Sep-93
	GE_EST19:A4728419	340	Corynebacterium glutamicum ftsA gene for fructose-bisphosphate aldolase (EC 4.1.2.13)	glutamicum	38,176	5-Jan-98
na01706_555	GE_PL2:Z439	93539	33598 CD4-5 Arabidopsis thaliana cDNA clone K2CRRP, mRNA sequence	Arabidopsis thaliana	33,381	21-Jul-97
	GE_OV:F03935	93539	Arabidopsis thaliana chromosome II BAC T00220 genomic sequence, complete sequence	Arabidopsis thaliana	37,917	9-Jun-96
	GE_EST5:H85355	535	Galus gallus T-box protein 4 (TBX4) mRNA, complete cds	Galus gallus	38,735	14-Nov-95
na01711_1281	GE_EST38:AR29867	427	y8800411 Soares retina N20bHR Homo sapiens cDNA clone IMAGE221682.5, mRNA sequence	Homo sapiens	40,299	26-Aug-99
	GE_GSS10:AQ217798	441	HS_2007_A1_A04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Pile-2007 Col-2 Row-A, genomic survey sequence	Homo sapiens	38,292	19-Sep-98
	GE_PAT:E09055	2053	Human DNA sequence from clone 570L12 on chromosome Xq13.1-21.1. Contains the PGK1 gene for phosphoglycerate kinase 1, the gene for a novel protein similar to TAF2G (TATA box binding protein) (TBP-associated factor, RNA polymerase II, G. 324D) (TAF101), EST's, STS, GSSs and a putative CpG island, complete sequence.	Xanthomonas oryzae	38,475	28-Sep-97
na01714	GE_PR3:HS570L12	143508	Human DNA sequence from clone 570L12 on chromosome Xq13.1-21.1. Contains the PGK1 gene for phosphoglycerate kinase 1, the gene for a novel protein similar to TAF2G (TATA box binding protein) (TBP-associated factor, RNA polymerase II, G. 324D) (TAF101), EST's, STS, GSSs and a putative CpG island, complete sequence.	Homo sapiens	38,292	23-Nov-99
na01715_819	GE_BA1:MTCY441	35187	Streptomyces coelicolor cosmid B65	Mycobacterium	36,216	18-Jun-98
	GE_BA1:SC165	14866	Streptomyces coelicolor cosmid B65	Myxobolus	58,807	11-MAY-1988
	GE_BA1:MSGB19:2C5_38503	L71538	M. leprae genomic DNA sequence, cosmid 01912	Streptomyces coelicolor	55,651	14-Jun-96
na01729_642	GE_BA2:CONCALS15_2221	MI69531	Corynebacterium glutamicum beta C-S lyase (aeoD) and branched-chain amino acid uptake carrier (aeoC) genes, complete cds, and hypothetical protein Y19w (Y19w) gene, partial cds.	Corynebacterium glutamicum	41,993	4-Jun-98

TABLE 4: ALIGNMENT RESULTS

	31806	U19103	Saccharomyces cerevisiae chromosome XII cosmid 8039.		Saccharomyces cerevisiae	37,685	22-Aug-97
na01754							
na01760	405	34037	GB_PL2.YSCL8039	GB_INT1.CELF43C9	Caenorhabditis elegans cosmid F43C9	40,345	16-Nov-95
		34037		GB_INT1.CELF43C9	Caenorhabditis elegans cosmid F43C9	35,484	16-Nov-95
		3405		GB_ROMUSOPF9	Mouse osteopontin gene, 5' flanking region	35,264	4-Feb-99
na01761	4587	133863	GB_PRR4.AC004600	GB_PRR4.AC004600	Homo sapiens chromosome 15q11-q13 PAC clone PDJ27301 containing Angelman Syndrome gene (UBE3A), complete sequence	37,037	11-MAR-1999
		118664	GB_PRR3.AC004259	AC004259	Human Chromosome 15q11-q13 PAC clone PDJ1412 containing Angelman Syndrome gene (UBE3A), complete sequence	37,037	3-Jun-98
		133863	GB_PRR4.AC004600	AC004600	Homo sapiens Chromosome 15q11-q13 PAC clone PDJ27301 containing Angelman Syndrome gene (UBE3A), complete sequence	35,995	11-MAR-1999
na01765	1065	370	GB_EST31.AB64883	AB64883	gb:EST31.NC004533.1 Caenorhabditis elegans cDNA clone IMAGE 244755.9, mRNA sequence m347.005.11 SwissProt: G05NMU16.5 Mammalian chromosome 15q11-q13 similar to protein 25 (MUSEL), mRNA sequence	35,566	3-Sep-96
		341	WB8857	WB8857	gb:Z23090.1 HEAT SHOCK 27 KD PROTEIN (HUMAN), gb:111639 Mus musculus heat shock protein 25 (MUSEL), mRNA sequence	37,353	
na01767	588	40997	GB_INT1.CELC39D10	U39878	Caenorhabditis elegans cosmid C39D10	39,590	2-Nov-95
		21721	GB_INT1.CEF16H9	Z50005	Caenorhabditis elegans cosmid F16H9, complete sequence	39,687	2-Sep-99
		32063	GB_INT1.CECCA	Z81490	Caenorhabditis elegans cosmid CCA, complete sequence	35,084	2-Sep-99
		156162	GB_HTG1.CEY26D4	AL022595	Caenorhabditis elegans chromosome I clone Y26D4, *** SEQUENCING IN PROGRESS ***, in unordered pieces	33,276	7-Sep-99
na01768							
na01769	554	130818	GB_HTG4.AC010034	AC010034	Drosophila melanogaster clone RPO188-4C3, *** SEQUENCING IN PROGRESS ***, 63 unordered pieces	35,740	16-OCT-1999
		130818	GB_HTG4.AC010034	AC010034	Drosophila melanogaster clone RPO188-4C3, *** SEQUENCING IN PROGRESS ***, 63 unordered pieces	35,740	16-OCT-1999
na01770	3888	360	GB_EST1.D08647	D08647	gb:K0352ZF.Yui Kohara unpublished cDNA Caenorhabditis elegans cDNA clone yK352Z.5', mRNA sequence	37,870	8-Aug-94
		4692	GB_INT1.SUSEND018C	L34680	Strongylocentrotus purpuratus calcium-binding protein (enr16) mRNA, complete cds	39,337	21-Jun-94
		535	GB_EST31.AF121178	AF121178	Strongylocentrotus purpuratus purpuratus	39,620	24-MAY-1999
		5134	GB_PRR1.AB011149	AB011149	AF121178 Homo sapiens liver (Chang L-Y) Homo sapiens cDNA clone PTT1A2.2, mRNA sequence	38,270	10-Apr-98
na01771	825	2936	GB_BA1.CGPRPOEN	Y12337	Homo sapiens mRNA for KIAA0677 protein, complete cds	100,000	17-Nov-98
		545	GB_EST33.A1778471	A1778471	C glutamicum proP gene.	41,187	26-Jun-99
		37714	GB_INT1.CET11F9	Z74042	EST259350 tomato susceptible, Cornell Lycopersicon esculentum cDNA clone cLES5M16, mRNA sequence	38,077	23-Nov-98
na01773	600	46387	GB_HTG3.U82212	U82212	Caenorhabditis elegans cosmid T11F9, complete sequence	42,142	09-DEC-1998
		46387	GB_HTG3.U82212	U82212	Homo sapiens chromosome 10 clone LA10NC01.23, C_3 map 10g28 1-10g28 2, *** SEQUENCING IN PROGRESS ***, 1 ordered pieces	42,142	09-DEC-1998
		46387	GB_HTG3.U82212	U82212	Homo sapiens chromosome 10 clone LA10NC01.23, C_3 map 10g28 1-10g28 2, *** SEQUENCING IN PROGRESS ***, 1 ordered pieces	37,748	09-DEC-1998
na01774	849	228174	GB_HTG1.HSA55TH15	AL076590	Homo sapiens chromosome 10 clone LA10NC01.23, C_3 map 10g28 1-10g28 2, *** SEQUENCING IN PROGRESS ***, 1 ordered pieces	38,054	23-Nov-99
					Homo sapiens chromosome 6 clone RP11-557H15, *** SEQUENCING IN PROGRESS ***, in unordered pieces		

TABLE 4: ALIGNMENT RESULTS

ra01775	887	GB_H1C1:HS4557H15	128174	AL078390	U00030	335600	131427	Z38747	Human DNA sequence from clone 3718 on chromosome 1p38.2-36.3. Contains a putative novel gene, ESTs and GSSs, complete sequence	Homo sapiens	38,054	23-Nov-96
ra01776	1575	GB_PR3:HS3718							Saccharomyces cerevisiae	Saccharomyces cerevisiae	39,110	2-Sep-97
ra01777	582	GB_H1G2:AC007475	185087	AC007475	AC000505				Drosophila melanogaster chromosome 2 clone BACRO4E21 (D592) RPOI-08 E 21 map, 49A-48B	Homo sapiens	35,038	23-Nov-99
ra01778	1260	GB_PR3:AC007475	185087	AC007475	AC000505				Drosophila melanogaster chromosome 2 clone BACRO4E21 (D592) RPOI-08 E 21 map, 49A-48B strain y, on bw sp. *** SEQUENCING IN PROGRESS ***	Drosophila melanogaster	37,333	2-Aug-99
ra01779	1542	GB_GSS10:QA174954	4132	QA174954	AC002881				49B strain y, on bw sp. *** SEQUENCING IN PROGRESS ***	Drosophila melanogaster	37,333	2-Aug-99
ra01780	408	GB_GSS8:AC038759	670	AC038759	AC003875				HS_321T_B2_C03_MIR_C01 Approved Human Genomic Sperm Library D Homo sapiens genomic clone P146-3211 Col-04 Row-E, genomic survey sequence.	Homo sapiens	43,171	17-OCT-1988
ra01781	384	GB_GSS14:HS4557H15	128174	AL078390	U00030	335600	131427	Z38747	H sapiens FGH gene.	Homo sapiens	41,166	15-Feb-95
ra01782	519	GB_PR1:HS6746	1032	X53705	AC000505				Human PAC clone from X223, complete sequence	Homo sapiens	35,080	14-Nov-96
ra01783	360	GB_PR2:HSAC000055	83578	AC000505	AC000505				Combinatorial intorsion P1L5 cryptic plasmid pP11, complete sequence	Comamonas testaceoloni	37,805	30-Nov-99
ra01784	582	GB_PR2:AF070397	13388	AF070397	AF070397				Comamonas testaceoloni P1L5 cryptic plasmid pP11, complete sequence	Comamonas testaceoloni	35,529	30-Nov-99
ra01785	1260	GB_PR3:AC002881	153568	AC002881	AC002881				Homo sapiens X223 BAC G52710412 (Genome Systems) complete sequence	Homo sapiens	37,305	22-Jan-98
ra01786	1542	GB_PR1:HS4557H15	128174	AL078390	U00030	335600	131427	Z38747	HS_321T_B2_C03_MIR_C01 Approved Human Genomic Sperm Library D Homo sapiens genomic clone P146-3211 Col-04 Row-E, genomic survey sequence.	Homo sapiens	37,305	14-MAY-1988
ra01787	816	GB_PR1:HS4557H15	128174	AL078390	U00030	335600	131427	Z38747	HS_321T_B2_C03_MIR_C01 Approved Human Genomic Sperm Library D Homo sapiens genomic clone P146-3211 Col-04 Row-E, genomic survey sequence.	Homo sapiens	37,305	14-MAY-1988
ra01788	408	GB_GSS8:AC038759	670	AC038759	AC003875				HS_321T_B2_C03_MIR_C01 Approved Human Genomic Sperm Library D Homo sapiens genomic clone P146-3211 Col-04 Row-E, genomic survey sequence.	Drosophila melanogaster	40,212	21-Nov-96
ra01789	1542	GB_GSS14:HS4557H15	128174	AL078390	U00030	335600	131427	Z38747	HS_321T_B2_C03_MIR_C01 Approved Human Genomic Sperm Library D Homo sapiens genomic clone P146-3211 Col-04 Row-E, genomic survey sequence.	Homo sapiens	38,000	7-Jul-99
ra01790	408	GB_GSS8:AC038759	670	AC038759	AC003875				HS_321T_B2_C03_MIR_C01 Approved Human Genomic Sperm Library D Homo sapiens genomic clone P146-3211 Col-04 Row-E, genomic survey sequence.	Mus musculus	36,907	30-Apr-99
ra01791	384	GB_GSS8:AC038759	670	AC038759	AC003875				HS_321T_B2_C03_MIR_C01 Approved Human Genomic Sperm Library D Homo sapiens genomic clone P146-3211 Col-04 Row-E, genomic survey sequence.	Homo sapiens	32,845	11-Jul-98
ra01792	519	GB_GSS14:HS4557H15	128174	AL078390	U00030	335600	131427	Z38747	HS_321T_B2_C03_MIR_C01 Approved Human Genomic Sperm Library D Homo sapiens genomic clone P146-3211 Col-04 Row-E, genomic survey sequence.	Homo sapiens	39,474	11-Jul-98
ra01793	360	GB_GSS14:HS4557H15	128174	AL078390	U00030	335600	131427	Z38747	HS_321T_B2_C03_MIR_C01 Approved Human Genomic Sperm Library D Homo sapiens genomic clone P146-3211 Col-04 Row-E, genomic survey sequence.	Caenorhabditis elegans	39,314	25-Sep-97
ra01794	582	GB_GSS14:HS4557H15	128174	AL078390	U00030	335600	131427	Z38747	HS_321T_B2_C03_MIR_C01 Approved Human Genomic Sperm Library D Homo sapiens genomic clone P146-3211 Col-04 Row-E, genomic survey sequence.	Oryza sativa	36,053	2-Jun-99
ra01795	609	GB_GSS14:HS4557H15	128174	AL078390	U00030	335600	131427	Z38747	HS_321T_B2_C03_MIR_C01 Approved Human Genomic Sperm Library D Homo sapiens genomic clone P146-3211 Col-04 Row-E, genomic survey sequence.	Human adenovirus type 19a	38,024	9-Jul-97
ra01796	519	GB_GSS14:HS4557H15	128174	AL078390	U00030	335600	131427	Z38747	HS_321T_B2_C03_MIR_C01 Approved Human Genomic Sperm Library D Homo sapiens genomic clone P146-3211 Col-04 Row-E, genomic survey sequence.	Drosophila melanogaster	38,372	21-Apr-95
ra01797	816	GB_GSS14:HS4557H15	128174	AL078390	U00030	335600	131427	Z38747	HS_321T_B2_C03_MIR_C01 Approved Human Genomic Sperm Library D Homo sapiens genomic clone P146-3211 Col-04 Row-E, genomic survey sequence.	Drosophila melanogaster	35,992	17-Jul-98
ra01798	360	GB_GSS14:HS4557H15	128174	AL078390	U00030	335600	131427	Z38747	HS_321T_B2_C03_MIR_C01 Approved Human Genomic Sperm Library D Homo sapi			

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TABLE 4: ALIGNMENT RESULTS

GB_GSS13/AQ48614	532	AQ48614	HS_3118_B2_F05_SPE RPL-11 Human Male BAC Library Homo sapiens genomic clone Plate-894 Col-10 Row-L genomic survey sequence	39,228	28-Apr-99	Homo sapiens
GB_BA1MTV029	3279	AL021427	Mycobacterium tuberculosis H37Rv complete genome, segment 1162	39,229	17-Jun-98	Mycobacterium tuberculosis
GB_BA1MITORREP	8400	X92504	M tuberculosis origin of replication and genes rnpA, rnpH, dnaA, dnaN, rnf	36,328	28-Aug-97	Mycobacterium tuberculosis
GB_GSS4/AQ272462	783	AQ272462	HS_5474_A1_C07_TTHAS_5474_A1 RPL-11 Human Male BAC Library Homo sapiens genomic clone Plate-100 Col-13 Row-M genomic survey sequence	39,451	15-Jun-99	Homo sapiens
GB_EST37/M835428	438	A935428	w854022.X1.C01.G3P.Jd11 Homo sapiens cDNA clone IMAGE 2462019 3' similar to U00185 c00185 SMALL ACIDIC PROTEIN 1; mRNA sequence	39,877	2-Sep-99	Homo sapiens
GB_GSS11/AQ28301	621	AQ28301	CTBIE1-250616.1F CTBIE1 Homo sapiens genomic clone 220616, genomic survey	45,556	27-OCT-1998	Homo sapiens
GB_HTG2/AC007596	199300	AC007596	Homo sapiens chromosome 16 clone 16B86, *** SEQUENCING IN PROGRESS ***; 42 unoriented pieces	37,572	20-MAY-1999	Homo sapiens
GB_PL2/ATA/C004521	104797	AC004521	Arabidopsis thaliana chromosome II BAC F41; genomic sequence, complete sequence	43,637	13-MAY-1998	Arabidopsis thaliana
GB_GSS13/AQ36125	508	AQ36125	HS_5049_B2_C12_77A RPL-11 Human Male BAC Library Homo sapiens genomic clone Plate-825 Col-2 Row-N genomic survey sequence	32,782	31-MAR-1999	Homo sapiens
GB_GSS12/AQ34210	674	AQ34210	RPL-11-121E5.TJ RPL-11 Homo sapiens genomic clone RPL-11-121E5, genomic survey sequence	37,269	06-MAY-1999	Homo sapiens
GB_STS/KLAJ9905	178	AJ229905	Kluyveromyces fragilis DNA fragment for sequence tagged site, clone olam560r	42,697	20-Nov-98	Kluyveromyces fragilis
GB_STS/KLAJ9905	178	AJ229905	Kluyveromyces fragilis DNA fragment for sequence tagged site, clone olam560r	42,697	20-Nov-98	Kluyveromyces fragilis
GB_GSS15/AQ61236	472	AQ61236	HS_5121_A2_D09_SPE RPL-11 Human Male BAC Library Homo sapiens genomic clone Plate-897 Col-18 Row-G genomic survey sequence	40,885	15-Jun-99	Homo sapiens
GB_GSS3/B2315	613	B2315	RPL-11-6J10.TV RPL-11 Homo sapiens genomic clone RPL-11-6J10, genomic survey sequence	40,164	9-Apr-99	Homo sapiens
GB_PP2/CNS00008	198287	AL049629	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-124D2 of RPL-11 library from chromosome 14 of Homo sapiens (Human), complete sequence	33,621	27-OCT-1999	Homo sapiens
GB_OV/A601393	4329	AF001393	Oryzias latipes Medaka OG-12 (MOG-12) mRNA, complete cds	35,511	30-Sep-99	Oryzias latipes
GB_GSS15/AQ44157	665	AQ44157	RPL-11-29012.TV RPL-11-29012 RPL-11 Homo sapiens genomic clone RPL-11-29012, genomic survey sequence	39,894	8-Jul-99	Trypanosoma brucei
GB_GSS15/AQ68704	685	AQ68704	Sheared DNA-24C24.TR Sheared DNA Trypanosoma brucei genomic clone Sheared DNA-24C24, genomic survey sequence	37,110	23-Jun-99	Trypanosoma brucei
GB_OV/GJ025125	6418	U25125	Gallus gallus protoporphyrin gene, complete cds	40,584	06-MAY-1995	Gallus gallus
GB_PP3/HS04045	119737	AL035695	Human DNA sequence from clone 4A4G5 on chromosome 1:25 2. Contains part of a human estrogen receptor gene, STSs and GSSs, complete sequence	34,793	23-Nov-99	Homo sapiens
GB_PP1/HSPT1CHG	8545	X82818	H sapiens PTP-10HCP gene	35,531	26-Jun-97	Homo sapiens
GB_PP3/HS04045	119737	AL035695	Human DNA sequence from clone 4A4G5 on chromosome 1:25 2. Contains part of a human estrogen receptor gene, STSs and GSSs, complete sequence	37,058	23-Nov-99	Homo sapiens
GB_HTG3/AC010869	38900	AC010869	Lashmania major chromosome 35 clone L7198 strain Friedin, *** SEQUENCING IN PROGRESS ***; 4 unoriented pieces	40,522	02-OCT-1999	Lashmania major
GB_HTG3/AC010869	38900	AC010869	Lashmania major chromosome 35 clone L7198 strain Friedin, *** SEQUENCING IN PROGRESS ***; 4 unoriented pieces	40,522	02-OCT-1999	Lashmania major
GB_OM/SSU12674	2190	U12574	Sus scrofa myogenic regulatory factor MyoD (myod) gene, complete cds	37,088	10-Feb-96	Sus scrofa
GB_PP1/CP2PVC	22172	L48605	Bacteriophage c2 complete genome	39,747	14-MAR-1996	Lactococcus lactis
GB_EST39/AN068009	641	AN068009	887004F38 p1 687 - Early embryo from Delaware Zea mays cDNA, mRNA sequence	40,000	12-OCT-1999	Zea mays
GB_PP1/CP2PVC	22172	L48605	Bacteriophage c2 complete genome	39,867	14-MAR-1996	Lactococcus lactis

TABLE 4: ALIGNMENT RESULTS

rs01623	873	GB_HTG2-A0020317	94832	AC02317	Homo sapiens chromosome 17 clone H017H10 map 17, *** SEQUENCING IN PROGRESS ***	8	Homo sapiens	37,012	20-Feb-98
		GB_HTG2-A0020317			unordered pieces				
		GB_BA1-G09844	29782	AC00644	Caenorhabditis elegans clone Y108G3Y, *** SEQUENCING IN PROGRESS ***	4	unordered pieces	37,176	24-Feb-99
		GB_HTG2-A00644	29782	AC00644	Caenorhabditis elegans clone Y108G3Y, *** SEQUENCING IN PROGRESS ***	4	unordered pieces	37,176	24-Feb-99
		GB_BA1-EC00W76	225419	U00039	E. coli chromosomal region from 76 to 0.815 minutes		Escherichia coli	38,902	7-Nov-96
		GB_BA1-G09844	2164	X95890	C. glutamicum parB, parC & xylB genes		Corynebacterium glutamicum	100,000	11-MAY-1997
		GB_HTG2-A007598	248427	AC007598	Homo sapiens chromosome 16 clone 16S91, *** SEQUENCING IN PROGRESS ***	105	Homo sapiens	38,469	20-MAY-1999
		GB_HTG2-A007598	248427	AC007598	Homo sapiens chromosome 16 clone 16S91, *** SEQUENCING IN PROGRESS ***	105	Homo sapiens	38,469	20-MAY-1999
		GB_INT-CEH1219	37427	Z98851	Caenorhabditis elegans cosmid H1219, complete sequence		Caenorhabditis elegans	32,793	18-DEC-1998
		GB_HTG1-CEY37A1	316170	Z83243	Caenorhabditis elegans chromosome IV clone Y37A1, *** SEQUENCING IN PROGRESS ***	in	Caenorhabditis elegans	32,793	03-DEC-1998
		GB_HTG1-CEY37A1	316170	Z83243	Caenorhabditis elegans chromosome IV clone Y37A1, *** SEQUENCING IN PROGRESS ***	in	Caenorhabditis elegans	32,793	03-DEC-1998
		GB_EST25-A1313027	520	A1313027	u98H06.x1 Sugano mouse kidney mRna Mus musculus cDNA clone IMAGE 1822267 3' similar to TR-00947 00947 COMPLEMENT COMPONENT 3A RECEPTOR 1, mRNA sequence.		Mus musculus	41,148	17-DEC-1998
		GB_RO-AF03757	8308	AF03757	Mus musculus complement C3a anaphylatoxin receptor (C3ar) gene, complete cds		Mus musculus	38,649	30-Jun-98
		GB_RO-BMUJ7461	2857	U77461	Mus musculus anaphylatoxin C3a receptor gene, complete cds		Mus musculus	38,649	28-MAY-1997
		GB_BA1-BRLPTSQ	3163	L18875	Brevibacterium lactofermentum phosphoenolpyruvate sugar phosphotransferase (psG) gene, complete cds		Brevibacterium lactofermentum	67,407	01-OCT-1993
		GB_BA1-CORP7SMA	2656	L18874	Corynebacterium glutamicum phosphoenolpyruvate sugar phosphotransferase (psG) mRNA, complete cds		Corynebacterium glutamicum	100,000	24-Nov-94
		GB_BA1-CORP7SMA	2656	L18874	Corynebacterium glutamicum phosphoenolpyruvate sugar phosphotransferase (psG) mRNA, complete cds		Corynebacterium glutamicum	37,008	24-Nov-94
		GB_HTG2-A004840	162485	AC004840	Homo sapiens clone U0607.02, *** SEQUENCING IN PROGRESS ***	12	unordered pieces	38,287	12-Jun-98
		GB_HTG2-A004840	162485	AC004840	Homo sapiens clone U0607.02, *** SEQUENCING IN PROGRESS ***	12	unordered pieces	38,287	12-Jun-98
		GB_V1-MC06315	190269	U06315	Molluscum contagiosum virus subtype 1, complete genome		Molluscum contagiosum virus subtype 1	37,650	17-Aug-98
		GB_GSS15-A0632158	445	A0632158	RPCL11-47387.T1 RPCL11-Homo sapiens genomic clone RPCL11-47387, genomic survey		Homo sapiens	38,095	17-Jun-99
		GB_GSS15-A0632158	445	A0632158	RPCL11-47387.T1 RPCL11-Homo sapiens genomic clone RPCL11-47387, genomic survey		Homo sapiens	40,275	17-Jun-99
		GB_EST16-C35275	300	C35275	C35275.Yuj Kohara unpublished cDNA Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone x44766.3, mRNA sequence.		Caenorhabditis elegans	37,688	18-OCT-1999
		GB_INT-CEL239H12	42835	U23169	Caenorhabditis elegans cosmid C239H12		Caenorhabditis elegans	34,477	13-Jul-95
		GB_GS1-CNS00GP0	1101	A1072364	Drosophila melanogaster genome survey sequence Tr and of BAC BACR33008 of RPCL98 library from Drosophila melanogaster (fruit fly), genomic survey sequence		Drosophila melanogaster	34,321	3-Jun-99
		GB_PRR1-HSL1RECA	12565	X94532	H sapiens gene for interleukin-1 receptor antagonist		Homo sapiens	42,079	25-Jun-97
		GB_PRR3-HS06590	33414	U6590	Homo sapiens IL-1 receptor antagonist IL-1Ra (IL-1RN) gene, alternatively spliced forms, complete cds.		Homo sapiens	42,079	21-DEC-1997
		GB_GSS15-A0293877	476	A0293877	HS_2254_A2_C03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone P1ater-2254 Colred Royce, genomic survey sequence		Homo sapiens	38,772	15-DEC-1998
		rs01656							
		rs01690							

TABLE 4: ALIGNMENT RESULTS

rx01961	603	GB_BA2	U67460	12589	U67460	Methanococcus jannaschii	section 2 of 150 of the complete genome	28-Jan-98	36,013	Methanococcus jannaschii
rx01962	893	GB_BA2	U67460	12589	U67460	LP04729 3prime LP	Drosophila melanogaster larval-early pupal pOT2 Drosophila melanogaster cDNA clone LP04729 3prime, mRNA sequence	17-Nov-98	39,130	Drosophila melanogaster
rx01963	784	GB_PR4	AC005397	91460	AC005397	HP08371 3prime LP	Drosophila melanogaster larval-early pupal pOT2 Drosophila melanogaster cDNA clone LP08371 3prime, mRNA sequence	01-DEC-1998	38,940	Drosophila melanogaster
rx01964	1426	GB_GSS13	AQ465174	437	AQ465174	Methanococcus jannaschii	section 2 of 150 of the complete genome	28-Jan-98	34,795	Methanococcus jannaschii
rx01965	784	GB_PR4	AC005397	91460	AC005397	Methanococcus jannaschii	section 2 of 150 of the complete genome	28-Jan-98	37,666	Methanococcus jannaschii
rx01966	684	GB_IN2	AC004283	80095	AC004283	Homo sapiens	Row-E genomic survey sequence	17-Feb-99	35,401	Homo sapiens
rx01969	489	GB_SY	SCU53587	4546	U53587	Homo sapiens	Row-E genomic survey sequence	17-Feb-99	35,401	Homo sapiens
rx01970	489	GB_SY	SCU53587	4546	U53587	Homo sapiens	Row-E genomic survey sequence	17-Feb-99	35,401	Homo sapiens
rx01971	489	GB_SY	SCU53587	4546	U53587	Homo sapiens	Row-E genomic survey sequence	17-Feb-99	35,401	Homo sapiens
rx01972	489	GB_SY	SCU53587	4546	U53587	Homo sapiens	Row-E genomic survey sequence	17-Feb-99	35,401	Homo sapiens
rx01973	489	GB_SY	SCU53587	4546	U53587	Homo sapiens	Row-E genomic survey sequence	17-Feb-99	35,401	Homo sapiens
rx01974	1008	GB_PL1	SC0320A	24000	Z68829	S cerevisiae	chromosome IV cosmid 9320A	11-Aug-97	36,528	Saccharomyces cerevisiae
rx01975	1008	GB_PL1	SC0320X	22253	Z70202	S cerevisiae	chromosome IV cosmid 9320X	11-Aug-97	36,528	Saccharomyces cerevisiae
rx01976	1008	GB_PL4	AC068210	186986	AC068210	Homo sapiens	Xp22:150 BAC GSHP-309P15 (Genome Systems Human BAC Library) complete sequence	31-DEC-1998	38,351	Homo sapiens

TABLE 4: ALIGNMENT RESULTS

na02006	595	GB_HTG3 AC011491	162134	AC011491	161 undordered pieces	Homio sapiens chromosome 19 clone C1978SK9_180A7, *** SEQUENCING IN PROGRESS ***	Homio sapiens	37,383	07-OCT-1999
		GB_HTG3 AC011357	160676	AC011357	161 undordered pieces	Homio sapiens chromosome 5 clone C17-HSPC_362D12, *** SEQUENCING IN PROGRESS ***	Homio sapiens	54,585	09-OCT-1999
		GB_HTG2 AC006901	294136	AC006901	undordered pieces	Caeonhabiditis elegans clone Y74A11X, *** SEQUENCING IN PROGRESS ***	Caeonhabiditis elegans	37,500	26-Feb-99
		GB_HTG2 AC006901	294136	AC006901	undordered pieces	Caeonhabiditis elegans clone Y74A11X, *** SEQUENCING IN PROGRESS ***	Caeonhabiditis elegans	37,500	26-Feb-99
		GB_HTG2 AC006901	294136	AC006901	undordered pieces	Caeonhabiditis elegans clone Y74A11X, *** SEQUENCING IN PROGRESS ***	Caeonhabiditis elegans	36,021	28-Aug-97
na02007	759	GB_BTG1 CEY70C5	224525	Z88978	Caeonhabiditis elegans chromosome V clone Y7005, *** SEQUENCING IN PROGRESS ***	Caeonhabiditis elegans	100,000	01-OCT-1999	
		GB_BTG2 CGU012203	2952	AJ012293	Corynebacterium glutamicum i/o gene	Corynebacterium glutamicum	38,740	13-Nov-99	
		GB_PR4 AC006285	150172	AC006285	Homio sapiens, complete sequence.	Homio sapiens, complete sequence.	38,701	15-Nov-99	
na02009	223	GB_PR4 AC004628	150556	AC004628	Homio sapiens PAC clone D08101069 from Tuz21 1-q21.2, complete sequence	Homio sapiens	38,701	15-Nov-99	
		GB_PR2 AP000953	100000	AP000953	Homio sapiens genomic DNA, segment 21q22.1, segment 2428, complete sequence.	Homio sapiens	38,672	17-Feb-99	
		GB_PR2 AP000953	100000	AP000953	Homio sapiens genomic DNA, segment 21q22.1, GART and AAT, related, SL55A3-A44 region, segment 48, complete sequence.	Homio sapiens	37,674	20-Nov-99	
		GB_BTG1 MTC1237	27030	Z84752	Mycobacterium tuberculosis H37Rv complete genome, segment 48/162	Mycobacterium tuberculosis	37,674	25-Sep-99	
na02013	649	GB_BTG4 AC010085	201581	AC010085	Homio sapiens chromosome unknown clone NH038K23, WORKING DRAFT SEQUENCE, in undordered pieces.	Homio sapiens	39,308	11-Jun-98	
		GB_BTG4 AC010085	201581	AC010085	Homio sapiens chromosome unknown clone NH038K23, WORKING DRAFT SEQUENCE, in undordered pieces.	Homio sapiens	37,206	29-OCT-1999	
na02014	630	GB_HTG3 AC010769	119431	AC010769	Homio sapiens chromosome 15 clone 28_B_17 map 15, LOW-PASS SEQUENCE SAMPLING	Homio sapiens	33,816	22-Sep-99	
		GB_HTG3 AC010769	119431	AC010769	Homio sapiens chromosome 15 clone 28_B_17 map 15, LOW-PASS SEQUENCE SAMPLING	Homio sapiens	33,816	22-Sep-99	
		GB_EST3 AC010769	320	A783738	Id45007 x1 NC1_CGAP_P28 Homio sapiens cDNA clone IMAGE 2253973 3', mRNA sequence	Homio sapiens	37,855	1-Jul-99	
na02019	524	GB_EST19 AA473389	318	AA473389	vd44909 r1 Barstead MPLRB1 Mus musculus cDNA clone IMAGE 803488 5', mRNA sequence	Mus musculus	38,153	18-Jun-97	
		GB_HTG1 CEY102A5_3110000	Z89711		Caeonhabiditis elegans chromosome V clone Y102A5, *** SEQUENCING IN PROGRESS ***	Caeonhabiditis elegans	38,857	9-Jun-98	
		GB_HTG1 CEY102A5_3110000	Z89711		Caeonhabiditis elegans chromosome V clone Y102A5, *** SEQUENCING IN PROGRESS ***	Caeonhabiditis elegans	38,857	9-Jun-98	
na02021	1071	GB_BT1 CGDNAROP	2912	X58985	C glutamicum ORF3 and anrP gene	Corynebacterium glutamicum	99,905	30-Nov-97	
		GB_BT1 CGDAPE	1986	X41379	C glutamicum dapE gene and orf2	Corynebacterium glutamicum	38,406	8-Aug-95	
		GB_BT1 SC7	34983	AL096743	Streptomyces coelicolor cosmid I7	Streptomyces coelicolor	38,782	1-Jul-99	
na02023	891	GB_BT1 CGDAPE	1986	X41379	C glutamicum dapE gene and orf2	Corynebacterium glutamicum	99,884	8-Aug-95	
		GB_PR3 AC004067	161328	AC004067	Homio sapiens chromosome 4 clone B396024 map 4025, complete sequence	Homio sapiens	38,651	8-Nov-98	
		GB_BTG1 CEY100925	145005	AC00925	Mus musculus chromosome 5 clone 388_N_17 map 6, *** SEQUENCING IN PROGRESS ***	Mus musculus	38,215	01-OCT-1999	
na02032	693	GB_PR4 AC006961	171419	AC006961	Homio sapiens chromosome 18, clone RP11-31P16, complete sequence	Homio sapiens	37,703	19-Nov-99	
		GB_PR4 AC006961	171419	AC006961	Homio sapiens chromosome 18, clone RP11-31P16, complete sequence	Homio sapiens	40,839	19-Nov-99	
na02038	504	GB_PR2 HSD179963	127639	AL078524	Human DNA sequence from clone RP427963 on chromosome 14q21 11-42, 3, complete sequence	Homio sapiens	35,557	22-Nov-99	
		GB_BT1 AOPC2A391	37941	A223998	Anycotolaps orientalis cosmid PC2A391	Anycotolaps orientalis	46,341	29-MAR-1999	
		GB_PL1 ATDNADL1	8747	Y14851	Anabropsis italiana dsl1 gene	Anabropsis italiana	33,223	23-Sep-97	
na02039	863	GB_PR3 AC005698	151970	AC005698	Homio sapiens chromosome 5, BAC clone 203013 (LBN1.H15), complete sequence	Homio sapiens	37,176	4-Sep-98	

TABLE 4: ALIGNMENT RESULTS

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TABLE 4: ALIGNMENT RESULTS

GB_HTG3 AC008672	131573	AC008672	131573	AC008672	Homo sapiens chromosome 5 clone C17878SKB_3B12, *** SEQUENCING IN PROGRESS ***	71	3-Aug-99
GB_IN1 DD06228	2865	U06228	2865	U06228	unoriented pieces	40,871	1-Feb-95
GB_PR2 CNU5/DRA	198444	AL110505	198444	AL110505	Dicystosium discoidium CRAC (dga) gene, complete cds	35,016	11-Nov-99
GB_PR2 HS230G1	125515	Z84468	125515	Z84468	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-816.8 of RPCL11 library from chromosome 14 of Homo sapiens (Human), complete sequence	35,013	23-Nov-99
GB_PR2 CNU5/DRA	198444	AL110505	198444	AL110505	Homo sapiens DNA sequence from PAC 230G1 on chromosome 4p11.3. Contains EST, STS and GSS, complete sequence.	41,751	11-Nov-99
GB_HTG3 AC008643	150208	AC008643	150208	AC008643	Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-816.8 of RPCL11 library from chromosome 14 of Homo sapiens (Human), complete sequence.	35,969	07-OCT-1999
GB_PR2 HS230G1	125515	Z84468	125515	Z84468	Homo sapiens chromosome 11 clone 63_H_13 map 11, *** SEQUENCING IN PROGRESS ***	35,966	07-OCT-1999
GB_BA1 MTC61	13540	Z86280	13540	Z86280	Homo sapiens chromosome 11 clone 63_H_13 map 11, *** SEQUENCING IN PROGRESS ***	35,966	23-Nov-99
GB_BA1 MTC61	13540	Z86280	13540	Z86280	unoriented pieces	38,348	17-Jun-98
GB_HTG3 AC008643	150208	AC008643	150208	AC008643	unoriented pieces	36,042	17-Jun-98
GB_PR2 HS230G1	125515	Z84468	125515	Z84468	Myobacterium tuberculosis H37Rv complete genome, segment 53/162	39,374	17-Jun-98
GB_BA1 MTC61	13540	Z86280	13540	Z86280	Myobacterium tuberculosis H37Rv complete genome, segment 53/162	39,374	17-Jun-98
GB_BA1 MTC61	13540	Z86280	13540	Z86280	Myobacterium tuberculosis H37Rv complete genome, segment 53/162	39,374	17-Jun-98
GB_BA1 MTC61	13540	Z86280	13540	Z86280	Myobacterium tuberculosis H37Rv complete genome, segment 53/162	39,374	17-Jun-98
GB_HTG3 AC008643	150208	AC008643	150208	AC008643	unoriented pieces	39,352	15-DEC-1997
GB_PR2 HS230G1	125515	Z84468	125515	Z84468	unoriented pieces	40,413	23-Nov-98
GB_BA1 MTC61	13540	Z86280	13540	Z86280	unoriented pieces	35,275	3-Aug-99
GB_HTG3 AC008643	150208	AC008643	150208	AC008643	unoriented pieces	43,041	2-Jul-99
GB_PR2 HS230G1	125515	Z84468	125515	Z84468	unoriented pieces	37,079	18-Sep-97
GB_BA1 MTC61	13540	Z86280	13540	Z86280	unoriented pieces	37,056	13-OCT-1997
GB_HTG3 AC008643	150208	AC008643	150208	AC008643	unoriented pieces	39,359	22-Jun-99
GB_PR2 HS230G1	125515	Z84468	125515	Z84468	unoriented pieces	39,357	22-Jun-99
GB_BA1 MTC61	13540	Z86280	13540	Z86280	unoriented pieces	39,357	22-Jun-99
GB_HTG3 AC008643	150208	AC008643	150208	AC008643	unoriented pieces	37,053	26-Sep-99
GB_PR2 HS230G1	125515	Z84468	125515	Z84468	unoriented pieces	37,016	12-MAY-1997
GB_BA1 MTC61	13540	Z86280	13540	Z86280	unoriented pieces	35,355	08-MAR-1999
GB_HTG3 AC008643	150208	AC008643	150208	AC008643	unoriented pieces	37,672	12-MAY-1997
GB_PR2 HS230G1	125515	Z84468	125515	Z84468	unoriented pieces	41,138	8-Sep-99
GB_BA1 MTC61	13540	Z86280	13540	Z86280	unoriented pieces	39,245	15-Jul-99
GB_HTG3 AC008643	150208	AC008643	150208	AC008643	unoriented pieces	35,399	8-Sep-99
GB_PR2 HS230G1	125515	Z84468	125515	Z84468	unoriented pieces	38,569	20-Nov-99
GB_BA1 MTC61	13540	Z86280	13540	Z86280	unoriented pieces	38,569	25-Sep-99
GB_HTG3 AC008643	150208	AC008643	150208	AC008643	unoriented pieces	38,569	20-Nov-99
GB_PR2 HS230G1	125515	Z84468	125515	Z84468	unoriented pieces	38,569	16-Apr-96
GB_BA1 MTC61	13540	Z86280	13540	Z86280	unoriented pieces	37,817	18-MAY-1997

TABLE 4: ALIGNMENT RESULTS

rxn02091	774	GB_BA1	OCU45336	3674	U43336	Coynebetaadonin glutaromycin heat shock ATP-inducing protein (cibB) gene, complete cds
rxn02094	840	GB_BA1	RCFCB	3874	X03476	Rhodopseudomonas sphaeroides fbc operon (fbcF, fbcR, fbcS genes)
rxn02100	910	GB_BA1	MMHC188A7	120990	AF109719	MUS musculus casein kinase 2 beta subunit (tnfrsf2) gene, partial cds; BAT1, A2020, NG20, NG20, BAT3
rxn02101	911	GB_BA1	OCU45336	3674	U43336	BAT1, A2020, NG20, NG20, BAT3
rxn02102	1281	GB_IN2	AF135118	10830	AF135118	ATP10A1, B144, lymphothion beta, TNF, and TNF beta genes, complete cds, IKBI, gene, partial cds, and unknown gene
rxn02103	519	GB_GSS3	OC00866	1194	B09866	ms30080.1 Life Tech mouse embryo 13 D5pc 1066001.4 Mus musculus cDNA clone IMAGE 13934.5 similar to gp U1580 Mus musculus (MOUSE), mRNA sequence
rxn02104	1245	GB_BA2	ECOMW07_022	11000	U18897	EST210312 Normalized rat brain, Noto Soares Ratus sp. cDNA clone RBRBK04.3 end, mRNA sequence
rxn02107		GB_BA1	ECONPNBW_4434		D96212	EST210312 Normalized rat brain, Noto Soares Ratus sp. cDNA clone RBRBK04.3 end, mRNA sequence
rxn02108	732	GB_BA1	D50912	128598	D50912	EST210312 Normalized rat brain, Noto Soares Ratus sp. cDNA clone RBRBK04.3 end, mRNA sequence
rxn02109	1044	GB_BA2	OC00866	1194	B09866	ms30080.1 Life Tech mouse embryo 13 D5pc 1066001.4 Mus musculus cDNA clone IMAGE 13934.5 similar to gp U1580 Mus musculus (MOUSE), mRNA sequence
rxn02110	1044	GB_BA2	OC00866	1194	B09866	ms30080.1 Life Tech mouse embryo 13 D5pc 1066001.4 Mus musculus cDNA clone IMAGE 13934.5 similar to gp U1580 Mus musculus (MOUSE), mRNA sequence
rxn02111	509	GB_BA1	OCU45336	3674	U43336	Coynebetaadonin glutaromycin heat shock ATP-inducing protein (cibB) gene, complete cds
rxn02112	509	GB_BA1	OCU45336	3674	U43336	Coynebetaadonin glutaromycin heat shock ATP-inducing protein (cibB) gene, complete cds
rxn02113	509	GB_BA1	OCU45336	3674	U43336	Coynebetaadonin glutaromycin heat shock ATP-inducing protein (cibB) gene, complete cds
rxn02114	509	GB_BA1	OCU45336	3674	U43336	Coynebetaadonin glutaromycin heat shock ATP-inducing protein (cibB) gene, complete cds
rxn02115	509	GB_BA1	OCU45336	3674	U43336	Coynebetaadonin glutaromycin heat shock ATP-inducing protein (cibB) gene, complete cds
rxn02116	509	GB_BA1	OCU45336	3674	U43336	Coynebetaadonin glutaromycin heat shock ATP-inducing protein (cibB) gene, complete cds
rxn02117	597	GB_BA2	AF094575	18754	AF094575	Streptococcus pneumoniae serotype 19A DaxB (daxB) gene, partial sequence, capsular polysaccharide biosynthesis operon, complete sequence, and diacylglycerol acyltransferase A (glaA)

TABLE 4: ALIGNMENT RESULTS

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TABLE 4: ALIGNMENT RESULTS

na02207 698	GB_EST71:AA482901	442	AA482901	vs6907.11 Stratiopene mouse macrophage (#637369) Mus musculus cDNA clone IMAGE:1276525 5' similar to gp.358543_nratRIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M1 CHAIN (HUMAN); gp.402927 Mouse ribonucleotide reductase subunit M1 mRNA, complete (MOUSE); mRNA sequence	Mus musculus	42,141	27-MAY-1998
	GB_EST8:W65369	558	W65369	na02204.11 Soanae mouse embryo NM163.5 14.5 Mus musculus cDNA clone IMAGE:408343 5' similar to gp.402927 Mouse ribonucleotide reductase subunit M1 mRNA, complete (MOUSE); mRNA sequence	Mus musculus	39,964	12-Sep-96
na02211	GB_PAT E14824	2379	E14824	CDNA encoding M1 subunit of human ribonucleotide reductase	Homo sapiens	36,812	28-Jul-99
na02212 621	GB_HTG3:AC009518	241128	AC009518	Homo sapiens chromosome 7 *** SEQUENCING IN PROGRESS *** 98 unordered pieces	Homo sapiens	36,342	1-Sep-99
	GB_HTG3:AC009518	241128	AC009518	Homo sapiens chromosome 7 *** SEQUENCING IN PROGRESS *** 98 unordered pieces	Homo sapiens	36,342	1-Sep-99
	GB_HTG3:AC009518	241128	AC009518	Homo sapiens chromosome 7 *** SEQUENCING IN PROGRESS *** 98 unordered pieces	Homo sapiens	41,982	1-Sep-99
na02216 329	GB_HTG2:AC007641	102402	AC007641	Homo sapiens chromosome 10 clone 644_M_3 map 10; *** SEQUENCING IN PROGRESS *** 7 unordered pieces	Mus musculus	31,307	22-MAY-1999
	GB_HTG3:AC007641	102402	AC007641	Mus musculus chromosome 10 clone 644_M_3 map 10; *** SEQUENCING IN PROGRESS *** 7 unordered pieces	Mus musculus	31,307	22-MAY-1999
	GB_LHTG2:AC007641	102402	AC007641	Mus musculus chromosome 10 clone 644_M_3 map 10; *** SEQUENCING IN PROGRESS *** 7 unordered pieces	Mus musculus	32,188	22-MAY-1999
na02217 786	GB_RO RN191516	1540	U91516	Rattus norvegicus oxytocin receptor (OTR) gene, promoter region	Rattus norvegicus	39,256	25-Nov-97
	GB_RO RN191516	1540	U91516	Rattus norvegicus oxytocin receptor (OTR) gene, promoter region	Rattus norvegicus	37,176	25-Nov-97
na02218 390	GB_HTG3:AC008656	43033	AC008656	Homo sapiens chromosome 5 clone C11978SK3_194J6 *** SEQUENCING IN PROGRESS *** 64 unordered pieces	Homo sapiens	39,864	3-Aug-99
	GB_HTG3:AC008656	43033	AC008656	Homo sapiens chromosome 5 clone C11978SK3_194J6 *** SEQUENCING IN PROGRESS *** 64 unordered pieces	Homo sapiens	39,864	3-Aug-99
	GB_HTG3:AC008656	43033	AC008656	Homo sapiens chromosome 5 clone C11978SK3_194J6 *** SEQUENCING IN PROGRESS *** 64 unordered pieces	Homo sapiens	37,598	3-Aug-99
na02219 1509	GB_PR3:HS475N16	113109	AL035587	Human DNA sequence from clone 475N16 on chromosome 6p12.2-21.2, complete sequence	Homo sapiens	35,286	23-Nov-99
	GB_PR3:HS475N16	113109	AL035587	Human DNA sequence from clone 475N16 on chromosome 6p12.2-21.2, complete sequence	Homo sapiens	35,255	23-Nov-99
	GB_EST10:AA142336	411	AA142336	ms0702.11 Stratiopene mouse skin (#637313) Mus musculus cDNA clone IMAGE:600267 5' similar to SWRC01_1 YEAST P40341 MITOCHONDRIAL RESPIRATORY CHAIN COMPLEX ASSEMBLY PROTEIN RCO1; mRNA sequence	Mus musculus	38,398	12-Feb-97
na02221 1485	GB_PR3:AC002422	160991	AC002422	Human Chromosome X, complete sequence	Homo sapiens	38,435	30-Jan-96
	GB_PR3:AC009755	199917	AC009755	Caenorhabditis elegans clone Y40C3 *** SEQUENCING IN PROGRESS *** 1 unordered pieces	Caenorhabditis elegans	39,229	23-Feb-99
	GB_HTG2:AC009755	199917	AC009755	Caenorhabditis elegans clone Y40C3 *** SEQUENCING IN PROGRESS *** 1 unordered pieces	Caenorhabditis elegans	39,229	23-Feb-99
na02223 601	GB_HTG6:AC008224	199774	AC008224	Drosophila melanogaster chromosome 3 clone BACR23J02 (D817) RPCI-68 20 J2 map 83d.43D strain Y, on bw sc *** SEQUENCING IN PROGRESS *** 37 unordered pieces	Drosophila melanogaster	35,333	24-Nov-99
	GB_HTG3:AC011511	158298	AC011511	Homo sapiens chromosome 19 clone C1TB-H1_2369P2 *** SEQUENCING IN PROGRESS *** 57 unordered pieces	Homo sapiens	35,593	07-OCT-1999
	GB_HTG3:AC011511	158298	AC011511	Homo sapiens chromosome 19 clone C1TB-H1_2369P2 *** SEQUENCING IN PROGRESS *** 57 unordered pieces	Homo sapiens	35,593	07-OCT-1999
na02228 1156	GB_HTG2:AC008690	298195	AC008690	Caenorhabditis elegans clone Y67D8 *** SEQUENCING IN PROGRESS *** 23 unordered pieces	Caenorhabditis elegans	36,810	24-Feb-99
	GB_HTG2:AC008690	298195	AC008690	Caenorhabditis elegans clone Y67D8 *** SEQUENCING IN PROGRESS *** 23 unordered pieces	Caenorhabditis elegans	35,433	24-Feb-99
	GB_HTG2:AC008690	298195	AC008690	Caenorhabditis elegans clone Y67D8 *** SEQUENCING IN PROGRESS *** 23 unordered pieces	Caenorhabditis elegans	36,810	24-Feb-99

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TABLE 4: ALIGNMENT RESULTS

na022741	GB_EST5:H08835	440	H08835	yx14f12.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE261743 3', mRNA sequence.	Homo sapiens	38,182	15-DEC-1995
	GB_EST5:N25530	586	N25530	yx16c03.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE 267652 3', mRNA sequence.	Homo sapiens	37,543	26-DEC-1995
	GB_BA1:CG143535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds	Corynebacterium glutamicum	38,812	9-Apr-97
na022330	GB_EST18:AA570388	527	AA570388	element MSR1 (respiratory element), mRNA sequence	Homo sapiens	41,086	9-Sep-97
	GB_PR2:HSU43030	1539	U43030	Human carboxidophin-1 (CTF1) mRNA, complete cds	Homo sapiens	38,335	9-Jan-96
	GB_PL12:ATA006429	64818	AC006429	Arabidopsis thaliana chromosome II BAC F15K19 genomic sequence, complete sequence	Arabidopsis thaliana	33,687	30-Nov-95
na022331	GB_PR3:AC004654	195142	AC004654	Homo sapiens Y522 BAC GSHB-59035 (Genome Systems Human BAC library) complete sequence	Homo sapiens	38,921	23-Apr-99
	GB_HTG2:AC007853	118280	AC007853	Drosophila melanogaster chromosome 3 clone BACR03.02 (DT66) RPL38.03 L.2 map 88B-96C strain Y, on bw sp. *** SEQUENCING IN PROGRESS *** 80 unordered pieces	Drosophila melanogaster	36,237	2-Aug-99
na022338	GB_BA1:MTCTC71B4	39150	Z80108	Mycobacterium tuberculosis H37Rv complete genome, segment 62/162	Mycobacterium tuberculosis	52,206	23-Jun-98
	GB_BA1:MTCTC71B4	39150	Z80108	Mycobacterium tuberculosis H37Rv complete genome, segment 62/162	Mycobacterium tuberculosis	36,935	23-Jun-98
	GB_VI:AF105451	801	AF105451	HIV-1 isolate A-D11-07 from Italy, envelope glycoprotein, C2-V5 region (env) gene, partial cds (IG-HGP)	Human immunodeficiency virus type 1	40,884	25-Apr-99
na022344	GB_PR1:AB016195	10558	AB016195	Homo sapiens ELK1 pseudogene (ELK2) and immunoglobulin heavy chain gamma pseudogene (IGHGP)	Homo sapiens	38,929	9-Apr-99
	GB_PR3:HSN21F1	39212	Z84162	Human DNA sequence from cosmid N21F1 on chromosome 22 Contains exon trap and STS, complete sequence	Homo sapiens	38,763	23-Nov-99
	GB_INT1:DMA001648	51889	AC001648	Drosophila melanogaster (P1 DSG03431 D102) DNA sequence, complete sequence	Drosophila melanogaster	36,884	22-Apr-97
na022254	GB_GS512:AQ380240	541	AQ380240	HS_5035_A2_E07_T7 RPL111 Human Male BAC Library Homo sapiens genomic clone Plac8-811 Col-14 Row=1, genomic survey sequence	Homo sapiens	36,388	06-MAR-1999
	GB_GS511:AQ384453	620	AQ384453	na020020L191 CUGI Rice BAC Library Oryza sativa genomic clone rib020020L151, genomic survey sequence	Oryza sativa	36,271	23-OCT-1998
	GB_GS514:AQ377777	568	AQ377777	na020091L171 CUGI Rice BAC Library Oryza sativa genomic clone rib0091L171, genomic survey sequence	Oryza sativa	39,456	2-Jun-99
na022255	GB_PR4:AC066332	153477	AC066332	Homo sapiens clone NH0375014, complete sequence	Homo sapiens	35,019	11-Nov-99
	GB_PAT1:E06669	1167	E06669	DNA encoding Bacillus sp. L-lactic acid dehydrogenase	Bacillus sp.	39,719	29-Sep-97
	GB_PL1:Y5CB02	3201	D35310	Yeast BOZ2 gene for Bop4p	Saccharomyces cerevisiae	35,769	8-Feb-99
na022266	GB_BA1:REGIONB	4061	Z13965	N meningitidis lpa and lpb genes for Lpa and Lpb proteins	Neisseria meningitidis	35,091	28-DEC-1993
	GB_HTG1:AP000588	136627	AP000588	Homo sapiens chromosome 21 clone B75382 map 21q21.2, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens	37,500	07-OCT-1999
	GB_HTG1:AP000588	136627	AP000588	Homo sapiens chromosome 21 clone B75382 map 21q21.2, *** SEQUENCING IN PROGRESS *** in unordered pieces	Homo sapiens	37,500	07-OCT-1999
na022267	GB_PR4:AC007263	127361	AC007263	Homo sapiens clone NH0536118, complete sequence	Homo sapiens	37,155	28-Sep-99
	GB_INT1:CEG540C	35500	Z77131	Caenorhabditis elegans cosmid C54C6, complete sequence	Caenorhabditis elegans	38,280	23-Jul-96
	GB_HTG3:AC008805	128915	AC008805	Homo sapiens chromosome 5 clone CTB-H1_2259114, *** SEQUENCING IN PROGRESS *** 40 unordered pieces.	Homo sapiens	35,985	3-Aug-99
na022271	GB_HTG3:AC007441	219832	AC007441	Drosophila melanogaster chromosome 3 clone BACR10E03 (D680) RPL38.10 E.3 map 88A-88B strain Y, on bw sp. *** SEQUENCING IN PROGRESS *** 188 unordered pieces	Drosophila melanogaster	33,284	08-OCT-1999
	GB_HTG3:AC007441	219832	AC007441	Drosophila melanogaster chromosome 3 clone BACR10E03 (D680) RPL38.10 E.3 map 88A-88B strain Y, on bw sp. *** SEQUENCING IN PROGRESS *** 188 unordered pieces	Drosophila melanogaster	33,284	08-OCT-1999
	GB_HTG2:AC008029	123106	AC008029	Drosophila melanogaster chromosome 3 clone BACR10C1 (D680) RPL38.01 C.11 map 84D-84D strain Y, on bw sp. *** SEQUENCING IN PROGRESS *** 82 unordered pieces	Drosophila melanogaster	34,315	2-Aug-99

TABLE 4: ALIGNMENT RESULTS

na02279	1581	GB_INT.AC003121	68822	AC003121	AC003121	Drosophila melanogaster (P1 D500329 DB8) DNA sequence, complete sequence.	35,046	26-Nov-97	Drosophila melanogaster
		GB_INT.AC003121	68822	AC003121	AC003121	Drosophila melanogaster (P1 D500329 DB8) DNA sequence, complete sequence.	35,220	26-Nov-97	Drosophila melanogaster
		GB_BA1.MTCY39	38500	Z4025	Z4025	Mycobacterium tuberculosis H37Rv complete genome, segment 88/162	39,685	17-Jun-96	Mycobacterium tuberculosis
na02280									
na02286	672	GB_BA1.MTV025	121125	AL002121	AL002121	Mycobacterium tuberculosis H37Rv complete genome, segment 155/162	38,953	24-Jun-99	Mycobacterium tuberculosis
		GB_PL2.AC002130	114738	AC002130	AC002130	The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence	39,216	8-Jan-98	Arabidopsis thaliana
		GB_PL2.AC002159	97146	AC002159	AC002159	Arabidopsis thaliana chromosome 1 BAC T3898 (genomic) sequence, complete sequence	38,090	17-Aug-98	Arabidopsis thaliana
na02287	675	GB_HTG3.AC003281	221178	AC003281	AC003281	Homo sapiens chromosome 10 clone 8_C_22 map 15. *** SEQUENCING IN PROGRESS *** 49	35,565	12-Aug-99	Homo sapiens
		GB_HTG3.AC003281	221178	AC003281	AC003281	Homo sapiens chromosome 15 clone 8_C_22 map 15. *** SEQUENCING IN PROGRESS *** 49	35,565	12-Aug-99	Homo sapiens
		GB_ROMUS.MURINC	4587	M85736	M85736	Mouse multiglobin mRNA, complete cds			
		GB_EST19.AA813194	308	AA813194	AA813194	a08012.1 Soares, testis, NHT Homo sapiens cDNA clone 1377190.3, mRNA sequence	39,787	27-Apr-93	Mus musculus
na02284	498	GB_EST19.AA813194	308	AA813194	AA813194	a08012.1 Soares, testis, NHT Homo sapiens cDNA clone 1377190.3, mRNA sequence	33,417	31-DEC-1998	Homo sapiens
		GB_PAT1.B94511	18318	I89451	I89451	Sequence 6 from patent US 5721354			
		GB_VI.HCU33331	18535	U33331	U33331	Human cytomegalovirus Toledo strain U37 region	38,859	10-Aug-98	Unknown
		GB_PR3.HS550H1	108803	AL038420	AL038420	Human DNA sequence from clone 550H1 on chromosome 20q11.1-11.22 Contains a pseudogene similar to HIGH MOBILITY GROUP PROTEIN 2A, a novel mRNA, ESTs, STSs, GSSs and CpGs islands, complete sequence	38,796	23-Nov-99	Homo sapiens
na02286	612	GB_BA2.AF065312	1694	AF065312	AF065312	Yersinia pestis hypothermal protein (YocG) gene, partial cds; thymidylate kinase (tmk) gene, complete cds; and putative DNA polymerase II delta subunit (hoB) gene, partial cds	41,351	16-Nov-99	Yersinia pestis
		GB_PR3.HS550H1	108803	AL038420	AL038420	Human DNA sequence from clone 550H1 on chromosome 20q11.1-11.22 Contains a pseudogene similar to HIGH MOBILITY GROUP PROTEIN 2A, a novel mRNA, ESTs, STSs, GSSs and CpGs islands, complete sequence	37,919	23-Nov-99	Homo sapiens
		GB_PR3.HS550H1	108803	AL038420	AL038420	Human DNA sequence from clone 550H1 on chromosome 20q11.1-11.22 Contains a pseudogene similar to HIGH MOBILITY GROUP PROTEIN 2A, a novel mRNA, ESTs, STSs, GSSs and CpGs islands, complete sequence	37,807	23-Nov-99	Homo sapiens
na02287	1260	GB_BA2.AF065312	1694	AF065312	AF065312	Yersinia pestis hypothermal protein (YocG) gene, partial cds; thymidylate kinase (tmk) gene, complete cds; and putative DNA polymerase II delta subunit (hoB) gene, partial cds	39,883	16-Nov-99	Yersinia pestis
		GB_RO.AF007836	5955	AF007836	AF007836	Reittus norvegicus rac3 effector (RM) mRNA, alternatively spliced, complete cds	37,844	15-Aug-97	Reittus norvegicus
		GB_IN2.EGU27015	2394	U27015	U27015	Echinococcus granulosus 18S ribosomal RNA gene, complete sequence	38,710	16-Jun-96	Echinococcus granulosus
na02298	1782	GB_BA2.AF116184	540	AF116184	AF116184	Corynebacterium glutamicum L-aspartate-alpha-decarboxylase precursor (panD) gene, complete cds	44,231	02-MAY-1999	Corynebacterium glutamicum
		GB_BA2.AF116184	540	AF116184	AF116184	Corynebacterium glutamicum L-aspartate-alpha-decarboxylase precursor (panD) gene, complete cds	42,007	02-MAY-1999	Corynebacterium glutamicum
		GB_BA2.AF116184	540	AF116184	AF116184	Corynebacterium glutamicum L-aspartate-alpha-decarboxylase precursor (panD) gene, complete cds	46,250	02-MAY-1999	Corynebacterium glutamicum
na02300	456	GB_BA1.MTV004	69350	AL009186	AL009186	Mycobacterium tuberculosis H37Rv complete genome, segment 144/162	39,882	16-Jun-98	Mycobacterium tuberculosis
		GB_EST22.A048692	172	A048692	A048692	ub30g4.1 r1 Soares 2N6MT Mus musculus cDNA clone M84DE 1379286.5, mRNA sequence	43,284	8-Jul-96	Mus musculus
na02301	840	GB_HTG3.AC008573	205756	AC008573	AC008573	Homo sapiens chromosome 5 clone C11-HSPC_36111, *** SEQUENCING IN PROGRESS *** 95	35,115	3-Aug-99	Homo sapiens
		GB_HTG3.AC008573	205756	AC008573	AC008573	Homo sapiens chromosome 5 clone C11-HSPC_36111, *** SEQUENCING IN PROGRESS *** 95	35,115	3-Aug-99	Homo sapiens

TABLE 4: ALIGNMENT RESULTS

na02302	1002	GB_LHTG3	AC008573	205755	AC008573	Homo sapiens chromosome 5 clone CIT-HSPC_55111, *** SEQUENCING IN PROGRESS ***, 95 unordered pieces	Homo sapiens	36,527	3-Aug-99
		GB_LHTG6	AC008076	200000	AC008076	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***, 18 unordered pieces	Homo sapiens	34,884	02-OCT-1999
		GB_LHTG3	AC008930	258026	AC008930	Homo sapiens chromosome 5 clone CITB-H1_2352M8, *** SEQUENCING IN PROGRESS ***, 168 unordered pieces	Homo sapiens	36,945	3-Aug-99
		GB_LHTG3	AC008930	258026	AC008930	Homo sapiens chromosome 5 clone CITB-H1_2352M8, *** SEQUENCING IN PROGRESS ***, 168 unordered pieces	Homo sapiens	36,945	3-Aug-99
na02303									
na02304	1014	GB_PAT	A69720	53799	A69720	Sequence 3 from Patent WO980788	unidentified	36,015	07-MAY-1999
		GB_BA1	AI0123012	53794	AJ233012	Amyloidosis mediterranea genes encoding fibrinogen polypeptide synthetases, ORFs 1 to 5	Amyloidosis mediterranea	36,015	9-Feb-98
		GB_BA2	AF040570	76199	AF040570	Amyloidosis mediterranea fibrinogen biosynthetic gene cluster	Amyloidosis mediterranea	36,015	5-Feb-98
na02307									
na02308	552	GB_LHTG3	AC009340	110415	AC009340	Drosophila melanogaster chromosome 2 clone BACR04E19 (D1026) RPCI-98 M.E. 19 map 34A-34E strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 103 unordered pieces	Drosophila melanogaster	36,066	27-Aug-99
		GB_LHTG3	AC009340	110415	AC009340	Drosophila melanogaster chromosome 2 clone BACR04E19 (D1026) RPCI-98 M.E. 19 map 34A-34E strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 103 unordered pieces	Drosophila melanogaster	36,066	27-Aug-99
		GB_LHTG3	AC009340	110415	AC009340	Drosophila melanogaster chromosome 2 clone BACR04E19 (D1026) RPCI-98 M.E. 19 map 34A-34E strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 103 unordered pieces	Drosophila melanogaster	36,066	27-Aug-99
na02314	564	GB_LHTG3	AC011247	206436	AC011247	Homo sapiens chromosome NH0541E12, WORKING DRAFT SEQUENCE, 1 unordered pieces.	Homo sapiens	36,201	13-Nov-99
		GB_LHTG3	AC011247	206436	AC011247	Homo sapiens chromosome NH0541E12, WORKING DRAFT SEQUENCE, 1 unordered pieces.	Homo sapiens	36,201	13-Nov-99
		GB_LHTG3	AC011152	142816	AC011152	Homo sapiens chromosome 7, H_4, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	35,548	01-OCT-1999
na02324	1299	GB_BA2	AF110165	20302	AF110165	Burkholderia pseudomallei strain 1026b (DBB (dbi)), general secretory pathway protein D (gsdD), general secretory pathway protein E (gsdE), general secretory pathway protein F (gsdF), GsdP (gsdP), general secretory pathway protein G (gsdG), general secretory pathway protein H (gsdH), general secretory pathway protein I (gsdI), general secretory pathway protein J (gsdJ), general secretory pathway protein K (gsdK), general secretory pathway protein L (gsdL), general secretory pathway protein M (gsdM), and general secretory pathway protein N (gsdN) genes, complete cds, and unknown genes	Burkholderia pseudomallei	39,670	2-Aug-99
		GB_BA1	PSEAMNH	5215	D80216	P. chlorophyllus genes for amidase (EC 3.5.1.4) and for nitrite hydratase (EC 4.2.1.84).	Pseudomonas chlorophyllus	51,254	7-Feb-99
		GB_PAT	E12519	4775	E12519	Nucleotide sequence of Rhodococcus rhodochrous genomic DNA region containing amidase and nitrite hydratase genes.	Rhodococcus rhodochrous	51,646	24-Jun-98
na02325	990	GB_BA1	GGPYC	3728	Y06548	Corynebacterium glutamicum pyc gene	Corynebacterium glutamicum	100,000	08-MAY-1998
		GB_PAT	AC006079	178109	AC006079	Homo sapiens chromosome 17, clone HRPX_855_D_21, complete sequence	Homo sapiens	37,807	12-DIC-1998
		GB_GSSB	AC008932	441	AC008932	CIT-HSP-2334L1.T7 CIT-HSP Homo sapiens genomic clone 2334L1, genomic survey sequence	Homo sapiens	42,359	11-Jul-98
na02331	489	GB_PL1	YKSGA11	4199	M88970	Kluyveromyces fragilis transcriptional activator (GAL11) gene, complete cds	Kluyveromyces fragilis	40,252	18-MAY-1993
		GB_PL2	YKSGA11	594	Y18890	Kluyveromyces fragilis gene for caseinase-9, intronic sequence (584 bp)	Kluyveromyces fragilis	40,529	08-OCT-1989
		GB_PL1	YKSGA11	4199	M88970	Kluyveromyces fragilis transcriptional activator (GAL11) gene, complete cds	Kluyveromyces fragilis	39,679	18-MAY-1993
na02336	303	GB_BA1	CGU35023	3195	U55023	Corynebacterium glutamicum thiosulfate sulfurtransferase (tsfR) gene, partial cds, acyl CoA carboxylase (accBC) gene, complete cds	Corynebacterium glutamicum	35,548	15-Jan-97
		GB_PL2	AF114171	183990	AF114171	Homo sapiens chromosome 18, complete sequence	Sorghum bicolor	41,414	25-Apr-99
		GB_PAT	AC009324	157310	AC009324	Corynebacterium glutamicum thiosulfate sulfurtransferase (tsfR) gene, partial cds, acyl CoA carboxylase (accBC) gene, complete cds	Corynebacterium glutamicum	41,786	11-Nov-99
na02337	1446	GB_PAT	AC009324	157310	AC009324	Corynebacterium glutamicum thiosulfate sulfurtransferase (tsfR) gene, partial cds, acyl CoA carboxylase (accBC) gene, complete cds	Corynebacterium glutamicum	100,000	15-Jan-97

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TABLE 4: ALIGNMENT RESULTS

GB_EST77	AK438343	610	AK438343	SMOATFAP31F05K	Onchocerca vivulus adult female cDNA (S98WMLW-OWAF) Onchocerca vivulus cDNA clone SMOATFAP31F05 5', mRNA sequence	Onchocerca vivulus	41,244	09-MAR-1999
GB_BA1	XANHRPA1A	1824	AM9173	AJ26535	Xanthomonas campestris HrpA1 gene, complete cds.	Xanthomonas campestris	37,520	14-Sep-93
GB_OV	CC245635	2455	AJ26535	Cyprinus carpio IL-1 gene for interleukin-1 beta	Cyprinus carpio	35,514	5-Aug-99	
GB_OV	AB070701	1213	AB070701	Cyprinus carpio mRNA for interleukin-1 beta	Cyprinus carpio	36,821	29-Jun-98	
GB_OV	CC245635	2455	AJ26535	Cyprinus carpio IL-1 gene for interleukin-1 beta	Cyprinus carpio	35,500	5-Aug-99	
GB_JNI	CEV40818	2813	AL022636	Caenorhabditis elegans cermid Y40B18, complete sequence	Caenorhabditis elegans	37,068	12-Nov-99	
GB_GSS12	ACQ74513	640	ACQ74513	RPCH11-145N15 TJ RPCI-11 Homo sapiens genomic clone RPCH11-145N15, genomic survey sequence	Homo sapiens	35,058	20-MAY-1999	
GB_JNI	CEY40919	2813	AL022636	Caenorhabditis elegans csmid Y40B18, complete sequence	Caenorhabditis elegans	32,800	12-Nov-99	
GB_BA1	MTVCY1A11	30650	Z78620	Mycobacterium tuberculosis H37Rv complete genome, segment 83162	Mycobacterium tuberculosis	64,510	17-Jun-98	
GB_PR4	AC049698	135572	AC049698	Homo sapiens clone DJ164D05, complete sequence	Homo sapiens	41,118	17-Jun-99	
GB_PR2	AC020091	181799	AC020091	Genomic sequence from Human 17, complete sequence	Homo sapiens	36,193	9-Sep-97	
GB_HTG5	AC069754	212878	AC069754	Homo sapiens chromosome 15 clone RP11-519C12, WORKING DRAFT SEQUENCE, 16 ordered pieces	Homo sapiens	33,008	17-Nov-99	
GB_HTG5	AC069754	212878	AC069754	Homo sapiens chromosome 15 clone RP11-519C12, WORKING DRAFT SEQUENCE, 16 ordered pieces	Homo sapiens	39,716	17-Nov-99	
GB_PR4	HUAC003108	164864	AC003108	Human Chromosome 16 BAC clone CT1987SK-327024, complete sequence	Homo sapiens	35,180	23-Nov-99	
GB_IN2	AC005650	60019	AC005650	Drosophila melanogaster, chromosome 2R, region 59B4-59B7, P1 clone DS02885, complete sequence	Drosophila melanogaster	40,397	30-Jan-99	
GB_IN2	AC005650	60019	AC005650	Drosophila melanogaster, chromosome 2R, region 59B4-59B7, P1 clone DS02885, complete sequence	Drosophila melanogaster	37,719	30-Jan-99	
GB_RO	AF081193	2250	AF081193	Mus musculus calcium and DAG-regulated guanine nucleotide exchange factor 1 mRNA, complete cds	Mus musculus	37,835	28-Nov-98	
GB_HTG4	AC009370	59409	AC009370	Drosophila melanogaster chromosome 3L/75C1 clone RPI08-35F4, *** SEQUENCING IN PROGRESS ***; 40 unordered pieces	Drosophila melanogaster	35,460	16-OCT-1999	
GB_HTG4	AC009370	59409	AC009370	Drosophila melanogaster chromosome 3L/75C1 clone RPI08-35F4, *** SEQUENCING IN PROGRESS ***; 40 unordered pieces	Drosophila melanogaster	35,460	16-OCT-1999	
GB_EST9	AA081446	311	AA081446	LOC111811 Staphylococcus aureus strain 8324/83, mRNA sequence	Homo sapiens	36,334	21-OCT-1996	
GB_BA2	SC776	18292	AL121600	Staphylococcus coelicolor strain F76	Staphylococcus coelicolor A3(2)	39,326	29-Sep-99	
GB_PR2	HS1022J11	137858	AL121600	Human DNA sequence from clone 1022J11 on chromosome 20q13.13-13.2, complete sequence	Homo sapiens	35,444	23-Nov-99	
GB_HTG1	AC002345	132645	AC002345	Homo sapiens chromosome 17 clone 20D5, *** SEQUENCING IN PROGRESS ***; 10 unordered pieces	Homo sapiens	36,106	25-Aug-97	
GB_GSS14	AQ579499	825	AQ579499	Oryza sativa genomic clone nbx0084D17L CUGI Rice BAC Library Oryza sativa genomic clone nbx0084D17L, genomic survey sequence	Oryza sativa	39,535	2-Jun-99	
GB_GSS14	AQ579499	825	AQ579499	Oryza sativa genomic clone nbx0084D17L CUGI Rice BAC Library Oryza sativa genomic clone nbx0084D17L, genomic survey sequence	Oryza sativa	38,213	2-Jun-99	
GB_HTG3	AC007810	140775	AC007810	Drosophila melanogaster chromosome 3 clone BACR14A01 (D720) RPI-98 14 A 1 map 90C-90C strain y, on bw sp, *** SEQUENCING IN PROGRESS ***; 89 unordered pieces	Drosophila melanogaster	33,331	17-Sep-99	
GB_HTG3	AC007810	140775	AC007810	Drosophila melanogaster chromosome 3 clone BACR14A01 (D720) RPI-98 14 A 1 map 90C-90C strain y, on bw sp, *** SEQUENCING IN PROGRESS ***; 89 unordered pieces	Drosophila melanogaster	33,331	17-Sep-99	
GB_PR3	AC005339	32390	AC005339	Homo sapiens chromosome 15, cosmid R33729, complete sequence	Homo sapiens	38,131	30-Jul-98	
GB_HTG3	AC003936	105005	AC003936	Drosophila melanogaster chromosome 3 clone BACR03P18 (D672) RPI-98 03 P 13 map 83A-53B strain y, on bw sp, *** SEQUENCING IN PROGRESS ***; 85 unordered pieces	Drosophila melanogaster	36,529	27-Aug-99	
GB_EST20	AA820427	436	AA820427	Drosophila melanogaster embryo p0T2 Drosophila melanogaster cDNA clone LD24042, 5' splice, mRNA sequence	Drosophila melanogaster	38,018	25-Feb-99	

TABLE 4: ALIGNMENT RESULTS

[illegible]

TABLE 4: ALIGNMENT RESULTS

na02554	747	GB_P1A_Q00482	171878	X54422	Mutalis gene for polyphosphic adhesive protein.	Homio sapiens PAC clone DJ07820 from 22. complete sequence.	Homio sapiens	27-MAY-1992	35.619
na02555	728	GB_GS11FR020318	466	AL013501	F rubripes GSS sequence, clone 042H13D6, genomic survey sequence	Homio sapiens PAC clone DJ07820 from 22. complete sequence.	Homio sapiens	27-OCT-1999	37.346
na02556	1125	GB_GS11FR020376	555	AL013459	F rubripes GSS sequence, clone 042H13D6, genomic survey sequence	Homio sapiens PAC clone DJ07820 from 22. complete sequence.	Homio sapiens	27-OCT-1999	38.440
na02557	1545	GB_PR3_Q004976	127425	AC004976	F rubripes GSS sequence, clone 042H13D6, genomic survey sequence	Haemophilus influenzae Rd section 145 of 163 of the complete genome	Haemophilus influenzae	22-MAY-1998	33.514
na02558	1753	GB_PR3_HUAC002038	161973	AC002038	Homio sapiens chromosome 2 clone D1143119 from 7p16-p15, complete sequence		Rd	10-DEC-1997	40.215
na02559	1753	GB_HT33_Q0010791	111643	AC010791	Homio sapiens chromosome 17 clone 6_M_14 map 17, *** SEQUENCING IN PROGRESS ***		Fugu rubripes	10-DEC-1997	40.215
na02560	873	GB_BA1_FT16SRNA	121	Z18191	F rubripes 16S rRNA		Fugu rubripes	10-DEC-1997	35.379
na02561	873	GB_BA1_FT16SRNA	120	Z18192	F rubripes 16S rRNA		Fugu rubripes	10-DEC-1997	35.379
na02562	873	GB_GSS13_Q0469318	553	AQ469318	CTBE1E1-2556420 TR CTBE1E1: Homio sapiens genomic clone 2556420, genomic survey sequence		Fugu rubripes	10-DEC-1997	39.718
na02563	765	GB_GSS12_Q0439003	485	AQ043903	HS_5058_B1_F07_TPA RPI1 Human Male BAC Library Homio sapiens genomic clone		Homio sapiens	13-MAR-1999	38.049
na02564	765	GB_PR2_A0147315	2889	AF047315	Plate-634 Coli-r13 RowE1 genomic survey sequence		Homio sapiens	6-Aug-97	35.689
na02565	765	GB_BA1_G0143435	2331	AU43435	Homio sapiens gely gene product tomobog mRNA, complete cds		Corynebacterium	9-Apr-97	38.165
na02566	431	GB_EST133_Q0743398	490	U176398	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds		glutamicum	29-Jun-99	42.084
na02567	431	GB_EST133_Q0743398	490	U176398	EST572548 tomato resistant, Cornell Lycopersicon esculentum cDNA clone cLER1810, mRNA sequence		Mus musculus	2-Sep-98	40.281
na02568	1258	GB_BA1_SC0D03	39776	AL008622	uc21005 r1 Soares mouse mammary gland NMMMG Mais musculus cDNA clone IMAGE 1389510		Streptomyces coelicolor	8-Jul-99	39.742
na02569	1545	GB_PR1_HUIM05	38945	U002105	Shiga toxin sequence from Shiga toxin-producing Escherichia coli O157:H7		Homio sapiens	29-MAY-1997	38.104
na02570	1008	GB_GSS15_Q0818143	592	AQ618143	HS_5168_B1_H08_TPA RPI1 Human Male BAC Library Homio sapiens genomic clone		Homio sapiens	16-Aug-94	34.183
na02571	1008	GB_OV_XLF61A1	2172	X64759	Plasma-744 Coli-r15 RowP7 genomic survey sequence		Xenopus laevis	15-Jun-96	34.874
na02572	1008	GB_PR4_Q0050339	151316	AF034976	X laevis mRNA for transcription factor (clone XLF61A1)		Homio sapiens	26-Jan-93	38.589
na02573	1008	GB_P12_A0343676	7130	AF034976	Homio sapiens clone H00512E16, complete sequence		Homio sapiens	14-Jan-99	33.575
na02574	474	GB_P12_A0343676	7130	AF034976	Playella littoralis ribosomal protein S14 (ps14) gene, partial cds, ATPase subunit 8 (p8b) gene, complete cds, rRNA-Ser gene, complete sequence, ribosomal protein S10 (ps10) and ribosomal protein L31 (p31) genes, complete cds, rRNA-Ser gene, complete sequence, T7-like RNA polymerase (p7ox) gene, complete cds, and unknown genes, mitochondrial genes for mitochondrial products		Mitochondrion Playella littoralis	22-Jun-98	34.690
na02575	1258	GB_EST30_A0655188	456	A655188	w607902 x1 NC1_CGAP_G05 Homio sapiens cDNA clone IMAGE 2310770 3' mRNA sequence		Homio sapiens	04-MAY-1999	39.198
na02576	1258	GB_P12_A0343676	7130	AF034976	Playella littoralis ribosomal protein S14 (ps14) gene, partial cds, ATPase subunit 8 (p8b) gene, complete cds, rRNA-Ser gene, complete sequence, ribosomal protein S10 (ps10) and ribosomal protein L31 (p31) genes, complete cds, rRNA-Ser gene, complete sequence, T7-like RNA polymerase (p7ox) gene, complete cds, and unknown genes, mitochondrial genes for mitochondrial products		Mitochondrion Playella littoralis	22-Jun-98	39.859
na02577	10000	GB_P12_A0000191	10000	AP000191	Homio sapiens genomic DNA, chromosome 21q22.1, D21S226-4HL region, clone 078C10-025E9, segment 1821, complete sequence		Homio sapiens	20-Nov-99	37.199
na02578	293	GB_EST133_A0349881	293	AA349881	EST56832 infant brain Homio sapiens cDNA 5' end similar to EST containing AU repeat, mRNA sequence		Homio sapiens	21-Apr-97	42.466

TABLE 4: ALIGNMENT RESULTS

na02585	1104	GB_EST32A078215	404	A078215	48,780	28-Sep-96
na02586	807	GB_EST32A078215	404	A078215	48,780	28-Sep-96
na02587	100000	GB_PH2_A0000115	100000	AP000115	35,502	25-Sep-99
na02588	100000	GB_PH2_A0000115	100000	AP000115	35,502	20-Nov-99
na02589	50188	GB_PH2_A000047	50188	AP000047	35,502	20-Nov-99
na02590	39730	GB_BA1_MTCY8D5	39730	Z02859	38,354	18-Jun-98
na02591	43523	GB_BA1_MTCY349	43523	Z39318	39,949	17-Jun-98
na02592	158841	GB_H1T2C_A0007579	158841	AC007078	36,635	31-Jul-99
na02593	39730	GB_BA1_MTCY8D5	39730	Z02859	63,368	19-Jun-98
na02594	42408	GB_BA1_MLCJ22	42408	Z05398	63,875	17-Jul-99
na02595	477	GB_BA1_CHBA7TPO2	477	L08777	24-Jun-97	24-Jun-97
na02596	984	GB_GSS1_CNS03963	984	AL057060	37,979	26-Apr-93
na02597	984	GB_GSS1_CNS03963	984	AL057060	27,208	3-Jun-99
na02598	714	GB_B1_PNA13P5	88829	AL034556	30,270	3-Jun-99
na02599	1553	GB_BA2_AE000030	23026	AB024026	40,057	04-OCT-1989
na02600	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02601	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02602	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02603	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02604	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02605	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02606	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02607	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02608	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02609	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02610	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02611	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02612	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02613	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02614	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02615	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02616	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02617	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02618	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02619	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02620	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02621	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02622	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02623	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02624	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02625	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02626	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02627	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02628	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02629	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02630	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02631	1521	GB_BA2_AE000030	1553	AB024026	38,865	15-Nov-97
na02632	1521	GB_BA2_AE000030	1553	AB024026	38	

TABLE 4: ALIGNMENT RESULTS

[illegible]

Table 4. Panel 89

TABLE 4: ALIGNMENT RESULTS

ra02715	513	GB_GSS13/AQ44067	534	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
		GB_ESTA/H37480	489	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
		GB_GSS13/AQ44067	534	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
ra02720	825	GB_PR3/AC005495	185254	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
		GB_PR3/AC005495	185254	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
		GB_BA1/AB003132	4118	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
		GB_BA1/BLT53	5546	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
ra02721	861	GB_BA1/BLT53	5546	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
		GB_BA1/AB003132	4118	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
		GB_BA1/SC61	40745	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
ra02725	735	GB_BA1/CG143535	2531	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
		GB_EST1/D40448	391	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
		GB_BA1/AF038430	8330	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
		GB_BA1/MTCY270	37586	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
ra02727	1035	GB_BA1/MTAG84	1458	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
		GB_EST1/D40448	391	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
		GB_BA1/AF038430	8330	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
		GB_BA1/MTCY270	37586	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
ra02735	828	GB_BA1/MTAG84	1458	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
		GB_EST1/D40448	391	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
		GB_BA1/AF038430	8330	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
		GB_BA1/MTCY270	37586	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
ra02736	1080	GB_EST1/D40448	391	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
		GB_BA1/AF038430	8330	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
		GB_BA1/MTCY270	37586	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
ra02738	927	GB_PR1/AB026988	270000	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
		GB_PR1/AB026988	270000	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
		GB_PR2/AF000498	100000	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
ra02751	597	GB_HTTGA/AC010127	196552	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
		GB_HTTGA/AC010127	196552	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
		GB_HTTGA/AC010127	196552	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
		GB_HTTGA/AC010127	196552	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99
		GB_HTTGA/AC010127	196552	Alou6569	87011	GB_PL2A1/209411	87011	Alou6569	34,249	9-Jun-99

TABLE 4: ALIGNMENT RESULTS

rs22756	1014	GB_RO_CUGR1P	2785	D38103	Hamster mRNA for GIP (gastric inhibitory polypeptide) receptor, complete cds.	8-Feb-99
		GB_HTG1 CINS91DRV	243272	AL118558	Homo sapiens chromosome 14, clone R-1017Q21, *** SEQUENCING IN PROGRESS *** , in unordered pieces	15-OCT-1989
		GB_HTG1 CINS91DRV	243272	AL118558	Homo sapiens chromosome 14, clone R-1017Q21, *** SEQUENCING IN PROGRESS *** , in unordered pieces	15-OCT-1989
rs22757	869	GB_RO_RNU35245	2051	U35245	Rat vacuolar protein sorting homolog -vps35b mRNA, complete cds	15-Jan-97
		GB_RO_RNU35245	2051	U35245	Rat vacuolar protein sorting homolog -vps35b mRNA, complete cds	15-Jan-97
rs22765	882	GB_EST1 H46883	459	H46883	Yp1096 r1 Soares adult brain N25bHB55y Homo sapiens cDNA, clone IMAGE 78403 5', mRNA sequence.	31-Jun-95
		GB_PL11 WT42335	3931	AJ009235	Nicotiana tabacum DNA fragment for K-alpha right T-DNA border	6-Feb-99
		GB_PL11 WT42335	3931	AJ009235	Nicotiana tabacum DNA fragment for K-alpha right T-DNA border	07-OCT-1989
rs22766	516	GB_GSS13.AQ48419	554	AQ48419	Homo sapiens chromosome 19, clone LNF-1, 1947b, *** SEQUENCING IN PROGRESS *** , 38 unordered pieces	24-Apr-99
		GB_GSS13.AQ48419	554	AQ48419	Homo sapiens chromosome 19, clone LNF-1, 1947b, *** SEQUENCING IN PROGRESS *** , 38 unordered pieces	24-Apr-99
		GB_PR3.HS90L6	160837	Z97353	RPCH11-246A3 TV RPCH11 Homo sapiens genomic clone RPCH11-246A3, genomic survey	23-Nov-99
		GB_BA1 MTCY273	35516	Z73419	Hsp90A DNA sequence from clone 90L6 on chromosome 22(11:21-11:23. Contains an RPL11 (60S Ribosomal Protein L15) pseudogene. ESTs, STSs and GSSs, complete sequence	17-Jun-98
		GB_BA2 AF038651	4077	AF038651	Mycobacterium tuberculosis H37Rv, complete genome, segment 57182	14-Sep-98
rs22770	1689	GB_LOV AF081275	6756	AF081275	Corynebacterium glutamicum dipeptide-binding protein (dcAE) gene, partial cds, adamine phosphotransferase (apt) and GTP pyrophosphokinase (rel) genes, complete cds, and unknown gene.	31-OCT-1988
		GB_LOV AF081275	6756	AF081275	Corynebacterium glutamicum dipeptide-binding protein (dcAE) gene, partial cds, adamine phosphotransferase (apt) and GTP pyrophosphokinase (rel) genes, complete cds, and unknown gene.	31-OCT-1988
		GB_RO MMSCSELN4	3840	X81756	Italicus punctulatus estrogen receptor type alpha mRNA, complete cds	03-DEC-1981
		GB_HTG2 AF129408	138885	AF129408	M musculus rearranged T-cell receptor beta variable region (Mb17a)	04-MAR-1999
rs22774	484	GB_HTG2 AF129408	138885	AF129408	Homo sapiens chromosome 21, clone PAC 31K18 map 21q22.3, *** SEQUENCING IN PROGRESS *** , in unordered pieces	04-MAR-1999
		GB_HTG2 AF129408	138885	AF129408	Homo sapiens chromosome 21, clone PAC 31K18 map 21q22.3, *** SEQUENCING IN PROGRESS *** , in unordered pieces	04-MAR-1999
		GB_PR3 AF064859	123571	AF064859	Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homolog pseudogene L23a.	2-Jun-98
rs22775	348	GB_PR3 HSU19F10	31474	Z81145	Human DNA sequence from cosmid U19F10, between markers DXS366 and DXS37 on chromosome X contains ESTs.	23-Nov-99
		GB_EST11.A421850	293	AA211850	TR002431 NC-CGK-CDB Homo sapiens cDNA, clone IMAGE 68974, 3' similar to TR002431, 5' end contains a 12bp 5' UTR, 3' end contains a 12bp 3' UTR, 5' and 3' ends contain ESTs.	13-Aug-97
		GB_GSS5.AQ096114	383	AQ096114	EST14441 Colon adenocarcinoma IV Homo sapiens cDNA 5' end, mRNA sequence	21-Apr-97
rs22776	465	GB_EST13.AA372532	400	AA372532	HS_3030.A2.01 MF C17 Approved Human Genomic Sperm Library D Homo sapiens genomic clone P146-3030 Col-22 Row-G, genomic survey sequence	27-Aug-98
		GB_RO AF139518	8827	AF139518	Rattus norvegicus A-kinase anchor protein mRNA, complete cds	11-Jun-99
		GB_EST12 AF782935	564	AF782935	BNLGH10366 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AF076274) contains similarity to rat p47 protein (GB AB020286) [Arabidopsis thaliana], mRNA sequence	16-Jun-99
rs22777	1230	GB_HTG3.AC009407	207973	AC009407	Homo sapiens clone NH023210, *** SEQUENCING IN PROGRESS *** , 16 unordered pieces	21-Aug-99
		GB_HTG3.AC009407	207973	AC009407	Homo sapiens clone NH023210, *** SEQUENCING IN PROGRESS *** , 16 unordered pieces	21-Aug-99
		GB_BA2 AE001137	44380	AE001137	Borella burgdorferi (section 23 of 70) of the complete genome	15-DEC-1997
rs22778	348	GB_EST37 AB940900	668	AB940900	s79408 y1 Gm-c1010 Glycine max cDNA clone GENOME SYSTEMS CLONE ID Gm-c1010-1192 5' similar to SW ITRA, SOYBN P10170 TRYPsin INHIBITORS A AND C PRECURSOR, mRNA sequence	3-Aug-99
		GB_HTG4.AC008940	131884	AC008940	Homo sapiens chromosome 5, clone C1TB-H1_2318M24, *** SEQUENCING IN PROGRESS *** , 3 ordered pieces	31-OCT-1999
		GB_HTG4.AC008940	131884	AC008940	Homo sapiens chromosome 5, clone C1TB-H1_2318M24, *** SEQUENCING IN PROGRESS *** , 3 ordered pieces	31-OCT-1999

TABLE 2: GENES IDENTIFIED FROM GENBANK

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moockel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; fusQ; fisZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the fisZ gene from corynebacterium bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; fusQ		Wachi, M. et al. "A murC gene from Corynebacterium bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	disR		Kimura, E. et al. "Molecular cloning of a novel gene, disR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	disR1; disR2	D-glutamate racemase	
AB020624	murI	transketolase	
AB023377	tki		
AB024708	glbB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep, and	Replication protein; aminoglycoside adenylyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	
AF036932	aroD	3-dehydroquinate dehydratase	

002290" 00250360

GenBank™ Accession No.	Gene Name	Gene Function	Reference
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the <i>Corynebacterium glutamicum</i> (Brevibacterium lactofermentum AJ12036) <i>odhA</i> gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
F01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E01377		Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937		Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 199278088-A 1 10/02/92
F04040		Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminoelargonic acid aminotransferase and deshydrobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
F04041		Deshydrobiotinsynthetase	Kohama, K. et al. "Gene coding diaminoelargonic acid aminotransferase and deshydrobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307		Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376		Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377		Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484		Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108		Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112		Dihydro-dipicolinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
F08649		Asparase	Kohama, K. et al. "DNA fragment having promoter function in corynebacterium," Patent: JP 1995031478-A 1 02/03/95
L08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
F08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
F12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12750, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	IlvA	Threonine dehydratase	Moockel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	IlvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Kailhauer, C. et al. "Isolation and synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)

0042930 00250360

GenBank™ Accession No.	Gene Name	Gene Function	Reference
L18874	ptsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A. et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in <i>Escherichia coli</i> and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H.S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in <i>Corynebacterium glutamicum</i> ," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from <i>Corynebacterium glutamicum</i> ," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxR	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the <i>Corynebacterium diphtheriae</i> dtxR from <i>Brevibacterium lactofermentum</i> ," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the <i>Corynebacterium glutamicum</i> pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986)
M16175	5S rRNA		Park, Y.-H. et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of <i>Brevibacterium lactofermentum</i> , a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	Sano, K. et al. "Structure and function of the trp operon control regions of <i>Brevibacterium lactofermentum</i> , a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of <i>Corynebacterium glutamicum</i> ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)

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GenBank TM Accession No.	Gene Name	Gene Function	Reference
U31281	bioB	Biotin synthase	Serebriiskii, I.G. "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thrR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	3'5'-aminoglycoside phosphotransferase		
U89648	aphA-3	<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Elkman, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fdx	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> fdx gene: structural comparison of <i>C. glutamicum</i> fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i>
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonmassie, S. et al. "Nucleic sequence of the dapA gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)

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GenBank™ Accession No.	Gene Name	Gene Function	Reference
X96380	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahn, H. et al. "D-pantothenate synthesis in <i>Corynebacterium glutamicum</i> and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," <i>Appl. Environ. Microbiol.</i> , 65(3):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer <i>Brevibacterium lactofermentum</i> (<i>Corynebacterium glutamicum</i> ATCC-13869)," <i>Gene</i> , 198:217-222 (1997)
Y00140	thrB	Homoserine Kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00151	ddl	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the <i>Corynebacterium glutamicum</i> hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y08964	murC; ftsQ/diVd; ftsZ	UDP-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from <i>Brevibacterium lactofermentum</i> ," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of <i>Corynebacterium glutamicum</i> and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from <i>Corynebacterium glutamicum</i> : characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from <i>Corynebacterium glutamicum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of corynebacteriophage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)

TABLE 3: *Corynebacterium* and *Brevibacterium* Strains Which May be Used in the Practice of the Invention

Genus	Species	ATCC	FERM	NRRL	QECT	NCIMB	OBS	NCTC	DSMZ
<i>Brevibacterium</i>	ammoniaenes	21054							
<i>Brevibacterium</i>	ammoniaenes	19350							
<i>Brevibacterium</i>	ammoniaenes	19351							
<i>Brevibacterium</i>	ammoniaenes	19352							
<i>Brevibacterium</i>	ammoniaenes	19353							
<i>Brevibacterium</i>	ammoniaenes	19354							
<i>Brevibacterium</i>	ammoniaenes	19355							
<i>Brevibacterium</i>	ammoniaenes	19356							
<i>Brevibacterium</i>	ammoniaenes	21055							
<i>Brevibacterium</i>	ammoniaenes	21077							
<i>Brevibacterium</i>	ammoniaenes	21553							
<i>Brevibacterium</i>	ammoniaenes	21580							
<i>Brevibacterium</i>	ammoniaenes	39101							
<i>Brevibacterium</i>	butanicum	21196							
<i>Brevibacterium</i>	divaricatum	21792	P928						
<i>Brevibacterium</i>	flavum	21474							
<i>Brevibacterium</i>	flavum	21129							
<i>Brevibacterium</i>	flavum	21518							
<i>Brevibacterium</i>	flavum			B11474					
<i>Brevibacterium</i>	flavum			B11472					
<i>Brevibacterium</i>	flavum	21127							
<i>Brevibacterium</i>	flavum	21128							
<i>Brevibacterium</i>	flavum	21427							
<i>Brevibacterium</i>	flavum	21475							
<i>Brevibacterium</i>	flavum	21517							
<i>Brevibacterium</i>	flavum	21528							
<i>Brevibacterium</i>	flavum	21529							

Brevibacterium	flavum								
Brevibacterium	flavum					B11477			
Brevibacterium	flavum					B11478			
Brevibacterium	flavum				21127				
Brevibacterium	healii				15527				
Brevibacterium	ketoglucanicum				21004				
Brevibacterium	ketoglucanicum				21089				
Brevibacterium	ketoreductum				21914				
Brevibacterium	lactofermentum							70	
Brevibacterium	lactofermentum							74	
Brevibacterium	lactofermentum							77	
Brevibacterium	lactofermentum				21798				
Brevibacterium	lactofermentum				21799				
Brevibacterium	lactofermentum				21800				
Brevibacterium	lactofermentum				21801				
Brevibacterium	lactofermentum								
Brevibacterium	lactofermentum					B11470			
Brevibacterium	lactofermentum					B11471			
Brevibacterium	lactofermentum				21086				
Brevibacterium	lactofermentum				21420				
Brevibacterium	lactofermentum				21086				
Brevibacterium	lactofermentum				31269				
Brevibacterium	linens				9174				
Brevibacterium	linens				19391				
Brevibacterium	linens				8377				
Brevibacterium	paraffinolyticum						11160		
Brevibacterium	spec.							717.73	
Brevibacterium	spec.				14604			717.73	
Brevibacterium	spec.				21860				
Brevibacterium	spec.				21864				
Brevibacterium	spec.				21865				

Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoadipophilum	21476							
Corynebacterium	acetoadipophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniaenes	6872						2399	
Corynebacterium	ammoniaenes	15511							
Corynebacterium	fujikense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							

Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum		B8183						
Corynebacterium	glutamicum		B8182						
Corynebacterium	glutamicum		B12416						
Corynebacterium	glutamicum		B12417						
Corynebacterium	glutamicum		B12418						
Corynebacterium	glutamicum		B11476						
Corynebacterium	glutamicum	21608							
Corynebacterium	glutamicum		P973						
Corynebacterium	nitrophilus	21419					11594		
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							

Corynebacterium spec.	31090								
Corynebacterium spec.	15954								20145
Corynebacterium spec.	21857								
Corynebacterium spec.	21862								
Corynebacterium spec.	21863								

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCITC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saitama, Japan.

APPENDIX A: DNA SEQUENCES

>RXA00003-upstream
CATCCATTTCGCACAGAACATGGTAATCCTTCTCTAGGCCCCACTCGAAGCCGGCGATAT
AAGCGCCAAGAAGGCCACCCTTGCCTTCGCGGTGCAGCAC

>RXA00003
GTGCAGGTGAGAACTCTCAGCAGCGAGCTTGTCTGCAGCCTCTCCGGTGCCATCGGGGGC
GTGAACCTAGATATTGCAGCACCGAAGCCCAAGAAGTCAGGCCGCGCCACACTCACAAAA
CCCGAATTGGGATGCCGTCAATTAAGCACTGTGTTAACGCGGGATACCGAGCCACTGTTTAACC
CCCACCAAGCACAGAACATCCGACAAAGCACCAGAACATCCATGCCCGCATTTGTGCGG
CTCACTCTCTCTCAAGCCGTTTCAGGGCTGAGAAATTGCCGAAGCCAATCAATTGCAGTGG
AAGCACATCATCGACGGTGACGATGGCATGCTCAATTAATGCCAGCGCCGATATTGTCAAG
GGCGGAAAAGGCAAGGAAAGAGGGCGGTATATCCCTATCCTGAGGGCCGACGTAGCGGAA
TACCTTGCCTACACACCGCGAGGACGACGAGCAITTCATCGTAGGCTCACCGACGACGACC
GCGAGGCCCTTGGGACGCGACGAAACGCGAGATGACAAAGTGCCTCCGAGCTATACCGGCAAAAT
GCAGAAGCTACAGGCGTGAAGACTCTTCAAGACCTCCGAAGCCACTCTTGGCGTGCAGC
CTGCACGGTGTGTACGCGGACGTGATGGACCCAGCTACACGCGCGCCCATTTTCGGGCCAC
ACCGAGCAGGTAGCTGAGGAGTACTACAAACGACCGCCAAAATATTGAATCACTACTGAGA
CAAGTCAAGCGCGCTACGCG

>RXA00003-downstream
TAATACGCTTAAAGACTACGCGT

>RXA00008-upstream
CATTTGGCGTGGTGATCGCGGCATTATCGCACAACTCACCTTCGCGTTCTACGTGAGGAA
ATAAGACTATTGAACTCCTTCCCGTAGACTTAGAAAAGACT

>RXA00008
ATGGCCAAAGAGAAAAGAAAGTCGACGAAAACAACCTCAGTTCTCGCGACCAATCGCAAG
GCCCGCCATGACTACCACATCATTTGATACGTGGGAGGCGGGCGTGGTGCTCTTAGGCACC
GAAATCAAATCACTCGCGGAAGGTAAGGTATCCCTCTGGATTCTCTTTGCCACCATTTGAT
AACGGAGAAATCTGGCTTCAGCATCTCCACATCTCCGCGAGTATTCATGGGCTCTCTGGACA
AACCACACGCCCCAAGCGCACCCGCAAACTTTTGTGTCACCGCAACGAGATTGATTCCTCTG
ATGGGTAAAGTCTCGGACGGCAACCGCACGTTGGTTCCGCTCAAGCTTTACCTCAAAAAC
GGTCGCGTCAAACTCGAACTCGGACTCGCAAGAAGTAAAGCAGGATTACGACAAGCGCCAA
GATATCAAGCGTCGCACCGAAGAACGCGAAGTCAACCGTGAGCTCGGCCGTCGCAATTAAG
GGAATCAACCGC

>RXA00008-downstream
TAAATGAGTATTACATCGCAA

>RXA00015-upstream
AAGACGCACAGAAGCTACACACATAGCTACATCTGTCAGCACCAAGCCGGAACAAGAACT
ACAGCAACCGACGACACTCAACGAGCGCGACCTCCAAGAC

>RXA00015
ATGATTGATATGTGCACCACCTCCTCGACAAGAGATCATGATCCGCGAGCAATTTAAGGAG
ATCAACAACCGGTAGGGTTGTACCTCATTACGATCAGCTTGAACAGCTCGCAGAGATTTT
TCAACTAAAGACTCAATCGACATGGTCAACGAGATCTCAATCGCGATACGGATTTTCTC
AGTAATGAAGGCACAATTTTATGGAATACATTTTCAACGGTGGATTCCATACGGACAAC
GGCTATCAACCGTTGTCTATGCATATGTTGAACGAGGCTTAGCGATCCGCCCTCCACGC
ATAGTGCTC

>RXA00015-downstream
TAGATATGACACAAATCGGTATT

>RXA00018-upstream
CAACCCGCCCAACAACACATACAATTAACTTCTATATTAGTAAATAAATAACTAGTAT

TTTTAATGACTTACAAATATCAAGAAAGAACTATTCCTT

>RXA00018

ATGTCGGCATATTCTAGACCGCACAAAGATCGCCACCGCGTTGCTGTCGCAACTCTTACC
CTCACCTTTGTTAGCTCTGCTGCGCGGTTGTCATGACGCGCAACAAATCCATCAGCGGT
CCAGAAATCCCTCGTGCCTTTTAATCAACAGCGTTGGGATGACAGCAAGTTAAGCTTGAC
GACACCATCGCTACGGCCAAAACTCATTTGGTACAAACAGGCGAATGCAACCGCAACGAA
CAGGATCTACTTTACTGGCTATCTTTTCCAGCAACCGCACAGCAATTTACCTTGCACTC
AACAACGCTTATGCCGATGCCGTAGCAATCAAGACAGCTTTGTCGGCCCAACATGTGAC
GGTCTTAAAGAGTCCAAGATTGCCAGCGAACACGCCGTCTGAGGTTGTGGGTGCACTG
AATGTACTCGCCCGAGCACAAAAGCGCTGCAGATTAATCCGACACCTACGAACAGCAA
CGTCGTTGTGATGCCCTTCGCTAGCAAGCGGAGATGAATCAGATGTTCTTATGCGCAT
GATCGACCATGCTGCAGCTTCGTGCACACTAGCTGACATTGACAGGGCGTCCACAGAC
ATTCGCGATATTCGGGCTCAAAACAAAGCTTTGAACGTGATCTTGCCCGGAGCAAAAA
GAGGCCAGCAGCAGCACGCTGCTCAAGCTGTAGACACTTCGACCAACCAACATCAAGC
ACAGAAGATCGTGTCAACGACATCTTAAAGAGTCCCGTACCGATCAGTGGCGACAGT
TACACGCGCTCAACGACAACGAGCGCACAAAGCACTGAGCGGATTTCTGCAACCAACCT
TCATATCTGTACGCTGCTCTCGACAGCTTGAAGCAGCTGCGCAGCATATTGATCTCAAT
ACCCAGTGCACAACTCGATGATCTTCGTGAACCTACCAACAATGACACGCGTGATCAC
ACCGGCTCCGCTCATTTCCATTGCCGATCACTCAGACATCAACCAATGAATCAATGAA
TTACCGGATGACACTTTTGCCACAGAGACGTTGCCAACAGCACAGGATCAGTAATT
GCTCAACGTGAAGAACTGCAACGAGCAAAGGAGCAGCTAGAGAACAACGCGACTCGCC
AAGAAGCAGAAAGGGCGCTCGCAACGACGAAATTCAGGAACGTGACGCGCGCGAAGCA
GCATGCGTGAAGCACAAAGACCTCCTCAGTGCCTCGATGACACAGGCAACGCAACAGT
GATGACACAGCAGCGCTAGTAGACGGTCTTCTCAATAAC

>RXA00018-downstream

TAACAAATCAGCAACACCGCTCAC

>RXA00020-upstream

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AATAACTAAGTAATGTAAGTAAAGGACTTTTAAATAACT

>RXA00020

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>RXA00021-upstream

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>RXA00056-downstream
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>RXA00058-upstream
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>RXA00058
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 GGCCTTTGTGACGGCGGGTAGCAGGTGTGTGGCACTGGTCTAGCTCTCGCGCTTTTG
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>RXA00058-downstream
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>RXA00059-upstream
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>RXA00059
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>RXA00059-downstream
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>RXA00063-upstream
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>RXA00063
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>RXA00063-downstream
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>RXA00065-upstream
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>RXA00065
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>RXA00065-downstream
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>RXA00067-upstream
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>RXA00067
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>RXA00067-downstream
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>RXA00068-upstream
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>RXA00068
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>RXA00068-downstream
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>RXA00071-upstream
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>RXA00071
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>RXA00071-downstream
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>RXA00077-upstream
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>RXA00077

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>RXA00077-downstream

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>RXA00079-upstream

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>RXA00079

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>RXA00079-downstream

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>RXA00080-upstream

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>RXA00080

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>RXA00082-upstream

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>RXA00082

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>RXA00082-downstream

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>RXA00083-upstream

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>RXA00083

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>RXA00083-downstream

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>RXA00087-upstream

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>RXA00087

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>RXA00087-downstream

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>RXA00093-upstream

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>RXA00093

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>RXA00097
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>RXA00101-upstream
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>RXA00101
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>RXA00108
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>RXA00110-upstream

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>RXA00110
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>RXA00110-downstream
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>RXA00114
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>RXA00114-downstream
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>RXA00117-upstream
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>RXA00117
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>RXA00120
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>RXA00121
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>RXA00142-upstream
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>RXA00150

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>RXA00151-upstream

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>RXA00153-upstream

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>RXA00153

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>RXA00154

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>RXA00155-upstream

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>RXA00155

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>RXA00159-upstream

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>RXA00159-downstream
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>RXA00161-upstream
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>RXA00161
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>RXA00161-downstream
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>RXA00162-upstream
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>RXA00162
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>RXA00162-downstream
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>RXA00167-upstream
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>RXA00167
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>RXA00169-upstream

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>RXA00169

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>RXA00170

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>RXA00173-upstream
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>RXA00173-downstream
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>RXA00174-upstream
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>RXA00174-downstream
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>RXA00175-upstream
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>RXA00175
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>RXA00176-downstream
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>RXA00179-downstream
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>RXA00180

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>RXA00183-upstream

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>RXA00183

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>RXA00183-downstream

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>RXA00185-upstream

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>RXA00185

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>RXA00199

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>RXA00199-downstream

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>RXA00200

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>RXA00200-downstream

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>RXA00207-upstream

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>RXA00207
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>RXA00207-downstream
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>RXA00211-upstream
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>RXA00211
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>RXA00211-downstream
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>RXA00218-upstream
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>RXA00218
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>RXA00218-downstream
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>RXA00220-upstream

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>RXA00220

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>RXA00220-downstream

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>RXA00222-upstream

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>RXA00222

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>RXA00230-upstream

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>RXA00230

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>RXA00230-downstream
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>RXA00232-upstream
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>RXA00232
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>RXA00232-downstream
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>RXA00233-upstream
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>RXA00233
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>RXA00234
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>RXA00234-downstream

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>RXA00236-upstream

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>RXA00236

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>RXA00236-downstream

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>RXA00237-upstream

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>RXA00237

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>RXA00237-downstream

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>RXA00238-upstream

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>RXA00238

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>RXA00238-downstream

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>RXA00239-upstream

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>RXA00239

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>RXA00239-downstream

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>RXA00240-upstream

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>RXA00240

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>RXA00240-downstream

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>RXA00242-upstream

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>RXA00242

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>RXA00244-upstream

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>RXA00244

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>RXA00244-downstream

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>RXA00245-upstream

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>RXA00245

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>RXA00247-upstream

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>RXA00247

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>RXA00248-upstream
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>RXA00285

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>RXA00286

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>RXA00373-upstream
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>RXA00373
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>RXA00375-upstream
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>RXA00375
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>RXA00380
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>RXA00394-upstream
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>RXA00395-upstream
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>RXA00399
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>RXA00408-upstream
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>RXA00411
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>RXA00416
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>RXA00418

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>RXA00422

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>RXA00423-upstream

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>RXA00423

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>RXA00424-upstream

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>RXA00424

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>RXA00428
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>RXA00430
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>RXA00433-upstream
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>RXA00535-downstream
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>RXA00540-upstream
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>RXA00540
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>RXA00540-downstream
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>RXA00546
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>RXA00546-downstream
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>RXA00547-upstream
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>RXA00547
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>RXA00549
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>RXA00549-downstream
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>RXA00550-upstream
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>RXA00550
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>RXA00552
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>RXA00553
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>RXA00553-downstream
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>RXA00554-upstream
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>RXA00554

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>RXA00555

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>RXA00560

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>RXA00563

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>RXA00573

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>RXA00574
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>RXA00587-upstream

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>RXA00587

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>RXA00587-downstream

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>RXA00589-upstream

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>RXA00589

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>RXA00595

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>RXA00595-downstream

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>RXA00597-upstream

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>RXA00597

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>RXA00598-upstream

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>RXA00598

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>RXA00598-downstream

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>RXA00601-upstream

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>RXA00611
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>RXA00614

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>RXA00616-upstream

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>RXA00616

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>RXA00617-upstream

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>RXA00617

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>RXA00628

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>RXA00628-downstream

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>RXA00631-upstream

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>RXA00631

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>RXA00647-downstream
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>RXA00649-upstream

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>RXA00649

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>RXA00649-downstream

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>RXA00652-upstream

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>RXA00652

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>RXA00652-downstream

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>RXA00653-upstream

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>RXA00653

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>RXA00716
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>RXA00719
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>RXA00720
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>RXA00722-upstream
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>RXA00722
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>RXA00729

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>RXA00731

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>RXA00743-upstream
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>RXA00746-upstream

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>RXA00746

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>RXA00746-downstream

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>RXA00747-upstream

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>RXA00747

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>RXA00747-downstream

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>RXA00748-upstream

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>RXA00748

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>RXA00749-upstream
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>RXA00749
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>RXA00749-downstream
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>RXA00750-upstream
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>RXA00750
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>RXA00750-downstream
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>RXA00751-upstream
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>RXA00751
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>RXA00752-downstream
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>RXA00757
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>RXA00757-downstream
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>RXA00763

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>RXA00763-downstream

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>RXA00765-upstream

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>RXA00765

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>RXA00765-downstream

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>RXA00767-upstream

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>RXA00767

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>RXA00767-downstream
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>RXA00768-upstream
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>RXA00768
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>RXA00768-downstream
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>RXA00769-upstream
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>RXA00769
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>RXA00769-downstream
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>RXA00771-upstream
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>RXA00771
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>RXA00771-downstream
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>RXA00781-upstream
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>RXA00781

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>RXA00781-downstream

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>RXA00785

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>RXA00788-upstream

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>RXA00788

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>RXA00788-downstream

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>RXA00795-upstream

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>RXA00795

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>RXA00795-downstream

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>RXA00804-upstream

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>RXA00804

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>RXA00804-downstream

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>RXA00805-upstream

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>RXA00805

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>RXA00805-downstream

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>RXA00808

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>RXA00808-downstream

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>RXA00812-upstream

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>RXA00812-downstream
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>RXA00814-upstream
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>RXA00814
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>RXA00814-downstream
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>RXA00815-upstream
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>RXA00815
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>RXA00826-downstream
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>RXA00830
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>RXA00830-downstream

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>RXA00831-upstream

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>RXA00831

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>RXA00835

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>RXA00835-downstream

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>RXA00836-upstream

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>RXA00836

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>RXA00840

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>RXA00841-upstream

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>RXA00841

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>RXA00846-upstream

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>RXA00846

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>RXA00853

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>RXA00854-upstream

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>RXA00854

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>RXA00854-downstream

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>RXA00855-upstream

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>RXA00855

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>RXA00861

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>RXA00862-upstream

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>RXA00862

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>RXA00869

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>RXA00874-upstream

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>RXA00874

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>RXA00876-upstream
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>RXA00876
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>RXA00881-upstream
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>RXA00881
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>RXA00882-upstream
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>RXA00882
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>RXA00883-upstream
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>RXA00883
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>RXA00887-upstream
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>RXA00895-upstream

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>RXA00895

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>RXA00904-upstream

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>RXA00904

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>RXA00908

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>RXA00915

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>RXA00916

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>RXA00917

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>RXA00930
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>RXA00946
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>RXA01008-downstream
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>RXA01011-upstream
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>RXA01011
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>RXA01011-downstream
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>RXA01016
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>RXA01017-upstream

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>RXA01017

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>RXA01021-upstream

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>RXA01021

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>RXA01023

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>RXA01028

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>RXA01028-downstream
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RXA01029-upstream
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>RXA01029-downstream
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>RXA01031-upstream
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>RXA01033-upstream
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>RXA01034
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>RXA01036-upstream

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>RXA01036

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>RXA01036-downstream

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>RXA01037-upstream

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>RXA01037

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>RXA01038-upstream

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>RXA01038

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>RXA01038-downstream

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>RXA01039-upstream

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>RXA01039

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>RXA01040-upstream

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>RXA01040

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>RXA01041-upstream

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>RXA01041

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>RXA01041-downstream

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>RXA01042-upstream

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>RXA01043-upstream

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>RXA01043

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>RXA01044-upstream

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>RXA01044

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>RXA01148-upstream

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>RXA01148

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>RXA01148-downstream

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>RXA01153

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>RXA01154

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>RXA01155-upstream

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>RXA01155

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>RXA01156-upstream

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>RXA01156

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>RXA01156-downstream

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>RXA01158-upstream

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>RXA01158

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>RXA01158-downstream
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>RXA01159-upstream
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>RXA01159
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>RXA01160
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>RXA01160-downstream
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RXA01163-upstream
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>RXA01163
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>RXA01165-upstream

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>RXA01165

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>RXA01165-downstream

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>RXA01166

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>RXA01166-downstream

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>RXA01167

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>RXA01167-downstream

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>RXA01169

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>RXA01169-downstream
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>RXA01170-upstream
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>RXA01170
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>RXA01170-downstream
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>RXA01171-upstream
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>RXA01171
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>RXA01171-downstream
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>RXA01173-upstream
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>RXA01173
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>RXA01173-downstream
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>RXA01174-upstream
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>RXA01174
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>RXA01174-downstream
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>RXA01176-upstream
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>RXA01176
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>RXA01176-downstream
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>RXA01177-upstream
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>RXA01177
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>RXA01177-downstream
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>RXA01178-upstream
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>RXA01178
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>RXA01178-downstream
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>RXA01184-upstream
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>RXA01184
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>RXA01184-downstream
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>RXA01186-upstream
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>RXA01186
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>RXA01186-downstream
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>RXA01187-upstream
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>RXA01187
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>RXA01187-downstream

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>RXA01195-upstream

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>RXA01195

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>RXA01195-downstream

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>RXA01196-upstream

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>RXA01196

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>RXA01196-downstream

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>RXA01197-upstream

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>RXA01197

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>RXA01197-downstream
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>RXA01198-upstream
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>RXA01198
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>RXA01198-downstream
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>RXA01206-upstream
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>RXA01206
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>RXA01207-upstream
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>RXA01207
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>RXA01207-downstream
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>RXA01210
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>RXA01210-downstream
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>RXA01213-upstream
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>RXA01213
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>RXA01213-downstream
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>RXA01218-upstream
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>RXA01218
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>RXA01218-downstream

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>RXA01229-upstream

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>RXA01229

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>RXA01231-upstream

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>RXA01231

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>RXA01231-downstream

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>RXA01234-upstream

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>RXA01234

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>RXA01234-downstream

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>RXA01237-upstream

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>RXA01237

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>RXA01237-downstream

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>RXA01246-upstream

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>RXA01246

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>RXA01249-upstream

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>RXA01249

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>RXA01251-upstream

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>RXA01251

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>RXA01251-downstream

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>RXA01263-upstream
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>RXA01263
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>RXA01266-upstream
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>RXA01266
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>RXA01313
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>RXA01364
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>RXA01401-upstream
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>RXA01401
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 GACACCTAGCGGTTGACCTT

>RXA01401-downstream
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>RXA01402-upstream

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GCCCACTTCCCCACGAACAAGTCCACGGCGTCGGCCCCCTC

>RXA01402

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TCCCGAGCAGAATTCCTAGAAACCCACGGCATGGACGCTTCTCAACGCCGAAAAAATC
CACGCCCAACCCAGCAACCGTAGGAACCCCGACACAGTCCCGACATTTCCGGCGAA
CTCCTCCCCCTGGGCTTACCGAGGCGCGCCCAAAGCGACCTCCCTCCAAAGAAAGAAATC
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>RXA01402-downstream

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>RXA01403

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CAACAGATCTTCGACCTAGAGAAACAAGCGAGCGCTATGTGTCTTTGCGGCAACAATG
AATCTCCAGAACACGGAAAATCAATCTGAAGAAATCTCGTGACATCTTCGATGCAGGATG
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>RXA01403-downstream

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>RXA01405-upstream

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>RXA01405

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>RXA01405-downstream

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>RXA01409

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>RXA01409-downstream
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>RXA01413-upstream
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>RXA01413
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 AAGGGTGTGAGGTTGTAGACCCAGTGGCAACCGCAAAGCGTGTGGTACCCGTGCGGTT
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>RXA01413-downstream
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>RXA01414-upstream
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 GTTTTAAGAATTTTATTACCTCTCTACAGGAGAACCCAGCG

>RXA01414
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>RXA01414-downstream
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>RXA01417-upstream
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>RXA01417
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>RXA01417-downstream
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>RXA01421-upstream
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>RXA01421
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>RXA01421-downstream
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>RXA01422
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GCC

>RXA01422-downstream
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>RXA01425-upstream
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>RXA01425
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>RXA01425-downstream
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>RXA01429-upstream
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>RXA01429
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>RXA01429-downstream
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>RXA01434
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>RXA01434-downstream
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>RXA01439-upstream
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>RXA01439
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GACGCC

>RXA01439-downstream
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>RXA01440-upstream
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>RXA01440
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>RXA01440-downstream
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>RXA01441-upstream
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>RXA01441
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GGCACACAC

>RXA01441-downstream
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>RXA01445-upstream
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>RXA01445
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>RXA01445-downstream
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>RXA01447-upstream
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>RXA01447
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>RXA01447-downstream
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>RXA01448-upstream
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>RXA01448
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>RXA01448-downstream
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>RXA01452-upstream
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>RXA01452
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>RXA01452-downstream
TGAGGAGGAGCATGGCTCAGA

>RXA01456-upstream
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>RXA01456
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>RXA01456-downstream
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>RXA01457-upstream
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>RXA01457
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>RXA01457-downstream
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>RXA01459-upstream

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>RXA01459

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>RXA01459-downstream

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>RXA01460-upstream

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>RXA01460

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>RXA01460-downstream

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>RXA01463-upstream

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>RXA01463

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>RXA01469
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>RXA01469-downstream
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>RXA01470
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>RXA01471-upstream
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>RXA01471

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>RXA01472-upstream
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>RXA01472
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>RXA01473-downstream
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>RXA01474-upstream

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>RXA01474

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>RXA01475-upstream

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>RXA01475

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>RXA01476

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>RXA01479

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>RXA01479-downstream
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>RXA01484-upstream
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>RXA01484
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>RXA01485
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>RXA01485-downstream
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>RXA01488-upstream
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>RXA01488
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>RXA01492
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>RXA01492-downstream
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>RXA01494-upstream
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>RXA01494

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>RXA01494-downstream

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>RXA01497-upstream

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>RXA01497

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>RXA01501

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>RXA01600
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>RXA01624
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>RXA01635-upstream

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>RXA01639-upstream

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>RXA01685
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>RXA01686
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>RXA01693
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>RXA1696
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>RXA01709-upstream

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>RXA01709

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>RXA01711

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>RXA01782-upstream

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>RXA01799-upstream
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>RXA01799
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>RXA01799-downstream
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>RXA01800-upstream
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>RXA01800
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>RXA01800-downstream
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>RXA01803-upstream
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>RXA01803
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>RXA01803-downstream
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>RXA01804-upstream
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>RXA01804
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>RXA01805-upstream
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>RXA01805
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>RXA01806-upstream
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>RXA01806
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>RXA01806-downstream
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>RXA01809-downstream
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>RXA0182
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>RXA01813-upstream

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>RXA01813

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>RXA01815-upstream

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>RXA01815

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>RXA01815-downstream

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>RXA01816-upstream

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>RXA01816

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>RXA01816-downstream
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>RXA01817-upstream
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>RXA01817
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>RXA01817-downstream
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>RXA01820-upstream
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>RXA01820
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>RXA01820-downstream
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>RXA01825-upstream

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>RXA01825

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>RXA01825-downstream

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>RXA01831-upstream

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>RXA01831

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>RXA01831-downstream

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>RXA01834-upstream

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>RXA01834

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>RXA01834-downstream

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>RXA01842-upstream

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>RXA01842

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>RXA01842-downstream

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>RXA01844-upstream

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>RXA01844

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>RXA01844-downstream

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>RXA01845-upstream

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>RXA01845

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>RXA01845-downstream

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>RXA01846-upstream

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>RXA01846

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>RXA01847-upstream

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>RXA01847

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>RXA01847-downstream

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>RXA01856-upstream

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>RXA01856

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>RXA01857-upstream

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>RXA01857

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>RXA01858-upstream
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>RXA01874
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>RXA01910-downstream
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>RXA01911-upstream
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>RXA01911
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>RXA01923
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>RXA01931
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>RXA01945
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>RXA01957

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>RXA01958-upstream

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>RXA01962-upstream

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>RXA01966-upstream
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>RXA01966
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>RXA01968-downstream
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>RXA01969
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>RXA01969-downstream
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>RXA01973-downstream
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>RXA01974-upstream
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>RXA01974
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>RXA01976-upstream

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>RXA01976

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>RXA01976--downstream
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>RXA01977--upstream
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>RXA01977
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>RXA01977--downstream
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>RXA01982--upstream
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>RXA01982
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>RXA01987-upstream
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>RXA01987
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>RXA01988
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>RXA01990
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>RXA01991-upstream
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>RXA01991
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>RXA01992
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>RXA01992-downstream
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>RXA01996-upstream
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>RXA01996
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>RXA01999-upstream
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>RXA01999
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>RXA02009--upstream

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>RXA02013

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>RXA02019
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>RXA02021-downstream
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>RXA02023-upstream
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>RXA02023
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>RXA02023-downstream
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>RXA02032-upstream
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>RXA02032
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>RXA02032-downstream
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>RXA02036-upstream
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>RXA02036
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>RXA02036-downstream
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>RXA02039
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>RXA02039-downstream
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>RXA02040
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>RXA02040-downstream
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>RXA02045-upstream
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>RXA02045
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GACATTTTCGGCACTGAAGGC

>RXA02045-downstream
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>RXA02046-upstream
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>RXA02046
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>RXA02049-upstream
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>RXA02049
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>RXA02049-downstream
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>RXA02050-upstream
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>RXA02050
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>RXA02050-downstream
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>RXA02051-upstream
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>RXA02051
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>RXA02051-downstream
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>RXA02053-upstream
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>RXA02053
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>RXA02053-downstream

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>RXA02057-upstream

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>RXA02057

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>RXA02057-downstream

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>RXA02058-upstream

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>RXA02058

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>RXA02058-downstream

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>RXA02059-upstream

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>RXA02059

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>RXA02059-downstream

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>RXA02066-upstream
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>RXA02066
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>RXA02066-downstream
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>RXA02067-upstream
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>RXA02067
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>RXA02067-downstream
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>RXA02069-upstream
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>RXA02069
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>RXA02069-downstream
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>RXA02070-upstream
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>RXA02070

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>RXA02070-downstream
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>RXA02071-upstream

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>RXA02071

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>RXA02076-upstream

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>RXA02076

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>RXA02076-downstream
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>RXA02080-upstream

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>RXA02080

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>RXA02080-downstream

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>RXA02081-upstream

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>RXA02081

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>RXA02081-downstream

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>RXA02084-upstream

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>RXA02084

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>RXA02089-upstream

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>RXA02089

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>RXA02090-upstream

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>RXA02090

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>RXA02091-upstream

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>RXA02091

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>RXA02094-upstream

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>RXA02094

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>RXA02097

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>RXA02102
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>RXA02102-downstream
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>RXA02108-upstream

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>RXA02108

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>RXA02108-downstream

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>RXA02109-upstream

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>RXA02109

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>RXA02114

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>RXA02117-upstream

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>RXA02117

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>RXA02121-upstream

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>RXA02121

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>RXA02123-upstream

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>RXA02123

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>RXA02124-upstream
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>RXA02124
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>RXA02151-upstream

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>RXA02163

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>RXA02169-downstream
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>RXA02170-upstream
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>RXA02170
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>RXA02170-downstream
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>RXA02172-upstream
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>RXA02172
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>RXA02172-downstream
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>RXA02177-upstream
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>RXA02177
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>RXA02177-downstream
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>RXA02178-upstream
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>RXA02178
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>RXA02178-downstream
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>RXA02180
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>RXA02180-downstream
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>RXA02181-upstream
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>RXA02181
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>RXA02181-downstream
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>RXA02183-upstream
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>RXA02183
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>RXA02183-downstream
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>RXA02185-upstream
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>RXA02185
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>RXA02185-downstream
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>RXA02186-upstream
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>RXA02186
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>RXA02186-downstream
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>RXA02187-upstream

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>RXA02187

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>RXA02187-downstream
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>RXA02199-upstream

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>RXA02199

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>RXA02199-downstream
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>RXA02203-upstream
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>RXA02203
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>RXA02203-downstream
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>RXA02206-upstream
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>RXA02206
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>RXA02206-downstream
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>RXA02207-upstream
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>RXA02207
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>RXA02211-upstream

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>RXA02211

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>RXA02212-upstream

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>RXA02212

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>RXA02212-downstream

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>RXA02216

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>RXA02216-downstream

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>RXA02217-upstream

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>RXA02217

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>RXA02217-downstream
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>RXA02218-upstream
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>RXA02218
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>RXA02218-downstream
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>RXA02219-upstream
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>RXA02219
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>RXA02219-downstream
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>RXA02221-upstream

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>RXA02221

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>RXA02223-upstream

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>RXA02223

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>RXA02226-upstream

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>RXA02226

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>RXA02227-upstream

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>RXA02227

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>RXA02227-downstream

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>RXA02230-upstream

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>RXA02230

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>RXA02230-downstream

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>RXA02231-upstream

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>RXA02231

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>RXA02238
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>RXA02238-downstream
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>RXA02244
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>RXA02244-downstream

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>RXA02254-upstream

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>RXA02254

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>RXA02254-downstream

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>RXA02255-upstream

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>RXA02255

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>RXA02255-downstream

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>RXA02266-upstream

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>RXA02266

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>RXA02266-downstream
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>RXA02267-upstream
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>RXA02267
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>RXA02271
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>RXA02279
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>RXA02280
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>RXA02280-downstream
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>RXA02285-upstream
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>RXA02285
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>RXA02285-downstream
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>RXA02286-upstream
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>RXA02286
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>RXA02286-downstream
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>RXA02287-upstream
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>RXA02287
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>RXA02295-upstream

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>RXA02295

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>RXA02296-upstream

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>RXA02296

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>RXA02296-downstream

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>RXA02297-upstream

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>RXA02297

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>RXA02297-downstream
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>RXA02298-upstream
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>RXA02298
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>RXA02300
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>RXA02300-downstream

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>RXA02301-upstream

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>RXA02301

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>RXA02302-upstream

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>RXA02302

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>RXA02303

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>RXA02303-downstream

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>RXA02304-upstream

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>RXA02304

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>RXA02307-upstream

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>RXA02307

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>RXA02308-upstream

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>RXA02308

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>RXA02308-downstream

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>RXA02314-upstream

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>RXA02314

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>RXA02324-upstream

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>RXA02324

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>RXA02325-upstream

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>RXA02325

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>RXA02331-upstream
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>RXA02331
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>RXA02336-upstream
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>RXA02336
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>RXA02336-downstream
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>RXA02337-upstream
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>RXA02337
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>RXA02338-upstream

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>RXA02338

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>RXA02339

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>RXA02339-downstream

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>RXA02340

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>RXA02340-downstream

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>RXA02341-upstream

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>RXA02341

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>RXA02347-upstream

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>RXA02347

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>RXA02347-downstream

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>RXA02349-upstream

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>RXA02349

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>RXA02352

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>RXA02352-downstream

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>RXA02356-upstream

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>RXA02356

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>RXA02356-downstream
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>RXA02358-upstream
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>RXA02358
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>RXA02358-downstream
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>RXA02360
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>RXA02360-downstream
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>RXA02361-upstream
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>RXA02361
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>RXA02361-downstream
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>RXA02362-upstream
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>RXA02362
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>RXA02362-downstream
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>RXA02367-upstream
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>RXA02367
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>RXA02368-upstream
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>RXA02368
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>RXA02368-downstream
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>RXA02374-upstream
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>RXA02374
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>RXA02374-downstream
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>RXA02381
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>RXA02381-downstream
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>RXA02383
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>RXA02390
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>RXA02393-upstream
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>RXA02393
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>RXA02395
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>RXA02396-upstream
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>RXA02396
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>RXA02396-downstream
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>RXA02398-upstream
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>RXA02398
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>RXA02403
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>RXA02406-upstream
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>RXA02406

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>RXA02407-upstream

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>RXA02407

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>RXA02408

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>RXA02409

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>RXA02412-upstream
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>RXA02412
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>RXA02417-upstream
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>RXA02417
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>RXA02421
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>RXA02423-upstream
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>RXA02423
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>RXA02427-upstream
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>RXA02427

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>RXA02428-upstream

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>RXA02428

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>RXA02430

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>RXA02433-upstream

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>RXA02433

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>RXA02437-upstream

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>RXA02776
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>RXA02776-downstream
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>RXA02777-upstream
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>RXA02777
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>RXA02777-downstream

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>RXA02778-upstream

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>RXA02778

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>RXA02778-downstream

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>RXA02779-upstream

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>RXA02779

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>RXA02779-downstream

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>RXA02780-upstream

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>RXA02780

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>RXA02780-downstream

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>RXA02781-upstream

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>RXA02781

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>RXA02781-downstream
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>RXA02782-upstream
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>RXA02782
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>RXA02782-downstream
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>RXA02783-upstream
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>RXA02783
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>RXA02784-upstream
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>RXA02784

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>RXA02786

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>RXA02786-downstream

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>RXA02789-upstream

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>RXA02789

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>RXA02789-downstream

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>RXA02793-upstream

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>RXA02793

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>RXA02796-upstream
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>RXA02796
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>RXA02798-upstream
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>RXA02815
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>RXA02823-upstream

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>RXA02823

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>RXA02824

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>RXA02825

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>RXA02827-upstream

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>RXA02827

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CAT

>RXA02838

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>RXA02840-upstream

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>RXA02840

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>RXA02840-downstream

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>RXA02841-upstream

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>RXA02841

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>RXA02842

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>RXA02842-downstream

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>RXA02845

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>RXA02846

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>RXA02847-upstream

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>RXA02847

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>RXA02848-upstream

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>RXA02848

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>RXA02849

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>RXA02849-downstream

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>RXA02856-upstream

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>RXA02856

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>RXA02856-downstream
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>RXA02858
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>RXA02858-downstream
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>RXA02862-upstream
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>RXA02862
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>RXA02867-upstream
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>RXA02867
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>RXA02874

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>RXA02874-downstream

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>RXA02876-upstream

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>RXA02876

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>RXA02876-downstream

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>RXA02881-upstream

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>RXA02881

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>RXA02881-downstream
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>RXA02884-upstream
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>RXA02884
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>RXA02885
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>RXA02885-downstream
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>RXA02888-upstream
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>RXA02888
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>RXA02888-downstream
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>RXA02892-upstream
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>RXA02892
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>RXA02892-downstream
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>RXA02898-upstream
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>RXA02898
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>RXA02899-upstream

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>RXA02899

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>RXA02899-downstream

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>RXA02905-upstream

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>RXA02905

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>RXN0022-upstream

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>RXN0022

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>RXN00154-downstream
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>RXN00162-upstream
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>RXN00162
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>RXN00162-downstream
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>RXN00167-upstream
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>RXN00167
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>RXN00171
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>RXN00171-downstream
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>RXN00194-upstream
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>RXN00194
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>RXN00197-upstream
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>RXN00197
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>RXN00197-downstream
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>RXN00216-upstream
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>RXN00216
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>RXN00216-downstream

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>RXN00222-upstream

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>RXN00222

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>RXN00222-downstream

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>RXN00232-upstream

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>RXN00232

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>RXN00232-downstream

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>RXN00236-upstream

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>RXN00236

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>RXN00236-downstream
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>RXN00242-upstream
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>RXN00242
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>RXN00242-downstream
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>RXN00247-upstream
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>RXN00247
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>RXN00247-downstream
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>RXN00256-upstream
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>RXN00256
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>RXN00256-downstream
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>RXN00264-upstream
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>RXN00264
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>RXN00264-downstream
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>RXN00267-upstream
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>RXN00267
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>RXN00267-downstream
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>RXN00271-upstream
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>RXN00271

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>RXN00271-downstream

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>RXN00272-upstream

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>RXN00272

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>RXN00272-downstream

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RXN00283-upstream

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>RXN00283

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>RXN00334-upstream
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>RXN00334
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>RXN00338-upstream
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>RXN00338
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RXN00915-upstream

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>RXN01128
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>RXN01153
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>RXN01154
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>RXN01155

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>RXN01167

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>RXN01169-upstream

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>RXN01229-upstream

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>RXN01229

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>RXN01251
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>RXN01263-upstream

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>RXN01263

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>RXN01266-upstream

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>RXN01266

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>RXN01275-upstream

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>RXN01275

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>RXN01769
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>RXN01769-downstream
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>RXN01771-upstream
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>RXN01771
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>RXN01771-downstream
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>RXN01774-upstream
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>RXN01774
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>RXN01787
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>RXN01803
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>RXN01811-downstream
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RXN01875-upstream

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>RXN01875

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>RXN01875-downstream

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RXN01877-upstream

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>RXN01877

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>RXN01879-upstream

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>RXN01879

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>RXN01896-upstream

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>RXN01896

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>RXN01902
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>RXN01945
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RXN01988-upstream

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>RXN01991

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>RXN02007-downstream
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>RXN02014-upstream
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>RXN02014
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>RXN02014-downstream
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>RXN02019
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>RXN02023
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>RXN02032
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>RXN02039-downstream
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>RXN02049-upstream
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>RXN02049

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>RXN02050-upstream
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>RXN02066-upstream
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>RXN02066
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>RXN02075
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>RXN02076

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>RXN02094-upstream

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>RXN02104-upstream

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>RXN02104

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RXN02107-upstream
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>RXN02108-upstream
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>RXN02108
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>RXN02121

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>RXN02121-downstream
TGAGTAGGCTGGCGGGCAGGTGC

RXN02138-upstream

TCACTCCGCGAGATCCGTAAAAAGGGGAGTACACTGCAAGCCTATGATGTCCGGCCCTA
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>RXN02138

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CGCGGCTGCTTGGCCCTTCGTTTACAGCTTTACTTCGACGACCGCACCCCTGTATGGCGAT
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>RXN02138-downstream
TAAAGAGATTCCGTTATGTAGGA

>RXN02151-upstream

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>RXN02151

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>RXN02151-downstream

TAACTGAAGCATAACCTGTGTGA

>RXN02169-upstream

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>RXN02169

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>RXN02169-downstream

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>RXN02180-upstream

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>RXN02180

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>RXN02180-downstream

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>RXN02185-upstream
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>RXN02185
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>RXN02185-downstream
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>RXN02186-upstream
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>RXN02186
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>RXN02186-downstream
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>RXN02207-upstream
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>RXN02207
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CCCCACCGACGAGGAACC

>RXN02223-upstream
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>RXN02223

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>RXN02226-upstream

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>RXN02226

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RXN02238-upstream

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>RXN02238

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>RXN02238-downstream

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>RXN02254

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>RXN02254-downstream
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RXN02271-upstream
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>RXN02271
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>RXN02271-downstream
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>RXN02279-upstream
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>RXN02279
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>RXN02279-downstream

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>RXN02296-upstream

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>RXN02296

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>RXN02296-downstream

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RXN02300-upstream

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>RXN02300

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>RXN02300-downstream

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>RXN02301-upstream

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>RXN02301

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>RXN02301-downstream

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>RXN02302-upstream

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>RXN02302

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>RXN02302-downstream

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RXN02303-upstream

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>RXN02303

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>RXN02303-downstream

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>RXN02307-upstream

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>RXN02307

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RXN02314-upstream
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>RXN02314
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>RXN02337
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>RXN02339
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>RXN02340
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>RXN02360-upstream
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>RXN02360

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>RXN02361
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>RXN02367-upstream
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>RXN02367
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RXN02368-upstream
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>RXN02368
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>RXN02381
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>RXN02381-downstream
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>RXN02383-upstream
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>RXN02383
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>RXN02387
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>RXN02398-upstream
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>RXN02398

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>RXN02406-upstream
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>RXN02406
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>RXN02407-upstream
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>RXN02408-upstream
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>RXN02408
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RXN20593-upstream

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>RXN20593

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>RXN20606

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>RXN02626
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RXN02680 -upstream
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>RXN02680 -downstream
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RXN02693 -upstream

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RXN02696-upstream

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>RXN02696

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>RXN02696-downstream

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RXN02697-upstream

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RXN02720-upstream
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>RXN02928-downstream
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RXN02931-upstream
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>RXN02931
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>RXN02931-downstream
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RXN02932-upstream

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>RXN02932

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RXN02934-upstream

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RXN02939-upstream

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RXN02950-upstream

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RXN02997

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>RXN03001

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RXN03010-upstream
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RXN03012
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RXN03017-upstream

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>RXN03018-upstream

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>RXN03018

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RXN03027-upstream

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>RXN03027

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RXN03047-upstream

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>RXN03053

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>RXN03055-downstream
 TGAACACCGCTTTCTGAGCGG

RXN03059-upstream
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 AAATCTTGGCCACGATGAACGGAATTGAGGATATTGCCATA

>RXN03059
 ATGAATTCGGGTTCCACAATGCGCAGAATCAGTCTGCGCAATATTGGCGCGCACAAAGTTC
 AGGCTGTTTATTGACAGTCTTGGCAGTGGTGTCTCGGCAGCTCTTTGTTTCCGCGCGGATG
 ATGTTTACCAACCGCGCTGTCTCTCACTTTTGATGAGGCTATTGCGCAGCAGCTTTGACGCG
 GTGGATGGTGGTTTACCAACCGGTGCATCAGAGGTGCGAGGTGTTCTGTTGAGACG
 GTTGAATCTTTGCTGAGGATTCGCGCATCAACCATCTCAACATCAACGGTTCCAGACT
 GTCGTTCTGGCGGATGCTGATTTCCAAGGCATTAACAACGACTGGGGATCGTCGTAAAGC
 ATTTATTACAGCGCGACGACGCGTTGCCCGAGGCCCTGAATTTGCTGAGGGAGAGGCA
 CCGACTGGCACCGAAGAGGTGCTTGCCCGAAGCGGGCGCTGAGGCGAATGGCTGGAG

>RXN03059-downstream
 TAGGGGACCGATCTTGGTCGTG

RXN03062-upstream
 GATGAGTATCTCTCCGAGGCAACGAAGTTAATATGTCCATGAGGGCGAAGTTGTAGACA
 ATAATTTGGCCCATATGGATAATTGACAGGAGTTTAACGCC

>RXN03062
 ATGGAACCCCAACCAAGACATGGATGTCGGTGGTTATACACCCAAAGCAGCTCAAA
 CTCGCCGAAATTCCTCCCAACAACAAAACCTTCGATGTCATCCAAATCAGCGAACTCGTT
 GACCCACCGACTTCATCAGGCCAACAGCGTGGTCTTATCCGTGGCATCGCTTCGCA
 GAAACGCCCGACGGGCTTCGCGATTGGGACACCGACTCGCCGACGCAGGGGTTCATCGG
 ATCGGTTTCGGCTCCGGCTCACCTTCCCACAGGTTCCGAGGCGCTTATCGACGCTCC
 CTCACCTTCGGCTCGGCCCTCTTTGAAGTCCCCCGTGAAATTCATTATCTCGATCACC
 TCCAGCGTGGTGATGAGCAAAACCCGCCGTGCCGGCCGCTGCAACAAGAACTCCTCCTG
 GAACAGGAACGGCTTAACTCCATCGCCATCTCCGGTGGCATCGAAGCCCTGTGCCGTGCT
 GCCCGCATATTGGTGGTGCAATAACCATCGTGGACAGC

RXN03066-upstream
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 CGAAATCCACCGCGCGTAATAGCACCAGCTTAAAAACCTT

>RXN03066
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 CGTTCACTGCTTGTCTGATCTAGGTTTGAATCGTTACGTTTGATGAAGTCGCTAAGCGT
 GCAGAGGTACCGATCGGCACGCTGTACCAATCTTTGCCAATAAGTATGTATTGATCTGC
 GAATTGGATCGTGTGGATACCGCAGAAGCTTCGCGGAGTTGAAGAAATTCCTCCGATCAG
 GTTCTCTGCTTGCGATGGCCGATATCCTTGATGAATTCATTGAGCACTTGGCTAGGCTC
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 CGTGCGACAGCTGCGCGCAGCGAAAAGAGATGCTGGAATTCATCGCGGAAGTTATGCGC
 CCGCTTGCCCGCGGTGCCGGCTACGAGGAGCGCATGTCACTGGCGGGATTGCTGGTGAC
 ACGGTAAGTTCCCTGCTTAACTATGCCGTGGTGATGTCAATAGTTCCGAAGAGGATTT
 GACAGCATCTGGGAAGAAATAAACGAATGCTGATTTTACCTCTTCTCCGTGGCTACT
 GGA

>RXN03066-downstream
 TAGTCAACACGCACGTTCACCCG

>RXN03067-upstream
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 TGAGCTGAATCTCCCTCTTCTTTCGATGAGGACAAAGTT

>RXN03067
 GTGATGACTGCGTGGGGTGCCTTTGGTGAGAAGAAGAAATACGGCAAGATTGTTACGGGT
 GTAATTCTGTTCCACATTCCTCATCAATGCTGACGAAGTGTGGCATGGCGAAGTACAAT
 GTTCTGTCAACTGGTCACTGGAGCGCATCGTCCGCAAACTACCGCGCGC

>RXN03067-downstream
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>RXN03068
 ACCAAGGAAGCATGCGATTTCCTGATCTTTGAGCAACCTCAACGATCTCGACATTGCT
 GTTGTGGCATTTCCCGGATCCGGTGACAAAGCTGGTAAGTTCCGTGAGGACCATGAGC

>RXN03068-downstream
 TGAACCTCCCTCTCTTTTCGAT

RXN03073-upstream
 CGAACATCTAGGCAACCGACTTTTATGTCTCTGCTTGAGTTGAAAACGTCTGCATC
 AAAGTGCCCAATGTTCATGCCGTGAGTTTGTGATTA

>RXN03073

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ACATCTGTACCTTTTATGACAGGGCTTGGATAATTGAGCGTTGGCAATTTTCACTGACAGAA
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GCAATCTGTGTTGGAATGGTTTCGCAAAATACCTTGAAGTCTGTGTTAGGTGTTTGA
CTGTATGGTCAAAAATAAGAGAGAGTACCAAAATGGTGGGGCTATCTCGTGTACTGGTT
CTGTGCATAATGGGCATTACTTCGTCTCTG

>RXN03073-downstream
TAAC TAGCGCATGTACTCATGAG

RXN03085-upstream
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CCGTGAGCTCGGCCGTGCGATTAAGGGAATCAACGCGTAA

>RXN03085
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GCTAAATCTCTCGAATTACGACCCGTTACACCGAAGAGCTCAACGCCAGCAACGACAAA
GACCTAGACGCGTTGTCTAGCGCCACCTCCCGCCACCCGCTAACCTCTCTACGGTGTCT
GCCAGACGCGACCAACCAACGCGCATTTGTTCTAGCCAAGTGGCTAAAGAAA

>RXN03085-downstream
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RXN03089
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CAATCCCAGTGGCGGTCTGTATGTTGGCGACTCGGGTGATGACGACTTCGGCGATGATGAC
CCCGACCCCGAACCGGACAAGCCTGAAGACGGCAAACTGATAGTGATAAAGCCCGTAGG
CCACGGATCAGCGCGGAAAAACACGCCATCATACCGACGAACTCCGCCCGCTCAACCCG
AATACCAACACCCAGCGCCGAGGAACACGCAACCAAGCCCTGAGTCAAGCGATCTGGCGC
ACCCGAGAAGCCTCCGACGTTGGCTACGCCACCAAGGTACCAACCGCGAACAACCAAC
CCCAACCCCATCAACGCCATGAAAAGGCGCTACCTCTCAGTAGGTAAACCCGATGCCGAC
AACAATGTTCCGATCAGCGGCCCTCGTGCCTCGAGCAACCGCAGCACTGATCAACCGCGAAC
ACCGCACTGCTTAAACCAACGTTGGCAACCTCGTGGATCTTACAGCAGCAGAAGATACGGC
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CTTGACGAGATCAACCAACGGTGATCATGGCGATGGCAGTCTACTTAAACACCTGTACCCC
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GCGTCAGCGAACCTGACTCAACGCATCGCGTTGTTTGGCTTCTGAGTTGGTGTGCTCGGCA
CCCAATTTGTGACAGGCGCGAGTTAGAGTGGCAGGTTTCACTATTAGATCCCTGGATGAGA
GGTGGGCTGACCAACCTGGTCAATCTACGCAATCAGTGTCTTAAATCAACCAACGCGAAC
GATGATTTCCAGGATGGGGTCAATGTGTAAGGGTTTATGGACCGGATCCCGTCACTGGC
AGAGTAGGTCACTACTCAGCAAGTGGTGAAGGGCGGGTGTAAACCGGTCCGCTGCTGCT
GATCGTTCCGGTGGTGCA

>RXN03089-downstream
TAGTCCAGACGTAAGCAATTATGG

RXN03098-upstream
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TTCCGTCAACACCTCTCTCGAGGCGGAGGCTTAAACACC

>RXN03098

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GCACGTGCCACCGGAATGGCAAGCTACATGCGGGATCAGTTTCTTTTCTCGGCATCCCA
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GACTTTGTCTCAGACTGCTTTGGCGCAGCTGAAACGGGAATACCAAGTATGTCGCTGCGAT
CACATCAATCGCGTCGGCATCACCGATTAGGTTTGGCAAAGCATTAGTGCAGACCAAA
TCCTGTGGGACACCGTCGATTCCCTAGCAAAACCGATCGCGCCCAAAACGATGATGAT
CTGATGAAAACGTGGGCGCTTGATGAGGACTTCTGGGTGCGCGCGCATCGCGATCATCCAC
CACTGGGCGCCAGAAAAACACCGACGCTGCCCTGCTGGCTGGATCATCGAGCAGAAC
CTCGGCTCCAGCGAGTTCTTTCATCAACAAAGCGATCGGCTGGGCACTGCGGGATTTCGCC
CGCCACGACCCAGCTGGGTCCGGCTTTTGTGACGCCACGGACCTTTCCCCACTGAGC
CGCGGAGAAGCCCTGAAGAATATT

>RXN03098-downstream

TAGCCCTCAGGCATCATCTGAGC

RXN03099-upstream

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ATGTCGCGAAACGATCTGATCATCTGCGGTGATGTCGGT

>RXN03099

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GTCATTGGAGTAGATGACCTTGATTGGGGTGCCGTTGGCCAGATGATGTTGTTGTCATA
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GCGGTTGACCAAGTCTTCTTCAACCATTTTTCGGGACACGATGGCGCGCAGACGAGCACC
GTCATACAGTGCTCGCGGAAACAGGATGCGGGCCAGCAGGGGACCGATCGCGCCGAA
ACCGTACAGCAGATATCAGTTGGTTGATGTCGGTTTCCGCACCAATACCGCGCGGAG
AGCGTCTCTCAGGAAGGCACGACGCTCGGTGCTTTCGATTTCTCGAAGCTGATAGGCCAG
CTGTCCCAAGGTGATGATGCGGTACCAAGTTTCATATCTACCAAGTTTCGCGCAAAATATC
CAAGGAGCTTTCCAGTGGAAGTTCTTGGATATGATGTGGGCGGCTAGCGGTGAGACTT
GATGATATCGATGTC

>RXN03099-downstream

TGAGACATTCACAAGGAGACGAC

RXN03104-upstream

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GGGACAGTGCCCTAACACAGGAAGAGTAGGTGTCGTATTC

>RXN03104

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GGAGCAGAGGATCAAAACCGTTATCCAAGTCTCGAGGTTTCAATGCGATCGTCATCTTG
GCGAACAAGCAGAGCTTGGTGGTAAGCAGGTATGGGCCACCGAAGTTACGCGACTC

>RXN03104-downstream

TGAACGCCACGCTTGATGGAGT

RXN03106-upstream

AAATGCCCTCTTGAAGTGAAGAAATCAAGCTTGCTTAGAGTCCTGATTACCTGCCAGAA
AGGCACCTCAGAGGTGCAATTATACACAACCCACAGG

>RXN03106

ATGTCGCGATCCTTTGATGACCCCAACCTCATCTCGCTTGCTGGACTGGTTCCAACCATG
CACTTAGCCGATGCTGCCAGCTGTCCACCTTGGCCAGGACCGGTTGAGCATCACCGGT
GATAAAGGTGCCAATGCTGTGTCGAAGATCGCCTCCTTAGTCGCGGCGATGTCGCGGT

GCTGATTCATC

RXN03107-upstream

GGATTATATCAATTTCAGGGCGTGGCGAGCTTTTAGTGATTCACGCTCCTACGGTGGGT
ATCACAAATACCTCACTAGTAGTAGGAGATGAGCACCAC

>RXN03107

ATGAGCGATTTTTCCAAACAGGCAGAGACCTCACAGGTAAGGCTAAAGAAGGATTTCGGC
GAGGCAACTGATAACGAGTCCCTCGCTGATGAGGGCGTGGCGATCAGGCTAAGGCAGAC
ATCAAGGATGCTGTGCAAAACGCCGCTGAAAAGGTAAGGACGCAGCTAACAAAGTTCTG
GGTGCCTTCAAGAAGCAGC

>RXN03107-downstream

TAA'TCCCGTACTTGTTCAGGATT

RXN03113-upstream

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CGGCAAGAAACCTCCTTAAAAAAGGGGAGTGATTGTGA

>RXN03113

GTGCTTGATTCTCTAGCTGCGAACCCTGATTGCGCTGGTGGTTATTTTGGCCGTTGGT
TTAGCAATTGGTCAGATTAGGGTCTTTTGGCCTTCTTTAGGTGCGCCGCGGTGCTGTTT
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CTGGGCTTGGCGATGTTTCTGTTTATGTCATCGGTTTGTCCGCCGACACGACATTTTTCAGT
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ATCGCAACCCGCAATTGTGGATGATCCACATACACACCGCCTCGCGGATCCAGATCTCGCG
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AAGGCGTTGGGTGAAGAACGCGAAACCAAAAT'TGAGGACACAGAGTGTATCTACACCCGC
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CACGGATTATGATTGCCCGTATCCGCCAGGGCGATTCTGAGGTAGTGCCTAAACCTGAC
ACCGTGATCAACTACTCTGACCGCATCCCGCGTGGTGGTTGCTCCTGGTGGTGGCTGAA
GTGGGACGATTCTTAGGGGACTCTGAAAAGTCCCTTGCTGATGTTAATCTGCTGCCCTTTA
GCCATCGGATTATCTTCTGGCCTGTTGTTGGGCGCGATCCCGATTCTCTTCCAGGCGCG
ACCACGATGTCCCTTGGCTTTGCTGGCGCGCGGATTATTTGCCGCCCTGATTTTGGGAGCA
CTCAAGACACAGGACCGCTGACGTGGCAGATGCCGTTCCACGCCAACCGCACGATCTCC
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GCCTCTGCGCTGCTGTGTGCTGTGATCGGCATGTGGGTACTCAGGTTGAGGTGGGATGAA
GCCATGGGTGTTGGCGCTGGCACCAACCAAAATCTTGCATTTATTTCTTACTCTGAATGGG
CAAAACCGGAACGATCTTGCCAACAGGGGATATGCCACTGTGTACCCACCGCGATGATC
GGTAAATCTCTGGCGCGCAGATATGTTCTTGTGCTGCTC

>RXN03113-downstream

TAAGTGATTTTGGGCGAGTGT

RXN03115-upstream

GGAACTGCTGGCAGGCAACGTCCTGATGGCGATGGTGTGCTGTGCACTGCGCCAGCG
CGGCCAGAAGCTCGACGTTTCCAGGGCGGTATCAACGGCTC

>RXN03115

GTGGGCAAGCAGGAAAAGCTGGCGATTCCCTCGATGTTCCGGAGTGGAATCAGAAGAG
GTAGGTGTAGAACTGCTTGCCGAAGGCTACTACCTGGTAGCCACTTTCGCCGCTGTGCGC

CAGGACTGTGCCCTGGGTGACGTCGTGCGGGCACATCATGTGTGATGAGGTCTTGAATTT
 CAAGAAGTGGCAGTTGTGCGGGAAACAAACCCCTCGGGTGCTCGTTGATGCCATCGCT
 GCTGACCACGTCGAGCCCACTAGAAACACTTGGGCTACACGTGGAAGCTCCCATGTCA
 GAAATGCTAACTGTCATATTGCCCCGATTCACCGTCGCACGGTTTGAGATCCTGCTC
 GATGATCTGCATGCTCAGGGGGTAATTTTCAGGGCGTTA

>RXN03115-downstream
 TAGAGCGCCTAATTGTAGAGAGC

RXN03122-upstream
 ATGGAACATGGCGGGATGAGTGAATGATGAGCGAGGAGACATGACAGCCCTCGAGGAC
 GCCCAGGGCACCAGGCTGCCCGGCTCTACCTTGAGCAG

>RXN03122
 ATGACCGCCCACTAGAGGGCGGGTCGATATGGCCCGCATGAGGTCACTGATGGCCAG
 AACCCGAGGCCATCGCTCTGGCTGAGCAGGTTCATGAAGATCAGGAGGCCGAGATCGCC
 GAGATGGAGCATATGCTCAACGAGCTC

>RXN03122-downstream
 TGAACAAGGACATTCCCCGACCA

RXN03134-upstream
 ATGCTGTTCATCGCTGGCGTTTTCGAGCCATTCGAGCTCTTCTCCGGGGAGAT
 CCAGTTTGTGATCAGCGGGTTGTTCGCGTGGGGCGTG

>RXN03134
 GTGGCTTGGCGCTCGGCCAGGTTCCCATGAGCATGACATAGTTGGGTCTCCGGCTTT
 GGATCCGAGGGCCGACGAGGATTTTTCAGCCCTCCGAAGGATGGCGTTGACAAATGGC
 CGCGGTGATGCGCGCGTTGACGTAGGCGTTTCCACATCGACGTGGTCAAGCCAGGTGCG
 GACTTTCGTGCGCGTCGAGGGATTTGAGTCCCGCGGTGAGTCCGAAGTCTGCGGTTTTG
 GAATTCGATGGCTTCATTGAGGTGCGTGCTTTCAATCAGGCCGAGGACTGCTCGCAATAC
 TTCGTGAGGTGGAAGAAGGTTCTTGGTTGACGCCCTCTTTGATGCCGGG

>RXN03134-downstream
 TGACCAGAGTCGGCCGGTGTCTG

RXN03135-upstream
 TTAGCTTGTGACGTCGCCCTCTTCCAACACCTCCGGCTTTGTGTTGTTTTCACCAAC
 CGGGCTCTGCTCGGTTGGCGACGGCTTTGTGCGCCACTG

>RXN03135
 TTGGTTTGGATGAGCGCTGGTGTGTCGGGCTCGTTGATAAATGGGACGAGGGGGG
 CTCGGAAGCGCTCTCTTTGCTGCGGTCTGTGTGTGGTTGGGGCCGGGCGGGCAGCTG
 GATGAGCTGGCGGAGGTTCAGATATGGAGGCGCGGAAGCGGCTCTCCTCTCTCGCTTGAAGGA
 CGGGTTGTGCGGCTCGAGTTCGAAGATGGGCGACATGAAGTTTTCGCTCGCGGCGTTTTC
 CTCGAGGCGCGCACGAGGTAAAGAAATGCCACGTGCAATTCTGTGGGCGCACGGCTGG
 TACGTAAAGCAGCAGCTCACCGACGTCAACGCTGACGGCGCGCGCTGATCGGACGCCAT
 GCCCTGCAGCATTTGCAACTCCACACGGTCCGCTACCCACGCTCCACAGAGAGCAAAATG
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 TTCCTTGGCGATCTGCAATAGAGGACGCGCTGTAAATTGCGATCGGTGGCTTGTGTTGA
 AGGTTCTGTGGCAACTGGCCAGCGGTGATCTGCGCGTGGACGTGCTCATAGGCAAAAT
 AGCACCTTGACAGGCGAACCTTAACGCCCGCCCGCTGTGTTGACGCGCTCGCGGCC
 GAACGTGCCCAAGTCTTGGATTGCACCGAGGGCATCGGGAAGGTACGCTGCAACACAAT
 TCCGGCTTC

>RXN03135-downstream
 TAGTTTCATGACGCTCTGGAATTGG

RXN03138-upstream

AGAATGTTCCAGTCTTGGCATCCAACCAGCCGATTCGCGTGGCCACACTGGGGCGTTGG
CGAGGTCTTTGGCGGTGTACAAGTTGAGGACTACCTTGAC

>RXN03138

TTGGATATTGTTCGGAAGGATGTCGCTGAAAGCTTCGCCGTAGGTGAGTCTGTTTTCTT
CGCGTGTGGGTGACGGCGTTCGTTGATGATGTGCCCGTCCACAGCATCGACGGAGGCTCC
GATTTCCGGCGTTCCGTTGCGGAGAAAGGTCACTCCGAAAGAGCTGTCGCTTTGGGTACC
CGCGAACCAGGTGGCTCTTTCGCTCGTCAAGCAAAATCTCTTATTTCCTTTATCTTTCGCTCC
TATGGACCGCCGGCTTGGCAGAACTCGTGTGGGGCTGGTGGCGGTGAGGTATTTCGTTGAG
GATTGCGTCCGGCGCCGGCGAGGTTGTCGGGTGATGCGCGCAGTTCGTTGCTTAATGTT
GATCAGTCGGGAGAGGTCGAGGTGTACAGCTTTTGTGTGACGGGCTTTGAGTTTCGGGCAA
GTCGGCGAGCGTGGCAACCGCATGGATATGCGGGAGACCTGCGCTTTTGT

>RXN03138-downstream

TAGACCTGTGACGATGGCGAGGC

RXN03140-upstream

CTCAAGCGATCGGTGGAACATCCACTAACGGGGTTACCAAAAAATCCTTCGCGGACACTCC
CGAAGGAACACTTCTTTCGGAAGGAAAGGAAGAAGCACT

>RXN03140

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GTCTCTGGATAGCATTCGAGAAGGATATGAAGGCCGAATCAACCGATTCCGCAAAATCTTC
ATTGAAATGAAAGCGGTTGAAGAGCTGCGCACCATCGCCGCCACCCGCCAAGCCACCTC
TTGCTGCA

>RXN03140-downstream

TAAGACACTTAAAGTTAAATAA

RXN03141-upstream

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>RXN03141

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CACGAAGCATTTGGCGCTTGTGGTTTTTCGTTTCGGTAAAGTTCGCGGCTTCGCGCGGGCG
GGCCTTTTCCAGGGCGCTCTTCGATGGGAGGTTGACTGGACTGCCCTTTTGAACGCCAGG
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>RXN03141-downstream

TGACAAACCTGGGCCCCAGAAGG

RXN03146-upstream

TAACTGGGGGTTTTTAAGCTTGCCTAGACATATCGTTTTTCGATAGATTTACATCTTGAA
ACGATACGCCCATCCACGGCGCATGCTTGAAAGGTTCCCC

>RXN03146

ATGAATCCCGCATCCTCATGCTGCTTCGCATCATTTTCGGCGCGGCCCTTCCTCGCACTG
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CTCTCCCCATCCCGCTCACCATTCTCGCGAGCTTCGTGATCATCGGTTTCGGGCTCGTG
CAGTTCATCATCGTCTGCTGTTTCGCGCTACTGCGTCTCTGTGAAGACGATGAAATCTTC
GACGCCACTCGCTCGCTGGGTTGATCGAATTGCCATCACCATCGCAGCGCGGCGGCTT
TTACTCTCCCAATGGCCTACATCGTGCAGAAAGTCGACGACGCCCCGGAGCCATCGTC

TTTCGGTCTCATCTCGCGATGCTCATCACGGCGTATCCCTGCTGGTAAAAATCATCGCG
GCACCTCTGGCCCGCCATCGGATTTCCACGGAAC TGGAATCGGTGATC

>RXN03146-downstream
TAAATGGCCATCATCGTCGACAT

RXN03147-upstream
CCC TGATCCCGAGGACGATGACCGCCAAAGCGATGGCGCCTCCAATCAGGATGTACTGCA
GTGGGATTGGGGGGCGTCATCGATGGCATCGATGCAGTT

>RXN03147
TTGGAAATCCTCTTTAAGAGCGGT TTGGGATTCTGTGTAATCATCGGTGCGGTGGCGAA
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GAGTACATCGTGGCTGGATCGCTGGAGAA TCCGCTGATGATGTC TTTGGCTTCGTGCTGA
TGTGTACTCCGTTT TGAAC TTTCTCGCGCTTGGGGTCTGCACGCTGGGATCGTCTG
GAGGAGCATGGC

>RXN03147-downstream
TAGGCTTCGCCGATTCGATGG

RXN03149-upstream
GCTTTACTAGAACGATGATCGGTAAACTACCTTTTAGTTGCGCTATTAGCAGTACAATC
TCTGTGCGCTGGGATTTATT TTAGTTACCGTATATCGAT

>RXN03149
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TTGAATCATTCAGCTGCAGGGCTAGGGAAGCTATTAGGTGTGCGTCTCGTATCTGAAGGA
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GAGTTGCCAAGAAGAAATATCATTATT

>RXN03149-downstream
TGAAAACGTGTTGAATTTGATG

RXN03152-upstream
GCAAAATATCAGCTTTGACCTGCACATATAGTTGCACAATGGTGAAAGTGCACATAAAGT
AACTTTCGTATTCGAATATTTAAACCTAAGGGTTTAGCA

>RXN03152
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CTGCACACCGTAGAAGAAGAAACGGGTAGCTCCAACGGATCTTCTGACATTGACTCTGAC
ACCATTTTGGATTACGTCGTCGTTATTACTGGCATCGTTGGCGTCTCAGCGCTGGTTTG
ACCTTCGCTACTGCTTTCCAGCGTTCATTGACG

>RXN03152-downstream
TAAATTTACGCTTATATCACCAA

RXN03153-upstream
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TTCACGGCCCTCGTTACGACTACAAAGATCGGGGTATTTT

>RXN03153
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GGAATCCACCACTCCACAAACCGTCACGGTAAACGCAACGCCAACGTCGGAGGAGGCTGCA
TCCACGGAGCCGACCAACGACATACTTGCAGCCAA TTTTATCCGTGTGAAGTACTCACG
CAGGAACAGTTCGAAGAAGTCGGATTGGGAGTCTTGATTGTTGAAGACGCTTACCTCGGC

TCGACAGGTTTAGGTTGCAGTTTCGGGAAAGCAGACAGAGAGGATTTTCAGGTACGTGG
CTCATTTTCAACTGACCAAGCAACACGACAATTTGTTGAAAACCAAGATCTAGAGACATTTG
GATTGGGGATCCAATGACAATCCAGATCTGTATGTGCATCAAAATGCCGAGACGGGTCTGT
CAATGTGAGGGCAGCAGTTGACTATGACTGGGGCCGGCTTACGGTTGACTATCTCGAATTA
GGTGAGGGCTGGGAGCCAGAAATTTGTGCTCTGATGCTGTGAAATTTAGAAAACTCTC
ATCAAGGAACCTAAGGGGAATCCA

>RXN03153-downstream
TGACATTGAAATTGATCCCTCG

RXN03154-upstream
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>RXN03154
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GATAACAAAGACTCCCAACTGGTGTGCTGTGGCCAGGTTTCGGCATGGGTGGCTATTAC
TATCGTCCGCTTGGCGCAGCGCTAAATAAAGCTGGATTCCATGTGGCGATTGGTGAACCT
CCTGGTCAGGGCAAAAGTTCGCGAAGGCTTCTCGGAAAAGTCAGTGGGGATACCATGAT
CTCGCATCGGTAGATTTTTCGCTGCAGATTGCGGCTGCGAAAAGGCGCTTGACCTGGAG
GAAGGCCATCCCATGAGGTTTGTGCGCATTCGATGGGTGGGCAGATTTCTTGCTTTTC
GCAGCGAGGCCGGAGGCTGAGAAATATAATCTTCGGGCGGATTTTCGGGTGGGTGCAGGG
TCGCCCTTAGGCCCTACGTTTAGTCCGAAAATGGGGAAGCGTTTGGGATGGGTGCGGTG
CTGCTTGGTGGGATTGGTGGCCACATTTGTGGGATTTTGGCCCGGCAAAAGTTTAGGAAAA
GACCTGGTGGGTTATGGCCGACATTCGGGAACCTCACATGAGGGAATGGCGTCGATTCCAT
AAGCAACATCTTTTGGACGATCTCACCGCGCAGGACATCAACTATGTGGAGGTGATGAAG
AAGGTGAGCATTCCTATTACTTTTAGTCGTTGTCTGATGATGAGGACTGCCCGCAGGCA
TCGATGATGGGTGGCGAGTTTGTGTCCGCGACGCGAGATCAAAATGATAGAAATTCCTC
GAAGCCTTGGGACATAACCGGTGGGCTCGGGAACCTGAATCAACAGTGAAACTCTTCTGT
GAACAAGCTCTT

>RXN03154-downstream
TAGTGACCGATGGAGCGGAGGTA

RXN03156-upstream
GTATCGACCTCGATGATCGCTTGCTGCAGAGATGACCATTTTAGGTCGCCCTGTGCCTA
AAGAAGGATAACCCACACCAAGAAAGTACCTCATT

>RXN03156
ATGGCTCGAACCAACCTCCACCAGCTGATGTACTCGACATCATATTTCACCGGTGAAG
CAGACCATCGGCATTGATCTTGCTGAACATGATTCAAGGCCGTGCACCTCGGCCAGGCTCAA
GGTGAGGCAACAGGCAAAAGCTAGTGCAGCAGCCCTTGAGCAGGCACCTCATATGAGCAG

>RXN03156-downstream
TAAATAACACACACCATGTGC

RXN03162-upstream
GGTCAATCAGTTCTCTGCCACTGCTCTGGCTTGCTGAGGTGTAATTTCGCCCGGAGAACA
GGGTTGGCGAGAAGTTGTGCGCGCCTTCTGCTGGCTTCTT

>RXN03162
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GCGTGGCATGAAACGATATCAACAGCATGCCGTTGTGCGCGATGATGTACTGGTCACA
GAAATTCATGAACCTCGCCGAGCTTTCGGGACTTCAGTTGGTTGTGCGACTGCTTCGGTGCA
CTGTGATTTCAGTGTCCAATGGCAGTGGGTGCTTGGCTCGATGGATGACGCGAGTTCTCT
GTCTACCACTGGACGCGCCAAATGCCGAGCCGTTGGAGCCACGGTTTGTCTGAGCAC
GCGCTCACCGAAGGACAGGGAGTTGGGAAAACCTTGTGGAAGTCTCCACGTCGTAGTA

GCCTCGGTGTCGGATGGCACCAGTTCGGTTTGGGA

>RXN03162-downstream
TAGCTTGACCAGCGCATCTTTTCG

RXN03167-upstream
GCCGCGATCGGGTGCTTTTGGCGTGTGCGTAAAAATAGTTTATTAAGGGCATTC
CCTGATTCACAGGTGGTGCCACATTGTTTATGGTGGAGAT

>RXN03167
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AAACGCGCCACCTACGATGCTCAATTAGAAGCTGGAGTTCCACTACCTTGGGCGCAGATT
CAGCATTTAGGAAACTTCGGCACCTTGCTTCCACCCCTACTGCGCAGCCGTTTTCGCGCA
CCTCAGCCGGAGCGCTCGCCGGAACCGCAACAGCAGTGAATAGCGGACAAAATATATGCG
TATGGCAATCCGACCATGGATTACCAAACCTCAGCAGAGCTACAACCCGATGCAGGACCAA
ACCCAGCGTCGATGTATGCGCAACCTTTTCGCGAACACCCCTGCACCGATGTACAACAGC
AATCAGGTTTTAAACAGGCTACTCGGGTACGCGTTTGGGATGGCGATCTTCGACAGT
ATTTTTCGCGCATCGTGTGGAAATGCTCCGGTATTTTCGGCTTTGGATCTGAATTC
CTCACAGTGTATCATGATTTTGGTGCTG

RXN03170-upstream
GTTAAATCATTTGCCGCCAGAGAAGACCGCGGGCGGAAATTTGGGCTTGGAGGGAACCA
AACGGCCACTTTTCCAGTCCAAACAAAGTATGAGGATTAAT

>RXN03170
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GCGCTTCCCACTGATTCTGGCGCGCAGTTTGATATCCACACGGCAGTATCCGCGCTCCCTTT
GCCACCTATGCCCAGCAACCTCACCTTGTGTTTCCACACCGCCGAGAAATTTAGGAACCCGC
CGCTGACGGGCTCGTGAATTCGAAGACACCGACGACCAACTCGCACACGCAATTGGAG
CGCCTGACA

>RXN03170-downstream
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RXN03172
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GAGCTCGACATCATCGGCGCACCAGCACTTCTTGGCGATCGCCCTCTCATCGCAAAACGTC
AAAACCTCTCCCGCATCTTCGTGTCTATGCGCAGCCTCGGCCACGTCAACCGCTGCCCTCC
CCAGTCAACCGTGTCTTCTTCTCTCCACTCCGTGCTCAGCAACGTTTACCGCGGATCCGAG
CACTACTCCGAGCCCAACGGCTTGGCGGAAATGGAACCTCCGTTGGTTCGCGAGTAGCCACC
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CGCGAGGCTGAAGAGCAAAATCGCCAAGGAAGAAGCCGAAAAGGTCGACCTTATCGACAAC
TCCCATGGGCTGCGCAGGCAATCGACCCCATCAAGGTCTCCATCGACGGACGCAACCAT
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TCCACCTTCAACAGCAAAAAATCCCTTCTGCGCTGGCTCGTCAACACGATGACCAACGAC
CTCGCCCGCGCTCCACCTGGAGCGACCTCATGCTCGGCACTCAACGCGCGTGAACCGAA
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TCCGTCGACGCCGTAGACACCCAAACAAATGGCCGCGCGCTACGAACCTATGCGCAGACAC
GCCAGCTGGGCGGACGACGACTCCATGAATTCCTACTTCTGGCCAAACCCACGATCGAG
GACTACATCTCTTACATGCTCGGCGGACGCAACCTCGGATATGTTCCTCTACGCAACA
TTCAACGACCACTCTGAGAGCTGGCGGAGCTGGAGGAGATGCTGATCAAGGATTCAGC
AAGTTC

>RXN03172-downstream
TAGGTCGCCATTTTGGGGTTCGT

>RXN03173

CTCAACCGGACACCCATCACCTGTGGGTGCTCTTAACCAACCGACTCCGACGACATTCGAC
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CGCTACTACTCTCTGAGCATCCGCTACCTCGCTCCATCATGATCGCCGTGGCCAAAGCA
GACCCACCTGTGGGAAGAACTCGACCTGCGCATCACGACGCTTAAACACCAAGTCAAC
GCAGGGGAAGTCAATGATCCAACTCCCTCACCTGTCCAAACGCATCGCCGCGTGGATCAAA
GAACCTGACCCCGAACCCACACGAGCGCCACACCGAAAGAGGACTATGTTACGCTCCAC
ACCATCTGATGAGCGCACTATGTCCGCATCAAAATCAGCGGCCCAACCGCTGATCTCTC
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CCAGGGTGTGCGTTCGCGCGAGTAAGTGCCAGGTGATCACAATATATCCCTGCGCGGAG
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ACCGATGTCGCTTTACTGCTGATGCTAATGGATTGGCGGAGATAGATGGAATTGGGCCG
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GCCCTCAACAAAGAAGAC

>RXN03173-downstream
TAGAAGCGCACAGGTTTTGCAT

>RXN03174-upstream
GCGATGCTCGAAGCGCGCAGAAGCTCCTGGGTAGACAAAGCGCTGCATACGATTTCGCG
TGGTCAGATCACTACCACCTGAACGTGATCTACTCTCTAAA

>RXN03174
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ATCGCGCGCGGATTCATCCGCGACATGCTGCTGGGACATACCCGCTGGTGTGGGTGGAA
AAGCCACTGTATCTACTGCTGATCATTTGGCGAGCCATTTGACAGATGTCCTATTCCTTC
CTGATGAGGACCTTCGCTGTGTGTCTCTGCTCGACGCGCGGGTCTTTCTGCAATTC
GCTGTGATCGGCACACAAATCGCACTGGAATGGGCTACGGATTTCATCATCGCAATGATG
GCATCAGTGTACAGGTGTATTCGCGCGGCTCATGCTGACCTTTTGTGTGACCGCATC
CCACTGTTATTTCAAAAAGAGCTCTACGCATCAATC

>RXN03177-upstream
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TATGGGTGAAACAATCTTAAGGAAATATCC

>RXN03177
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TCCGAACCTCGACGAGCGCCCACTCGAAGCAGAGCCATTACATAACCTGCTCATTGATGGT
TCAGAGTCTCGGCTTGGACAAATGCCACTGAAGGAAACGACACCTCATTAAGTGGCCAAACC
ATCAATCTTAAGTGGTCAACGGTGCCTTTAGATATCGATGGCTCCTGCGGAAAAGCCCTC
CAAGCTGTAGAGGACGCTCAATCTGGACAGCGTAGCTAGCGCATCCAGGGGCACTGGCATCC
GGGCAACAAAGTAGGACATCGCCATGTACTCAACCGCCGAAGCAACGACATCTCACCA
ATGGACCTCTACGAGACATCGCGAATGCTTGGGAAGACCCCGTCGTCGATTCTTCCGAC
ACACCTTACACCTTCGGCAAACTCGATGATGCTCCGACGCGCGCGGTGGATTACCCCTC
GACATTTGAAGTCAACCTTGACAAATCAAGGCTCCACCGTGATGATGATCAAGAAATAGGA
AACCACACATCATGTCGAGGACTTGAACCAACCCGAGAAGAAACCGCCACTGCTCTTC
GAAGCACAACGCACCAAACTCGAAGAAGGCTTGACGCTTAAACAGAAATTTGGCAGCTTGG
TGGGTT

>RXN03177-downstream

TAAATGCGCCCAACCTAAGAAAA

RXN03182-upstream

ACTCGACACCACCGTCACCAACTTCATGATGGTCATCGCACTCTTAGGATTCATCAGCTC
TGTATCCGTAGCCCCGCTTCCGCAAGAGGGATGGTGCCTAA

>RXN03182

ATGACCCCTGCAACTATTACCGACATCGTGCTCTGGTGTTCATTCTCAGCGGCGCATTC
TTGTCAATTCTCCGCATCCATCGGCCCTCATACGATTCAAAGACACCATGTCCAGAGTCCAC
GCCATGACCAAAACCCAAACAACCGGCCCTTATCCTCACCGTTGTAGGCGCAATCATCCGC
ATCTTAGGCCGACGAACACTTCGATCAATCACAACGCAGTGACCTCGGAGTCTTGTCTCTC
CTCGTACTGTTTGCCTGCTCACCAGCCCAGTG

RXN03184-upstream

GCACAACGTCGCTGGTCAGTGCCATTAGTCACGCAAGAAATGGGCGGGTCCGGTGAAGA
CTGGCCTGCTGTTTGGTGCCGCGGGC

>RXN03184

ATGGTTGGCGCGTTTGGCGGTGGCGTTCTCGGGGGCTACATTCCTGGCAGATTTTGATG
ATCGCGTTTGGCTCATGATGATCGCCACGTCGACTGCGATGTTGGCGGGGCGTAAGCAG
AAGAAGGGGGCGTCGAAAAGCTCTCTTTGGCGCGTCTTGTGTGATGGCTTGGTGGTCCGC
GCGGTGACCGGGCTTGTGTGTGCGGGCGGGCGCTTTTGGTGGTGCCGGCGCTGGCGCTG
CTCGGGGGGCTGTCATGCGCGGTGGCTGTGGGCACGTCGTTGGTGGTGATCAGATGAAG
TCGTTTGGCGGGCTTGCGGGGTATCTGACCAGCGTGCAGCTGGATTGGGGGCTGGTGTCTG
ATGGTGACTGCGGCGCCATCGTCGGTTCGCTTGCCGGTTGCGCCCTTGGCGGGGCGCGTG
CCTGAGACTTTGCTCCGCAAGGGTTTCGGGGTGTTCGTGCTGGTGCATGGGCGCTGTTCGTG
CTCGGCTTGTGAGCTTTTA

>RXN03184-downstream

TAAGCTTTTCGACGTCCTCC

>RXN03185-upstream

AGCGCCCAACCGTTTCAGACCAGCGGTTTCTCTGAGGATGCAAAGTCCATGATGGGTNAGG
TCACTGAGCTGTCCGAAACCACC

>RXN03185

ATGAATGATCTTGCAGCTGAAGGTGAAACGATCCTTACCGCATGGTTAGCAGCTGCGC
CGCAAGCTCTCTCGCTTCGTGAGCAGAAGTGAAGCGCCAGCCGGTCATCATGCCAACC
GTCATTCGGATGACTGCGGAAACCACGCACATCGGTGACGATGAGGTTCCGCGCTTCACGC
GAGTCCCTG

>RXN03185-downstream

TAAAAGCATTTTCGCTTTTCGACG

APPENDIX B: AMINO ACID SEQUENCES

> RXA00003 (1-741, translated) 247 residues
VQVRILSSSEL VCSLSGAIRG VNLDAAPKP KKSGRRTLT PEWDAAVHKHL LTRDTEPLLT
PTKHKNIQRS TKNIHARIVR LILLQAVSGL RIAEANQLQW KHIIDGGDGM LINASADIVK
GRKGKGRGRY IPLRADVAE YLRTHREDDE HFIVGSPPTT ARPWDATNAD DKVPELYRQI
AEATGVKTLQ DLRSHSWRAT LHGVYADVMD PATRAAIFGH TEQVAEEYIN DRQNIESLMR
QVKRAYA

> RXA00008 (1-492, translated) 164 residues
MAKKKKKVD E NNSVLATNRK ARHDYHIIDT WEAGVVLGT EIKSLREGKV SLVDSFATID
NGEINLQHLH IPQYSMSGWT NHTPKRTRKL LLHRNEIDSL MGKVRDGNRT LVPLKLYLKN
GRVKLELGLA QGKQDYDKRQ DIKRRTEERE VTRELGRRIK GINA

> RXA00015 (1-309, translated) 103 residues
MIDMCTTFRQ EIMIREQFKE INNGRVVPHY DQLEQLAEIF STKSDIDMVN EILNRDTDFL
SNEGTFIMEY IFNGGFHTDN GYPLSYAYV ERGLAIRPPR IVL

> RXA00018 (1-1299, translated) 433 residues
MSALSRPHKI ATGVAVATLT LTLCTSAAGV VHAAQQSISG PESSCAFNNQ RWDDSKVKLD
DTIATAKNSL VQTGELHRNE QDLLTGYLQF QPHSSNYLAL NNAYADAVAI KDSFVRPTCD
GSKESKIASE HAVSEVVGAV NVLARAQKAL QINSDTYEQQ RRCDALRLAS RDSDFVLMRI
DRTMLQLRRT LADIDQASTD IRDIRAQTTS FERDLAREQK EADAARAQA VDTSTPTSS
TEDRVNDILK ESRTDHSQDS YTRSTTSTAQ STEPDSATNT SYLSRRLDLS ERSAGHIDLN
TQCDNLDDLRL ELTNNDTRDH TGSVISIADQ LTDITNEINE LRDSFTATRD SAQQAQDQVI
AQREELQRAK EARLEEQRLA KEAEEGARNA AIQERDAAEA ALREAQDLS RLDDTGNATS
DDTAALVDGL LNN

> RXA00020 (1-780, translated) 260 residues
MTVTTAQRIA DEFQRGISIG PWDLCCEVPAG DDYLEHTTKV RRRHSTAVEI HTDSLIIICAP
EGSTYSNRT KAGLASTGTV TYPVKGLSEP VKLSLNLAD YGNSFDTVHD DLWQRELREQ
TRGQLLTLNA VSGLGDSDVA IMGTFWGDGL TGEANTIKGR EHFVMAAGC RFEDGYGRHA
LREDRHVRHQ ARAGEDSTAH HCWLLKGTVF GKELTGDAVT AAMTVFSDVV VTVDEGRIFG
MKSGQPFMSA TRLRASSAPV

> RXA00021 (1-1773, translated) 591 residues
MSDPTDSDHP ATSPTVDSAA SGTSDDPNQKP KKKFTIIRKV NMIAITAIDD CINRLGPDVV
TMSSEDIADQ VVNSINVAIA RENTRAQDAN AAVRYTPIFK LDFSHYAVILM RRLHVIINIA
PSHNSDDPDS MLAIYDNPFR SEHYGIYRST EAEIRRVARE YCPDLTSAQF RELQMALSDS
APRKVRHKQR DLI PVKNGIF NYSTKQLEPF SQEFVFLAKS AVNYPNPAQN PVITHPQDGS
VWDVESWMND LSDDPDEVNVL LWEIIGAIVR PYVSWNKSAS FYSEAGNNGK GTDVELMRNI
GALAEAYSISQ LSDFSKEFHL ESLTRAQALV VDENDVGAFK EKSANLKAIV TNVDISINRK
HKTMLSYQFY GFVMQOCINGF PKVKDQSESF FRRLQLEVPFE KSFTGAERYK IKDDYMSRTD
VLEYVLRHLV HMNYDNLSTP AAALAVLDEY KEFVDPVRAF WNEFSDQFVW DDLPLQLFYE
FYRKWFRDSD PSQSVLGKRS PIQKITTIAV DSGQWEYPLT AQRPGGDMAV PEPLVIDYDL
TEWQNATVPK GHVNVKGLPLP LKANYRGLLR KPLTTPATPF AAPVNPPTPT P

> RXA00022 (1-735, translated) 245 residues
MSAPTIYPGT KTSIDPITMD DARIIFFDIE SLHNIFTVAT YDLSLHHVDV FYLLDHTTSP
QITVLPMSMD YFDQTRSDAV MAALIEQNPA FAEIKGSPIT TADVALHNLG DTMANNRWQS
NVLLARLLG ISVRGEVPEH QSHNHAKQF AEATLVTRDF DVNYDPTSAH PFTAGFNSIN
YDTTLLSLYF AMLTSNIGST PTYFPVITAQ ELRAHNKLF SPEFIKNMFK YFWRDSDGAG
LRAAS

> RXA00025 (1-1437, translated) 479 residues
MAWMNVSVIV PGSDDEL FVK GLFTGEGLTW LITNLGANYI GPPPLLTVPIL ILLAVGVAER
SGMLAALIRK LFSGAKKIVL PYAVGVIGVT ASIMADAAVF VVPPLAAMVF KAAGRHPVAG
LLGSFAAVGA GYSTAIVPTS LDALFAGITN AVMETLPGIA TTEVNPVSNI YNIASSIVL
GLLCGFLIDK VLEPRMRQK IATEYAESIE PTAADDEEI SATLTAQENR ALTISMWTTL
ATAIIVLVVV LIPGSPWRNE DGGFLPTSP LSSVVFIVFL FFMVMGLAYG MVVGITKMDL
DVVNMMEGAI KDMIGFLVLA FILGQFVAF NWTGIGTWTVA VQGAAGLEAI GLTGFPATIA

FIILASCLNL LIISGSAMWT LMAAVFVPMF ALLGYEPSFI QAAFRVGDSA TQVITPLNPY
MIVILGLLR YEPDAGLGLT MSRLIPFVIP FWLAWATLLA IWFYADPLPG PGSALFLEG

> RXA00027 (1-366, translated) 122 residues
VDESRFRARS VFPPGEEPPD RFTLANERTF LAWTRTSLAF LAGGIAFEAF QISGLSDTVR
TTIAVFIIAV GMIIAAGAAV RWMNVERAMR KQKPLVPVPAI IPFLSTIAALV ASAAVLVLII
VQ

> RXA00028 (1-1947, translated) 649 residues
MTLTASSLEA GKMSFSGGYI VGETMIFLVD PDEVEIRRSF NSLHVLNRGS DILRRNEHHC
WVFENFNKPI DPPVRLGPRD IICPSALAWV LQQHSISRSL SHLHADKITL AGSIADGRPTW
ILREPTSTGG QDP SRLVSLE IDQEHGVILA VETQERLEA TEISFPDTLP NPEWGWAEWP
FHYPDSTPHT APDVAEIPGY IQSLPPQSED PRRLRVFVNE IALEGDFPDY QQQSVRLTL
GISSSPVPLE GMTTRRRGRV RNLGEEASPG DDGMPQWPIL LTGDGWTALA YTPIPKRGA
EIQQWFFYYSA YGIVDVP TDL RVERIFAGIG TSGTNERLWQ EIDNTSSAYH SEDWIRDRVV
LDVTLDGAVP PPLRRDVFTA VDPVIVAGDKL WLCDVHFVPA RCWETTTGRY LGQTLXPAPL
RDRSVVLELH SDQQLGAVAA SGKSGWILT QGAVATKAPD WTPPTATLAD YQVPSWEIV
AVRGQGLFEL QVETSRRTAL GRVNATGGVD ILGPPNGYT ISSVVOIGDE YIVGWRVEEY
RLNSKLEVIS TKELDISASG WKS KGT VAYL SEDTHICFD QVSGAELPSL GIAEGHQGEV
MSATSSSESV LIYRRNPNS MSIVPTSVAT YDNGTWTMP LQEAPEALS

> RXA00031 (1-402, translated) 134 residues
VAAGQWLGN IGEIDHVLCS DATRTQLTWE RVQGLGATAK GSSFHNDIYE NOVSEFKHLI
TGLPDVVGTA LLIGHWPGVE ELAHYFGIRD EHPGWDQMEF KFTPSAIAVL ENFTPWSKLE
RNSARLIDFV IPRG

> RXA00036 (1-1416, translated) 472 residues
MLERTQVFVD TSYLLASFYN SWETGARAQL EIDLPEVVGV LGRMIEQQLK QPVQRQMWYD
GIPDSGPHRY QDARLTCDGV QLRAGQLIEW GERRTQKAVD TRIVADLWLA GVRGQCSIDI
LVSGDADMIPI GVQEAANAGL RVHLYGFGWD SMSSQLRHCC DTTITLDPRE DFAECMQLVQ
LEGPLPPVVR VKPINDAEPI EDLDFTFPVPG VASPFEEVSA KDEKFSRPRS EPAEALSQV
CEAQVEISKH EQQTADSGEI TESFEAAEIK VTEFFGEPAE PVAESGVPEA TPEALTPPEA
AKPTPAKPKT PKAEPQKQES PKGPTPKPKA PSPADIPPKA PADTECHSEV EABIEDSRPK
IPSPMMAPR RKLRSRYVL PNEVWATAGF QTPYDVGGQY ASNWFENAT STQRDAQHLL
SGGGLPPEID RFLQFACET LHEYTLTEAQ RVALRDGFHS GIRGVLLNQR DS

> RXA00037 (1-873, translated) 291 residues
MANPLSKGWM YLMASFDNKI DENADPKIOI QQATEAAQKQ HQQIMQHASQ IIGQQKQLEM
KLNRLVTDAD KLQEQARQAI QLADKSANEG DSVKAQEFNN TAEVFSQVLV AVEQQLQGT
ALHQAEALLA KDAVAKSKES EMRLKEQMSQ IDALRAQADQ AKMQESVTKS MDSLQLEGTQ
DSSVPTLDV REKIERRYAD ALGAQELTQN TVSDRMAEIA QSGTDMRASA RLAEIRAEAL
GTSATPKGQL EAGVEDAEEL IDETSTFSAT PETASPEADA PEASADESEK K

> RXA00049 (1-687, translated) 229 residues
MPTPSQKHDA STAQTDNQVP TGRRAQKREQ TRARLITSAR TLMAERGVDN VGIAEITEGA
NIGTGTFYNY FPDREQLLQA VAEDAFESVG IALDQVLT KL DDPAEVFFAGS LRHLVRHSLE
DRIWGGEFFI MGAAPVLMR ILGPRARRDL LHGLETGRTF IEDLDLATTC TFGSLIAAIQ
MALADQDSN DDKQIFAAA MLRMVGVQAA EAREIASRFL PETSPVKPQ

> RXA00052 (1-711, translated) 237 residues
VAFILFNFKV TNDTSTSNVQ SESTAETVSE TNGVLSDGAE NIASQSDESK SGVEIIDSGF
GQSSNSAMAI VIAKTSGGSL AGEFVTATVN FLDESGAVVA TEDQVETLSW EDQELVLVPS
HYKEDSSRPE TISIEAFLSV TDYGSQGPDE TALPVLETTD ISNPYAGSYN ASFALKNDSS
DDFNLRVGI VCYNEQTDII GGGFKFPNLV PAGGSIRMDA SVTVSEMPAS CKAYLNH

> RXA00054 (1-2913, translated) 971 residues
MSPFDSLGR DTHFGFLDKT TASQQLLNS LISNEDPHTM LQAIKLELRT AQSFSTFVAF
ISSRGIALK QALLDFKKGK RIITSRYLDF NDPTMFRELL TLENVEVLH QGDGFHSRGY
VFHHDVGITA VVGSSNLTDN ALLVNREWNL KFSASKNGDI AFQLDDATNR QIERSTPLTP
EWISEYEATR RVPERLVSON IPLEDQSNAG TIVPNVMQDE ALDALLSLTE KGEKRGVLI
ATGTGKTI LA ALATRLMKPE RVLFVHVHREQ ILDKARSEFI KVLERPAVDF GKMSGSTKEL

DKPFVFGTIQ TLTKEATLSQ ISPTDFDLVI VDEVHRAGAE SYLALLNHLQ PQFLGLLTAT
 PERTDGFNIY ELDFNVFPYE IRLQAALASN MLVPFHYGV TDFTLDSETT VTDTSKLSAL
 VSEERVHHLI EALKTYGHPE NVRGLIFCSK TEEAEELSKL LDQSLFNGSL LKTKALSADK
 SIYREEEVA ELESGLDYI LTVDFNEGI DIPSVNQIVM IRSTQSSIVF TQQLGRGLRK
 AAGKDHRLVI DFIGNYANNY LIPIALFGDN SRNKNSIRRR LIESDIDGTI SGVSSVNFDP
 IAQERIFAAL KAKILDSKAK FKQDIVQLQD RLNHVPALLD FARFNTVDVF LLATHSGNYW
 SLSSSVKFPVD HAPSESEKYF LDFLTGELLN GKRPHELLLI QELMKQPETS TEEFRKLLQA
 QSTSSDEQTI NSVERILSQE FYTGPNRKKF GEHPILSVQN RTYSFTPEER RALDESLEV
 DRDEAAQNFK FHVQDIDTG LFIARNNGFW QGNLVVGERY SRRDVCRILN WERNNESTIY
 GYKVDSTYST CFIPIVTHKA DDVSESTRYQ DELVDPNTLH WYSRGNRKKT SNEIKFIAAN
 AVDLHVFVYKK DDAEGLDFEY LQQAHSSENSK QSSMPGNKGV VQPVVMTDQL FDTPEVQSLE
 EYLSTNLAVT E

> RXA00056 (1-750, translated) 250 residues
 LLNRVSRVAG ASAITLCIGL TTILSPTSTA QSLQITPLP ESAIDLNAEI HVNTSDISAE
 QILGAQDEIT TMYDSHPYE YFDTLTDIEQ RSIIAALKRD PSSLQQRQET RLAQSQDPYK
 IYISGLEMLS CINLVVVVSC GIANQAATKA NNEAVARYPG DSLRNGKGDG FRHCWSNALM
 TIRIGSNGAE RIATNHETIG DGPADENAMD LFNNAQGRQI GAGFINSKDE TSALAICALW
 TNLGLRKLTK

> RXA00058 (1-564, translated) 188 residues
 MKFFGFGYRPI ALIAGITVSA SILTSVATAA ESPTSFAQIT PAFSSSSAPE ADAEANTSEA
 TADLLYVAEN QLLIKLSNAV VEDVNGEILM KDNKGTLLN LTAELQAQPG FSEKVDSTHT
 ALLTMNPDEV PDLQWRCGV GALS GG VAGV VATGLALAL GVATGTGFA VLAAGLAGLY
 GTGAVANC

> RXA00059 (1-282, translated) 94 residues
 VLTGILLAMV STALAIRFGS GVAIAATVLW TVISITLGGD VLAETMLVLV AVPSWPETAD
 TTTRFLIAML LQAVLITGT IWAIREIRDS ERRG

> RXA00063 (1-285, translated) 95 residues
 MTDGDLADAI SPRQIGLMTT RTVVEIVRLR HMIAQQLERA TIMENEYLKE IAALKKELAH
 YKQGDHGNQM VVDILGKAIG TRPNFEGELD EEDAT

> RXA00065 (1-273, translated) 91 residues
 MANLPQEGFS VVHGILADPR IWGFEIPYVR EEAGQVNVEA PDEAGDLARL TLPLQLILLT
 EEEFAIALNE GSDVMFERMA EQEVDLLDLK R

> RXA00067 (1-486, translated) 162 residues
 MVDAQRPKAG IFGSHTTEETW VWLGNELFDE SGEVIADVRS DVLYVDRERL LIESTPGTMR
 FRCRATLSGG EYVTMTQNSF TVGDLTAVCG RRTYSLKRVS FWRKERLIIT NGVEVARLRP
 MSGVGVFEIF GTAGSEALPF VDAVFLSWAC VLVDASVRRP KI

> RXA00068 (1-582, translated) 194 residues
 MTSKDLIVTS YTSWGKRFKN DGKLFINLLR STTDSADEKV LATFGEVPSPK SFETTATVID
 QQWELSFSDI GTATAKLPDG RVFSANAGEK TFTRSKRRIE LMDGTAMAAR NEDKNWIID
 DSEENKVAQF TGMNNGVRRR IVEFEPDVEV TQEQEIFLSW VARKTLESRM LGSSWGLTLF
 LIILPPIIIF LTFS

> RXA00071 (1-1452, translated) 484 residues
 MSITHVQAL TIALNAIDNH LASMXDHGVT PDQYKALEPD LIALEHTINH HATIAAQTXA
 LAERTXXXXX IGSTHLIDYL TTFGLSKAR AHHRINLAHS LYPIPKPNSG SGNNGNGGNP
 DGGPDGDSG DDDSGDDDDP PEPDKPEDGK PDSKPRRRP ISAEKHAIIT DELARINPNT
 TFSAEEXRXQ ALSXAIWRTF EDLRTWLRRH VTTANKNNPN PITAMKRRYL SVGKPDADNM
 VRISGLVPAA TAALITANTA PLTKRGNLVD LPAEDMRTR GORHADALHH IMEIYNHGIV
 TPARGGTASI ISMTTDDLD EINHGDHGDG SLLNNLYPTN TGYSNLNAEI MNLIAAKYDF
 AVLLDGETGQ PLNVNRMQRS ANLTQRIALF ASELVCSAPN CDRPQLCECH HHLDPKMRGG
 LTNLVNLTHQ CFNHHPRNDD SRSGVNGKGF MDRDPVTGRV GHYSASGEGP VFNRSAADR
 SGGG

> RXA00077 (1-1362, translated) 454 residues

MNDENIQSSN YQPFPSFDDW KQIEVSLLDV IESSRHFSDL KDSTDRSALD AALERAKRAA
 AVDTNAIEGI FQTDGRGFTHT VATQVGAWEQ QMAMKGGKHKV PAFDDTLEGF EYVLDAVTGR
 TPISQQWIRN LHAVILRSQE SHEVFETAVGV QNQLAKQEGY KQPNSPQRS DGSVHAYAPV
 EDTPAEMARF ISELESKEFL AAEKVIOAAY AHYAFVCIHP FADNGRVAR ALASVFLYKD
 PGVPLVIYQD QRRDYIHALE AADKNNPLLL IRFFAERVD TINSIIVOLD TPIAGKSGSA
 KLSDALRPTR VLPELHDAAH RLQESLFTET SRRLDEEGRK NGLEFLLRQI FIGHSPFNLE
 GYNAPFDSYC LTLAFNSNSP KQIFHPLSIV IAARDGKRAS SDLVAATSIG YNFHAYGREV
 EPVVTESFRE RVKIYADGIV DHFLTALAKK FQQN

> RXA00079 (1-222, translated) 74 residues
 MGLVHTEFTP INTYGIILDHV VTLPGDGTKVL NPFVRVPHDT GSELIFTVRP NENFEEDCQA
 VAADLERLVA LAEK

> RXA00080 (1-420, translated) 140 residues
 MIVLLFINLP FAQLWAKLLL IPNHLYLSGI ALFCGLGIYA TSGAVFDLLM LLGIGVVALI
 MRRYGYPLAP LMIGMVLGPL AETSLRDALL SSVGDFSIIV SSPITWSLYA VLAIFIAVSV
 ITAIRGRKKH LITSQLETIDA

> RXA00082 (1-564, translated) 188 residues
 VNVTEQSGES HIDIPESHQL PGPRFVGEGT FWEGRSGLIM FAILTAFSLY LLIGVLNMDV
 GNAAFPGPRF FPTILGIAGL LVAVALTIQT IKYPMHPENE SGRSWFHSDD YVSLAWAIGG
 FFAFAVLLPY LGWVLGSL LFWTMTAFRGS KRPGFDVLVS LMMSSVVVLA FDVGLGLNLP
 SGLLGGGF

> RXA00083 (1-300, translated) 100 residues
 VLALPSSIID PLWCQFAALI PPVTDTHPLR CHRPRIPDRI IFDKLIQVLV LGASYAKIAD
 TTCSATTLRN RDEWITAGI FEQLEQICL FIDRIVGLDL

> RXA00087 (1-528, translated) 176 residues
 MIGGIIGLIL SVIIMAEKLA ILEDPGHITS CDFNAVLACG DVMRSQANA FGIPNPLIGI
 AQGFAVAIIG AGIILAGGGRF GWFWFGAQAG LTFAMMFCHW LAYQSMVIR ALCPYCMGVW
 TVSIIMFVLV TAWNVTFFSG SDSTFVNALY KYKWVIAIYW LLLIAAAVW SFRYMF

> RXA00093 (1-2223, translated) 741 residues
 VTTLLAATRP TLRDAFKHPN RSLAAILLVA VPMFLVSFFL TYDQSINNAA SYPGSOVQAH
 YDGEAGAYQLL QENLPEDFHL ELFANGYPEV SFGDEEVNFF VVQSTNVQQA SFPADALDVL
 GATIGDTVTI HGTPVEVQSI SFTNILLPEG TLFSLNFFSE SETFSGTWYF PGSNFTEENR
 QALEAVGFVE NEYRRGPISV DPNLIPSYIM GFLSTTILAV VALMLISPVF TISASRQTRT
 FALLASQCAT PRHIRWAVLT YGLFAGLVGA SIGLVLGQIG IYGWKWTYP EFSLTTPNLV
 LVGFWALAI IASTIAAFLPA VFVSRSSIIN GIYGGISDKI IRWSPRMLIG FVWIAAAVI
 ALFIDGGEWG GVVRQCLFLA AVIALPASPV AVLWALGRLP GLTFKLTARD MLRRSMHSIP
 ATGALAAVIM LGTFMQTTGL ATQASDREAT ASVYPEAVFL RGDTQIPGLM GQKIDVYDGN
 HGFGIYELDV DFYSANYVPA LTSFFGGPVI ATPKILDMFG VHEQADIYAP STYNSGLQEY
 AITYPGDETYM LDTAVLPLPL YSHVLLSPET FEELGGQTEF LGTIVLPQEL DDQTVQAINR
 SRDAHFSHDG HNSLASSAA LTAVAIVVVS LVIVLANRKL QQHALAIGA TPGTIYKYNA
 LNAALLALVG GIMGLVSSGI AALLTGTTDE IVDGAILNNG TLEHMLLPWF LLVSLLVVAP
 LVCVAVIGAI SPSGRHQEAS I

> RXA00096 (1-303, translated) 101 residues
 MTNAGDNFEI RMPSGTDDPL SDAEIQKYRE EINRLDREIL DAVKRRTHKS QTIGAKTRMS
 GGTRLVNFEI VAINQFREI IEEGEPALAG ILLRMGRGKL G

> RXA00097 (1-1161, translated) 387 residues
 LFTNFFAVNN PDSPPARQKT KLRELEHREWF QEHLPGDDDD HSTAISLLAI VTGLTKAQVS
 RISIAFATLA DLPELAKLQO KLYHLDLSSL ITISNELAGI NPDNLADAGI ILTEYLATAS
 PNQILPSFAS IGRKIKEIRD LLDDARATGS RGTQDDSSFG VTFSPOGTAE IGASVDAVDG
 HIINDAVTQH AKKNDLTYGE AFSDILRNNI QVKVVLNLYT AKDLANAPVW ASSIGWLDAK
 TGTFWSEKAN KEQMDMAAAK ISTDKHDPSP ALRDALIGRD GTCRFPGCSV PALKTQADHR
 IPYEEGGETC LGGTGCLCQH HHNMKTDDGRV TYLLDPFSGI IVWLMDGGTW AVSEPNGLPN
 PVNARMAQTV AQHRRARHHR VVKEDAK

> RXA00101 (1-408, translated) 136 residues
 MRLIINLIWL FFGGIWLALG YVFGIITACI FIVTIPAGIA SFRMANYALW PFGRTVVVRNP
 KAGGSALSIN GLWFIITAGLW LAIGHLTTAA AQATTIIGIP LAIANIRMIP VTCFFPGKEI
 YDSNRIPFGY EPMVKF

> RXA00108 (1-543, translated) 181 residues
 MKKFFVAGAV LSSALVMAAC SPANQSDSTS TSVETTSSSS TQVSDAVITT ENAVVRASVE
 QSDMTAVFAT LVNNSDDEIN VSGFTADVDA ASFEVHEVVD GVMQEKPGGF VIPAGESIEL
 APGGDHLMIM GLANPIEAGD EVTVTLELAD GSEVKLDPIP ARTIAAGDED YDGLGTGEGHE
 G

> RXA00110 (1-549, translated) 183 residues
 VSNKDGFLT D GNSTFAPKVD SIPLSDVDTS VSGEASIGTL ISNATSQMSS LFRAEVELAK
 TELAGEAKKA AIGGGAFSVA GVIALYSSFF FFFVVAALLS EWIKPMAAFL IVFLFMLVIA
 AALALFGWRK VKKMGAPKNT IQSVNQLKNL VPGQASEKLE KANKRGLYTS ASFHSFGAIT
 GDH

> RXA00114 (1-489, translated) 163 residues
 MKLLFFAAAG FATALAGACT QTESLVIATIE SATSAAQASG NDVEGDQTS A FELSVGECFN
 DTYEEIEISEV PIVDCAEPHD NEIYYLYDIE GDDFTDIT TGVEGCLPTF EGFVGAPYET
 SIYEVYPMPT TFGSWTNGDR EVVCSVYLAT GEQMTGTAAG TAQ

> RXA00117 (1-591, translated) 197 residues
 MTSAGPITVS DAQTLKSWID KHEGLTVIDV RTAHEFSNLH IKGSYNVPLT TLAHSEIEIS
 SRVGHEVVLV CQSGIRAGQA QQKLAPLGIS TVAVLEGGIN SFAKADGDDV RGTQVWDIER
 QVRFAAGSLV LAGLAGGKFL SPKVRTLSGI IGAGLTFSGV SNTCAMGKAL SALPWNKTKP
 VPTETETLSK LPSPEKN

> RXA00118 (1-255, translated) 85 residues
 MQLNPDEITP VLNRLKRAQG QLTGVIRMLD EGEDCKAVVT QLAAVTKALD RAGFAIIATG
 LEQCILNTPDG DMDKKELEKL FLSLA

> RXA00119 (1-759, translated) 253 residues
 MLEFPADVIP ENIKHIAQTK FQTEATSVED IRRAINLLSD QAERAGASFN PGFILAQVGS
 TIVEVYGGAP VAWLDAVELL ISPDVEWVGV HGSRKLDINV SGELSGVISA GDKLGGELLG
 DWTINIVHGE YKIQIEDARP STAFADATE LINQANSEIV PFHVRMLSNS KIVMSGFSDBY
 SLAGDAITSA GKLAELARPF AHWKENVIPT TEIAMDYEPS EVADLWQGD S SETPEFFDDF
 ERLLREEMLI PEI

> RXA00120 (1-654, translated) 218 residues
 VESLYFDSAD LRCYTEKIEG LKFRRLKRIR TYGDGVLTPE STVSVEIKQR VNKVTKRRRL
 DLPFTYALAL GDSTGAARVE QVDVEKLEI SPENQHALIH EMASFAKNVR LRPIATTKYH
 REAFVGADEA ESSRVITDHG VSGRDRDFLL QQDLEDRPTV AQGLAVVEIK CDERPVFWLT
 DMTAQLEMS V IRMSKYCETI EAFHNRPSA FGAVDPF

> RXA00121 (1-711, translated) 237 residues
 MSLDLSIFD FQDLSGTSFV VDVLTITLVLS FVLTSIVGVV YQKTHRHSY S QSFVQTLVL
 VGMVTAIIML VVGSNIARAF ALVGALS VIR FRNAVKE TRD VGLFLAMAI GMTCCGRFVY
 LAIAATVIVC GVLFIMYRFD WFKADIQRQV IKVQVPADGQ ADSGRSYAEF VELILAQYCT
 SFEMMSAESV RGGALTEFSY TAQMRKNVKP HELVAKMRDV NYGQKATVLT GHQDQTV

> RXA00122 (1-1623, translated) 541 residues
 MNRLRLCTGS AALIAVGGVL GGVQVVPYIS SGEIQTSASS TATIDVGAGN VDFIDTSVSH
 EISLQVSQES LDEMLADYQE DGSKTWVKAT ITIDGVITEN VGIRLKGNS LSGLGRTSEE
 GGPQAPEGVE EFTDLSEEEI AQFEEQFAAQ QETTDASETG ETAENEETRG PGGMGGGGGM
 GGMTSVDAAD VSTWPLLSIF DKYEDGRVYQ GMTQLALRPG TTVVNEAMAL ALTAETGQVS
 QQSSFTTFSL NDEPSTTRLL LKHPDENYAD ALNGVLFKA DSNSSFTYQ EDQTEYDQGF
 KQINGDNGND IQPINLLKW LDTASDEEFA EHLSDYVDVE SFARYVATQN LLVNSDDMAG
 PGSNNYLYWD YDTGLISVIS WDLNLA MGS TDAGPDDEIS MGGGGGGGGM PGGTDTTEIE
 GTATEDMFD GMNQQRERPE GMPDMGEMPD MGDREGGGSM GGNQLKERFL ASDAFETIYE
 QVYWELYEEM YSGGTAEIEL DEIAASIPET DAVTADEIAT EVASMREWIT ARTEALALQ

E

> RXA00127 (1-456, translated) 152 residues
 LSPYDGPHRN VLIALKEHGR ADLVAFFVAV VGASISYLAA QGEIEHDITL VPAPTRATSR
 RRRGGDPVER VCNASRLSTF PCLQISSRTP DSVGQTAQQR RLNMRLVELR QPRGSVLIID
 DVVTTGATIS ASANVLRAAG VQVRGALTYC QA

> RXA00128 (1-1704, translated) 568 residues
 VSKISTKLKA LTAVLSTVTL VAGCSTLPQN TDPQVLRSTF GSQSTQEIAG PTFNQDPDLL
 IRGFFSAGAY PTQQYEAAKA YLTEGRTRSTW NPAASTRILD RIDLNTLPGS TNAERTIAIR
 GTQVGTLLSG GVOYPENAEF EAEITMRRED GEWRIDALPD GILLERNDLR NHYTPhdVYF
 FDPGQVLVG DRRWLFNESQ SMSTVLMALL VNGPSPAISP GVVNQLSTDA SFVGFNDGEY
 QFTGLGNLDD DARLFAAQA VNTLAHADVA GPYTLVADGA PLLSEFTLT TDDLAENYPE
 AYTNVTSTLF ALQDGSLSRV SSGNVSPFLOQ IWSGGDIDSA AISSANVVA AISSHENNEAV
 LTVGSMGEVT SDALRSETIT RPTFEYASSG LWAVVDGETP VVARASATTG ELVQTEAEIV
 LPRDVTGPIS EFQLSRTGVR AAMIIIEKVY VGVVTRPGPG ERRVTNITEV APSLGEAALS
 INWRFDGILL VGTSPETPL WRVEQDGSAT SSMPSGNLSA PVVAVASSAT TVYVTDSHAM
 LQLPTADNDI WREVPGLLGT RAAFPVAV

> RXA00134 (1-570, translated) 190 residues
 MAVHLTKIYT RTGDDGTGL SNFERVPKDD PRLIAYADSD EANCIGQVL ALSSPTEDMA
 TLLRTIQNEL FDVGADLATP TEENPKYPL RVLPEYIERL EKECDKWNED VPALDSFILP
 GGTAAALLH TARVITRRAE RAAWIAVREF PSTTSTLPAQ YLNRSLDLFF ILSRVANNNGN
 DVKWVPGGKR

> RXA00140 (1-186, translated) 62 residues
 MSDESIEEQE KELAALKAQI DELEKKDKQN KLIIEILSKA VEKNVAEAEA KRARKYPFNP
 LW

> RXA00141 (1-462, translated) 154 residues
 MTTDSNSATI PTPKPIPTI DRISLIMKEF GIDLSIADEQ GTGSQVASAN LNGHHVMFAV
 IGSVLIVRAD RATEMPVSDG NPAWHLACNG VNCFNFAAKA VVVDRTDNIV IRAEKDVPIA
 AGLNDIQLSA MLKNAIDHVL AIQDAVANAG KEIG

> RXA00142 (1-477, translated) 159 residues
 VPQSPTAHDP NDIQEFNLDA VAGILQDEKL DYRIDEHGDG KVIRTGFINA AISFILLDGS
 LTMEAMWRGA PSTDAAAQVL AATNEWNLTQ FAPTIRFFEL NEGTLAINAL RHVVVSAGMS
 HNQVGSVYMS SIESAVQCQE WLEQQFFDLV TWKDEHHDH

> RXA00150 (1-774, translated) 258 residues
 MVFSMHDKGE TQENPADMSG RLNTPISTVF HFFSSLFHDA LRSVAQWSAW KKIADVSVIV
 AIIISVTLVD VPPISVYRDW ANNAGDAFVL VFCAFYILIT QFPIPTVLT LASGVLFGPV
 LGSVLVLSGT TVSAVISLII VRGLLDGDWA PRLTHPAVS INTRLEQQRG LIATSLRMIA
 AIPFSILNYV AALTSVPFVS FAIATLIGSA PGTIVTVVLG DAVTGSNGWT AVAFTVFLAI
 LCVLGIPLDQ KMPKPKPK

> RXA00151 (1-597, translated) 199 residues
 MWALHARYRG RDTRRAELVK RFEEALSTLE GAGQFEVIGV EDIRAHITSP LTTCDDVMAL
 LAAGDWAIGI GVITPVDTGT DESDEAIIQ VVKTISSDALR PTLAKCTVKV RIATSLKRONI
 QAFNISAAFT LIGQVLKSKRT IEGREATLV RSLGNQNEAA QELGISKQAM SQRLQAAGWQ
 AESAGWQLAV NLIEQAGKR

> RXA00153 (1-426, translated) 142 residues
 VGAIIWFIGA LVLAGLELAV GEFTLLMLGG AALATAGVAL IGPVWVAEFV TFAVASAALL
 MFIRPAIRKR LLKPKVLDSR PRALVGHRAE VLEDVGATSG QVRLDGSISW ARSMDPTHTF
 AEGEIVSVID IQGTTALVWK EA

> RXA00154 (1-843, translated) 281 residues
 MSFSDPYAGN IFGGSARNKQ PEYPDVPAKF GLVVEVRGDD FVGAVTFGER TYDGFVRLLE
 DRGRDALYK LRKGAFMIDG QIVNLTRFEV KQAFRKSNSG SRRVENAQAK VAAPSRIWVE
 GIHDAAIVEK VWGHDLRVEG VVVEYLEGLD NLEERLAEFQ FPGRRIGVL ADHLVEGSK

TRMTKSLPAD VAVTGHPPYID IWAAVKPERL GLKAWPEVPY GEDWKTGICK RVGWSDPKEG
WHRVYNAVNS FRDLDYTLIG AVERLVDFVT NLDLSKEDVL A

> RXA00155 (1-783, translated) 261 residues
MEIRANVYSP LQNTAVWLGA WLYELVPTED VIDAFVDLGG PHTFGDGLL DMLRTLKELT
STLIDAFPHG PILTLALSGP GQVPALFAGS RAAVLASASK EGALVLGGVD KQHSWALIPT
RGKDATEWNL VEVGFLPAI ATVSPGEADQ LLQATDQAA NIELSGVYAS LAFKSLKNPR
LTVGMLSDFY DTPGLPYAVE ERSAKLFARA DRVAIAETV QETIGDHSLD PQLIFLWSHI
RTARMAGVSY ALAEFARDYH S

> RXA00159 (1-1182, translated) 394 residues
MENVSSTVSD GSVADVHAER WQELLARLDA DAPDIAEGTA AKLLATIPGY ELVDAGPIRE
SSIRNTALII RVINAGTEPK AEDLPEALRL ADERIAQNVF LGSVLHGFRM SLGEILEHLV
QLGPEYNIDP GRMLRWSTLM WAVNDAFSTR ATRVYRDHEV ATAIADSVRR SEWIGKAVSE
GSELSELLGW AAMYDVDPADT PLRALAATSP DHAKAETQIQ KWTQRAQVRV LASVQPSVIV
GIVIGEPKRN VDGPGFAVLG GRAEVLASKLA DSYKDSLVL KAADNLKLINE VQRAQDLSWK
LAIHASPRTV ELIAQKYVKP LRESGEFAHE IVESLRAVYD NQMNIFAAAR SIPVHVNTLR
YRLRRFEELT GCYLEDTSTV IEVSWVLEVF GREL

> RXA00161 (1-462, translated) 154 residues
MSEPGSPGVK EKKKVKKASHI VFLLCIFIAA CALAWWQWSR FQSGSGTQFN LGYAFQWPLI
GAFFVYAYRK YLYQVENESIE LENMEAKMMA EQGKTPVAQS EQEDSFFVQLS HRPSLVEDDS
VKEIDESFLP SRPTMDVEEF NRLNDPHARR RRAKA

> RXA00162 (1-354, translated) 118 residues
VSTTTPHPE RKKKVRQALT MFSIAAWVTG VFLALVAEM IMKYIIGMDL PEWARFVPVIA
HGWWYIVFLM TTLNLGLKAR WNPTRWVTTA IAGVVPLLSF FVEHNRREKVE TQTFQLNS

> RXA00167 (1-261, translated) 87 residues
MYLLNPPVTE PEILTVNEIP TVVAVFDNHP MNDMPAAFDQ TYQVLFPTLG AKGIAPIGPG
FALYTSEPTD TVSEFVGMPV SQPLEGE

> RXA00169 (1-2073, translated) 691 residues
MSLGNPAAML AAYNTSTQVA PQQPLGPRAG EVQLSSEQQA MIDYVLAKGD VIVDATVGS
KTTAIQRLCS IMGADHDVLY LTYSKLLKVD AQQRVRGAKV QNYHGIVYPH LLKAGIKCGI
SESIREFNKN FKHSIRTFPS YDLLVIDEYQ DINEDYAEEL RNIKSVNPLM QVVMVGDLQ
KVRSDTTLDP QEFPAQLCED PVFAPFTQSF RIGEMAAGL ADANKPIVG ANTAQQIEYR
SFAEAVVLII STEPSKLLCL GSRNGQMSDA LNVVERKSPA KFNKKTVFAS IRDGDQSIAH
PNDAAVFTIQ DSSSGLERDT CVVFDYDEEF WDMRLGYPNV DPVVMNRNVL VAASRGKKNV
VFVRSDSLQA AYEAGADWAA GLAVGVVDNN TEVAPEVDAH TPAEESKGDV GEVQSQIERM
MGFIPVSVFK ELPELAPSEY ARPISVTEAF DFKYAENVEA CFDLLDVKRL DNGKGAAIEV
NRSDDLDLS PTVGNFQEA VFFKDYNVHTA LSAYPSQFAK NLKRLVKRNN SVWRNCLIVT
AASTEQMRYY DQVRSSIPVA AEKALVSRLS TRLNADSRNQ IPLILDGEAV QSKVVRTFMS
FAGVADAVHK GVLVELKFVS ELTHPMFLQL AMYLVMSGMK DGLWNTRTD EAWQVRVPDP
KRFLNAVVLG VSKQDYRVGN FDLPTGGGA R

> RXA00170 (1-1854, translated) 618 residues
MLLAIGVASP VAQAQVDQDF ELVKEISDEQ FADDGVDYVP RNRNAPTVEQ LEDFESAHP
VVIEYHEHVN DSKDNVEELP LPKRDIVAGE MRSDVIELPE GVSKDEADQV EVAEARLNEG
ARLMAATGCE AMWPTGFCFVC GRILDAYRQV GGQLSWLGGP KSNELTNPDG VSGRSEFVCG
AIYWHPTDGA YAVTLDGLRQ WGTILNWESGP LGYPTSCPM TNYPLTQRT FQCGDNYNYP
LTGGAVWGDI KQRYEELGGS NHAIGIPITN ELPSGTSEYFY NNFNGTISW RNDRTQTRFY
LATQRVWDAL GREYGRGLGP EADETEPVSG LFHGVNFAER LFHGVNFAER GVIAWNGILG ARELYGDVYS
LWLQYQNTDT PLGWPIPSLT SLNESLEQEF TRGVVLGSGD ALTWIPDDEE RSLEDFLPIG
SSGSSSSSQE MTLFSSQRAQY VDCKNLPLD EQRKTENNIE KTFSGPKKEV VSGRSEFVCG
FVVRKGHYDR YRNEGWWYLY NYCKHNFANH AMAEAVVDKA VIDYSSSPGT SYKFEKTVY
FLDCRTYTFN KNSGCKEMHA POWVTIYNP HTFTGANSNR PKGVISAOWN STPPGGIEHE
PEISQCPDHW NLYNKLRI

> RXA00171 (1-231, translated) 77 residues
LAAEVKRLRE RDDARDQQLG VLNEAMFSLG GDGLDRFRES GDEASFNAAL NYQAVVAPEM

EFTVYGVDPDS TGEPIPT

> RXA00173 (1-333, translated) 111 residues
MSTTIKAAAP YSLHADLEQ LAVDLTLVTT FDSNAAVDVT PTHTEAPGFT LHEGTDTPAM
APTLLVVPIS DISTAVSEIS TLVQQARTDA ASATHEAEAE FYNQLAAVLA Q

> RXA00174 (1-285, translated) 95 residues
MPNHPISTF DRRRSAMREG ITDYLANNTA NGLGGYSISD THLDNLAEKF TRTHGEAQYD
AGFDPNLEP ETFVRDIEMS WDERAIDRAL IHTQL

> RXA00175 (1-630, translated) 210 residues
MAVCQLPQPE KTTLIKDL LMTSTTNSTA MFNDHLIPMA ELDEQALRDS VGSWAQYKHP
LDQRKEPELV LIRRVNSSLR VVWLSFTDLR ADAGLVPRST PNADPSNIRN TIFSVAVRDL
VLDRSLPRLL NLNGQPPAGE WEEGFVYVDY DQSDTVDGYL IEHSEPVSE SQTGMEMHYF
DKVPGGVAVT NNPDGTEQGD ARRWVSHWES

> RXA00176 (1-159, translated) 53 residues
QLMYSTSSFT TVKQTIGIDL AELIQGRALG QAQGEAQGKA SAAALEQAPH NEQ

> RXA00179 (1-459, translated) 153 residues
MIAIHAIHAI LFLGPATVAN SQFHVRAYDA HNGNTQAAGS AKTLFKISQS YGMLSLVLPL
LGIATMLLDW SPYKSEQGFH AIAIALSVITW ALLLVFIFPR QKKMMGALDL LEDDEQAQAKT
YEIENWDKAK SQLSMFGGIW ALLWVIIAVL MFI

> RXA00180 (1-540, translated) 180 residues
MKNFIRVLIA FSVFLCIYTV APHIGRGGPD LAPVTAIPQR ATVLGVDRAS MFGGWLGGVR
EGIVDEAGDT DPYSGNRLDL SSAEVDHILP LSAAWDLGAH RWSAGERISF ANDPLNLVLV
SKAENQEKSD QLPSEWLPSD RSARCWYVER LFAVANAYEL PLPENDIRVG RKQCGFAKFW

> RXA00183 (1-852, translated) 284 residues
MTESRRVKMD NVIYANFGSK QRVSTPDDRT QVINKSRHKQ FSPAGTRTVM LTEKNADSGR
RSRGEQYYRN GNVTGMTVLE GRVECTVAGS QNEPFTVTTV FPYRSSEKLR EATYAAIADTP
NGLRLVRDGH LTSSMLDHLV GSPDESIYFD CTCPRSLVC KHAVASAYHV AEKMTANPGL
ILDIRGQGMA GLEALIRTYH TKVETEPEDN DSFWNGRELP ALDPKPIAPA IDSDSINYHL
KALRMVSYTS LEQLRAVSDI EDMYEILVAN HPDNQQVYEE EDTD

> RXA00185 (1-2628, translated) 876 residues
MRIHEIINDN FRAIEHLELR DIPDQGVIVI HGDNEQKSS ILEAIKTVLN SKHRTTSKTI
KAIQPVDRDV PISITL EATV GTVRFRIHKK FLKSTAAELQ VIEPRPSNHR GLEAEAAALAE
ILESHTDLSL LDALFMKQGE VEAGISAVGI PTLTALNAQ NGNTEDATED TALMEAVEKE
YLFKYTNSGK ANTRFLQFSK QVETLRLTDLD EANAEEVAKLS SHVDVRVKLE IDRDQATAQL
PKAEELLAGR KAELEEAQKV KAQATEILAQ FSRAEEQLEQ ATGAQKRKE LRNKLELAQL
EVEKAEAGQE NLAQESAREE EEFALSEKF EAAARAAETLA VEKVKAARQS VAGIKNRDRK
EHLTVMLGEL DRIGQRLYEL RSVQHSSVRV SQRDIDALQK AITEVDIQT LVEAQGSSTI
LSASTPTDIQ LGDDTVSATD AGTTVALDRE LTVVVGVDL VINPGKTAEE SRTDFESAEA
ALAEELDQLD VSDLDQLRER FTAQEQRDAD IAEVLVREQQR MSGTETTVL VAELEGLHVP
EDLDPSISVD DAQTQLNEAE ESRELAEEAH KHANAALDGL RSRPVDKALT VFNAQLAALQ
RNLSAQAQVEL DRAVAETSDD EVDAAVQRC EALAGVRVQK QEIEQVLAKT NPMAQRLCD
AAEANVRYSYK TAVSDATTEL VRLEGLIGVA AGAKERLDKV KSALETAENR FESEQRRAHA
ARRLVALMVF QLAITSRKYA APFADKLSRL AASVFGESAD FDLDELKTS SRSIGPRTVD
LANLSGGAKE QLAITREAI AELVAESSAQ GAVPVFIDDA LGSTDPERLT RISTLFSADG
KDSQVFLVTC VPDYRYNVEV TQKHSIESLK TANALL

> RXA00194 (1-285, translated) 95 residues
VAGSSHTIEP EYRGVSTLD EPSAAWGHG LKRNTIQLAG WISVLFMLGY NFGNHKGHVE
TWLVLITAL LVGLILHLF EPKALPGSHH HFSQQ

> RXA00197 (1-1011, translated) 337 residues
VAAVLLGVVL FFLGIAVITA LHEWGHFITA RIFGMKVRFF FIGFGPTVFA KRRGETVYGL
KAIPVGGFCD IAGMTAQDEL DPEDLPRAMY LKPWNQRIIV LSGGVIMNLI VGLVLVYGVA
VSSGIFNPVD DTTATVDTVQ CVPETQISAT ELSSCVSGSP AGDAGIEHGD KILAVNGQEM

ASFTAIRDAI LELPGETATL TIEREGTLFD VDLQVASVTR LASDGSSEITV GAVGMSSLLPP
TDVYKKGPI EGVGATARET GDMISATWLD LKAFFPAKIPG VVASIFGAER DVESPMSSVVG
ASRIGGGEFE RSMWDMFMM LASLNFFLAL FNLVPLP

> RXA00199 (1-1419, translated) 473 residues
MEDLEIFDRH LQHSDFEDQG SIGLELELNL VDKHMOPALA GHAVLSHLDD EYQSEIGNFN
VEMNHPPLSV KGDALRRLEQ GITSRLGRVR AAATSENVNV AMIGTLPTIT PEFLEDPAMW
TQENRYRALS NAVMESRGEL VHINIADREQ IHDFTDLAP ESTCTSIQLH LQLAPNKFAA
AWNASQAIAQ VQAALSANSF LFLGRRVWHE SRIPVFQQA DTPTPELVNQ GVRPRVWEGE
RWITSVDFLF EENVRYFSPL IAESRALSQT PMMKGKSPAL HYLNHLNGTV WRWNRIYAP
GEERSHLRLE NRLLPAGPPT IDITADAAFY YGLVKYLAEE NRPVWSRLFF PDAENKFGSG
ARSGFLARMT WFTLQGVNVA NLVQEHLPQ ARIGLERLEV NKDLIDQYLG IITERAKSRQ
NGATWQLRSL NLEAHGSMF GSDARKAGLA AMLQYQLQNG ESGQPVHTWA IGS

> RXA00200 (1-303, translated) 101 residues
HYAGVTEIPE YRISPDHGGK STLSPFDQWA GGGSMGTAE VNNAYEIPSY LRNDWGRDVG
SIERYSLRTN SNGDAPKQAD INLETIQRSQ LWNPGHMKVD E

> RXA00207 (1-318, translated) 106 residues
MEMKLKASQ VSTATVVAAG LIGGWLTAEE SGIRPLGTIP LAASGALAAR SWNEKKGPAP
ATGLLATYVG AFGLSHPLAK KIGAWPAVLV VTAGAAAIAY AVSDSQ

> RXA00211 (1-663, translated) 221 residues
MSFLIRVLLS DTPGSLALLA EALGIVEANI QSVDDVERFP NGTVMDDLVI SIPRDMVADT
IITAEEVDG VEIDSIRPFS GTVDRRGQIQ MAAVAHQRR DITAAEEMV DVIPTMTSG
WALVIDLKG ITRIAGSLAA PEDDGTYPEN IVLKEARMLN PENDPWIPES WTLLDSSLAI
APIGKHGLAL IIGRPGGPDF LASEVEHLQG VGDIIGAMLQ K

> RXA00218 (1-1140, translated) 380 residues
MSARNPRPT EGVSPTVLAG RDSLLQSPKL GLAEGPGSPF RALLISGSRG MKGTVLLNEF
EDAAASQGV TLRAYPNMS VDLVNSAIP EALQNLDDGP SKRMLSGVAI PGATVTAIA
DPTKKDPTPT LISRRLRELAT RLQKHGSGIL ITLDELQSAN VDLLHLVATA VQOLLRDDFD
IALVAAGLPE GIDRLLQHEG TTFIRRAERI LLNPVNHEDS VEMFLDTAAE GQRHMTSEAA
ELAAQISKGY PYSQMLTGS L AWAARSTLDNS DTIQAEQVDA VRDEVVRMRG MQVHEPSLHQ
VPDGLTILY ALQKSKNGE MVSTGDIHL MGVPKPNALSM QRKQLLSRGL VEVPKYGFLN
FTLPYMRHL LNSPHHRPIT

> RXA00220 (1-504, translated) 168 residues
MSAFHIAEQ SHDISAIHDV TEAAFTGIEH SDGTEQDLVD KLRAAKALS GVAEADGEV
IGHIAAEVSL IGGGVQGWGF IGPVSVRPDK QQQGVGIALM GSALDGLRAE SAGGIVLLGD
PGYYRRRGFE VVPLGLVYPA PAEFFMAVCL NAPAFFPGVV EYHSAFGG

> RXA00222 (1-1146, translated) 382 residues
MTPTADIWFK DTLAAHFTRD GDQTTFSYTA DYAGPPIATS LPINSEPVIT RSGAIPPFPA
GLLPEGRRLS SLRRNIKASA DDESLLLAV GADPVGAVAI FPHGENTQPA PPTVDFDEL
DFSAALETSG IADPVALAG QDKASARTIA VPVASDAILK LSPPEYPYLV ENEAACYQLL
TKNKLRIELS KVEVLHDKHG RSGLLVHRFD RTPKGKIPVE DAGQVLGIWE ADKLVLSYED
IAQALTQVCA SPILAMRNLA FQIAVAWLSG NGDLHAKNIS IINKGRGFEI SPYIDIPATA
VYGDDTMALE IQGSKKDLQ KFKLKFCTSI GLPEKTAMSV ANAALLATEN AAETILASGN
FDTMRNDRLA RVLKRRSAW GA

> RXA00230 (1-720, translated) 240 residues
LIHEQDVQKL LNYITSHFVG DPERWFHPEG YQSIALAILD SIYSTGNRYT GVLNLVNRVC
GLRANEGSHP EADTATDLIE TFRWGGVDE FVLKTNRRWR TSSKIHAPYK AYAALAAKVV
LAGHSIESIS DVUGRFDSRE SREHSDIARE WLMITGQSSA LTWSYFLMLV GVPGVKADRM
IVRFVTHVLE RPKEISRHEA SRLIEEVADI MCVNYIYLDH TIWRFSQGRF YLEDSSPFE

> RXA00232 (1-510, translated) 170 residues
MNDRAHQRIQ DIERSQALDR LGSYFADGYL DIDEFDTRTG AAAIARTAGE IDVLFTDLPE
QQASTAVTPV QDDTEKELDL VLQRGKKLQK IDSIAWAVM VSFFLGLFVF NVPYFWVVFI
LGGASASAGR FLLKVDDADE KLFEELHSKE QSEREARLRI AAQRRELEQ

> RXA00233 (1-417, translated) 139 residues
MSVNEADLNA VEEQLGRAPR GVLDISYRSP DGVPGVVMTA PKLDDGTFFP TLYYLTDPRL
TTEASRLLEVA LVMKWMTDRL STDEELRADY QRAHEHFLAK RNAIEDLTGD FSGGGMPDRV
KCLHVLIDYA LAEGPHHFL

> RXA00234 (1-540, translated) 180 residues
MAKQKKTTHKG LVPVSSRERA SESVSATRAP FRLGAVGIGA IALVLLILF VIAIPVRNYF
QLRSIDIAETE ASIEAKEQOI QKLESDLNRY QSEAYIREQA RLRLGVIEPG ETAFRIVDPA
LDTDTSVTSD GNEEKPLGAW YENLWDSVTK PEALGEEIEA PPAVEGEVPT LAPTEEATVQ

> RXA00236 (1-726, translated) 242 residues
MVISFVGWAL SEMDGTAPIR QLQIPEVDV PARGVEVPQI DTEADGRTSN HLRFWAEPPIA
QDGTGVSQAII AAYGNAELIA STAWPGCNLG WNTLAGIGQV ETRHGTYNGK MFGSSSLDEN
GVATPPIIGV PLDGS PGFAE IPDTDGGELD GDTEYDRAVG PMQFIPTWR LMGLDANGDG
VADPNQIDDA ALSAANLLCS NDRDLSTPEG WTAAVHSYNM SNQYIMDVRD AAASYALRQP
AI

> RXA00237 (1-378, translated) 126 residues
MKLSHRIIAM AATAGITVAA FAAPASASDF ANLSTSNKEL SPQYNWVACG ILEGLKKAAG
VLEEGQYNNR LAEAIAAKGE GFWTTQFPQI GDWNEDQAAA LADRAQTCGL VKADTYLSEL
SSNFSS

> RXA00238 (1-369, translated) 123 residues
MKKLRFATIA AATVALTASL TFSASAQDFN QIIONFDCGI LQTAIYTTGL AHENSTRSEL
AANLRNSAAV GQLDFPLNIA ATGYSERIAN RALTCGIVKE DPQDFLSQLQ LLSSNLSSSF
FTA

> RXA00239 (1-585, translated) 195 residues
MRVVVVDPKH PVLVPVSFLEA VLGRGEPVSI DPDPFFDIEK WGIKTSTSAF WFIIAKPFQT
LLIDAPLNPL HEAVGVMMRAA VGRGEWERTQ THESLIPYLE EESQFIEAI HGGDDEHMK
ELGDVLLQVL FAEIAARQG RFDIFDVAAS FVAKMQSRSP YLFDGSGTGIV DTDEQQLWA
QGKAQEKLS EEGRR

> RXA00240 (1-210, translated) 70 residues
MGIFDEAKKK ATEFLDSDSG EQKSDGLLAK AADKAKGLLG EDKADQINKV RDAVDERIGK
NNGGEENPAN

> RXA00242 (1-1203, translated) 401 residues
VNEWRTVSLV DSTALTIIIS VAVFTSAVAL LGVVKKRSRW RVLGALISSA VLTSGAWVVI
EKLWKPFPDP NPWTIYLSAG LAVPILLSIL FRTGRTRILM ATLTVALVIA TAIVINVIYQ
PYPTILGSFNP VPTAVSMSYA DFESQTTAPT QDDREVGAIV QVPLAGTTDD STSGFDARDA
YAYIPPAWFD NESLQLPVLV LMPGNFGQPD MWFSSGNADQ TADNFQATHD GISPIVISVD
GTGFSFGNPA CVDSDAQSVM TYLSHDVPMPL IKQKFRVNDQ QRTWTIGGLS YGTCALQIM
TNHPEAYGSF LDFSQEEPT LGTRQQTVDQ LFGGDEDAFK AVNPEDLLNQ AISSGAHTYS
GISGRFIAGS NOKSAVSALS HLDNLSNQAG MSTTFDTVAG G

> RXA00244 (1-636, translated) 212 residues
MNDQLWEGDT GTLTGSRKA LVQLLKGPV NALQHVVEWR AITTDQDALN AVLNNLFLLEL
VLDEADAGVAF TRPANRQGEV LVGNKNTTEAM PKVLRTEELS HFDTLIILL RQELTMAPPG
ERVIVDREIE REQVLLYRVD EERDEAKLAK RFDAAFRRIV DYSLAKKTET PERFEVSPAL
RQIFDADTVA GVRAEYEFKN KAAHDGNEEE QK

> RXA00245 (1-1485, translated) 495 residues
MTVVSHALGF KRFRQESLEL SLLRSDNFPV VLAVVAQYFP QGAIKAPASE LYQLLSDDDR
VLREEGFELP KSPSDYVSDW VKSRWFVRRP GSSQTGETVE PSEELLAVLD SVQRWONPHR
SISASRIEEL TQALQTLALE SDPSTAKRLA ELERERDRIE RQIEAVHAGE FEVLTTVQIG
DRVADILDLA ASIPADFARV RHELSDLNRR LRRQLLDPED SRGDLVEEIF RGVDLIGDS
AGRSFNSFFD VLLDRERSSL IDRWIREVLG RDEAIDLDSK LRTGLYRIFR DMEDASFEVN
GEMTGLARS L RHYVTTEFA ESRRMIQLLR DTRSAAAKAA EAGEVTSLSNM MDTPLVRIGM
DVRSIAGLKL KNPGEERVED LPEPVEEQEL DTEVLMQIR ASEIDFEELE EAVSLVLAEQ

SHATITEVLE HFPATQGLAS IVGLLYLAMR DGVPTGRAQI VEWESDDATH RRRITGWQFI
RGLNSEDLAE SEMDK

> RXA00247 (1-927, translated) 309 residues
MQTLIFIAIA GVAQQLVDGG LGMGFGVTST TILIMLAGLG PAQASAVVHT AEVGTTLVSG
LSHWKFGNVD WKVVVRLGIP GAIGAFAGAT FLNISTEAA APITSLILAL IGMNLVWRFIS
KGRIRRDYSD RPHSRGFLGG LGIVGGFVDA SGGGWWGPVT TSTLLSLGRIT EPRKVVGTVN
TAEFLVSLAA TLGFVVLWD DLVANLSAVL ALLLGGAIAA PIGAWMISRV NATVLGGFVG
TLIVTLNLPK VLVVVGGLDFI PTGLIQVTVL LIGLPLTYLG FRRYRKNLLN ETISSEVVSE
PKGQKIKST

> RXA00248 (1-723, translated) 241 residues
MIPLITLSHG SRKKSAAAGI TALTHEAGRM LETPAVEAHL ELAEPQLDQV VATLSAEGVT
RAALVPLLFY NAYHAKIDVP EAVKDASEKY GVLLVGPPL GTGSDVASVLT AQLRLSADVT
DAHVILYSVG SSHVSANESV IDLAHTIALI TGFSVEVVPA TGGPGAGGAG VIEVASKHKA
VHILPLFVTE GLLLDRAIDQ SANIAAATGT NPTYSEPLTT DLAPLVAARY HAALSALLAH
I

> RXA00250 (1-216, translated) 72 residues
ALGAALGQFD FVRNNIDLIF LLIVFISVVP GLVGMARKLA DGHKQANTEP QENPAVQTAP
VKTQEAQEP QN

> RXA00252 (1-243, translated) 81 residues
VFAGGVGDVA GWWSVAGAV VDDBAACGRA EGGQELATQL GRDNDEIVEKV CVPFPGTAGF
DGRVTRHRRG VHQRIHVVEV F

> RXA00256 (1-771, translated) 257 residues
MFMSLKTTRI FGALAVLSGI SFSAIATPAA SAQELVVSTS AVNEFGVVTS DITAEQILQA
QDLIAEMKQS EDIYEYFGAL SDVEQRSIIA AVKENPYLIE NESPRMRVQS ETPDEETPDK
KKPSKTYKLY MSILEMMSCI NLVDVPSCAQ ALKAANIAER EAKARYPDSV TNGKGDLARH
CAWSALMTIR IGKDAAEERIG NAHETVVRGE PEEREMDLIN NALGRDIGER FIINGDETGA
LSTCVSMANI GLRLTL

> RXA00257 (1-456, translated) 152 residues
MKIKKFSITA LASVLMLTGC ATNHSSPLYS YLNASTSTTV EQVRLSDLYG EQWTEFALVC
PYTTKDEVKE EGLIKINTYL TDSTDDSSND IVLRDKDGSY DWIYFNRFDI VYLCNGSAEN
LKIYPIPSVL EFEHRDDYGT WKLSAITEPG NQ

> RXA00258 (1-672, translated) 224 residues
MRHTTSATST TSIIKRAMTI SAAVLIASAV GLTTSASSLN TLSATSPESP DQAATVSQAE
SDSELDDGKM KLATKILNRA DNAENDDTG KNLNDDKKL NTKQPORPAE KVAQAIELSL
DTTNAEKPD KSFHHEKPVN AYTVSVSYNK SNTWTIKPS DSAVNTPTND AERISNIIEQ
ARDLGLSDDE SLTQQIAFHA HAANYLVTEW VLRGYQLANP KVLFP

> RXA00260 (1-1176, translated) 392 residues
MHSDAVLAGA SIRAKIGALA TIYGAQNLEN VIHSVSFTDR RISPDGQLSK ELFREAWSAN
LLIPDPSVD EAFAWSEKNS TELAGGIFVE KMLFTVPDGT RSNNRVQSFS EELRNHISLK
DMYSTQREEL LDLAYELMVG EAVRFANFRL YDQNLPLTE ANIDKLRALH REAASASLG
VLYLMVWRSV KDAQAAHTKH TRMSKENATT HSVTKVSIFV DQLLSGTFFC SKPFHESSQV
PLSEATKIVF NLIMESPEME TEPVSLRNSL QHSDWELLQ QCDEKIPDRE FLMEWLYEQE
TWTAEQFFDA LAMVSSSEFR ICAPGCAHQV SADIATQVLE FHDRVSFHDD RKSAMLAEEA
TTIGNKIGSQ ARAGDFVLGE VITKLQNIQ EV

> RXA00261 (1-429, translated) 143 residues
MYSKLLILL LSEQDSSYEC CVGLLDGSDG RDYIEKLLKG RKLKNHFLEW EDINKADVAD
EEIYKQLVH LVFVTALSTP GEISFVFPQG SLMSATLEED FAALVLEER TSFRPDLSHL
WSLPVGVWAP GLEGFVERNS EAA

> RXA00264 (1-378, translated) 126 residues
LLVDSGDVQL EGVTVPTQL AYTGINETQL RIRNIGTPA RTVLLGGEFF TEDIWMWNF
IGRSHEEIAE YRKQWQAEAD RFGITHGYIS HHKDGLTRLP APELPNAAIK ARKNPAPTAR

PETRID

> RXA00267 (1-270, translated) 90 residues
 VSVAVITRIA SSPSFIAIVA IIVAAIALFV GLNSRVGTKL VDQPVVFTQE QIDQLKELKS
 RDQEAARQ AQLWSRSGSS EAVAEAVRKL

> RXA00271 (1-990, translated) 330 residues
 MFSSRSKSLV SIFTVGAIAL ASCSSDSDS STSTDAAGD SYRVGINQLV QHPALDAATT
 GKKEAFEEAG VDVTFDEQNA NGEQGTALTI SQQFASDNL LVLAVATPAA QATQNTIDI
 PVLFTAVTDA VSABLVSNE APFGNVTGTS DIAPIEQQLL LLQQLVPDAK SIGIVYASGE
 VNSQVQVDEV TKAAEPLGLS VNTQTVTTVN EIQQAVEALG DVDVIVVPTD NMVVSIGSSL
 VQVAEQKQIP VIGAESGTVE GGALATLGID YTELGRQTGE MALRILQDGE DPATMPVETA
 TEFTYVINED AAEARQGVETP QEILDKAERV

> RXA00272 (1-372, translated) 124 residues
 MPEPETSTMG SIQKSGEWLV PAYSAYKING ADLFLDIRHA TAAAPVITFD VNMTMGSMTL
 IVPPGVYVEV QMASKNWSDF KVQTTNPLFG APRVFTTGA RASGLKVFTK HPHEPFGFWQ
 KMFE

> RXA00273 (1-1113, translated) 371 residues
 MSLKLNRRRL ASIAVAVAVG VSGVAAVGAA PATAQQVQAG TPIHVNNLDR TVVDVPTGDI
 TFHFTDGTFF TLKAGVDGKD GTDGDQGVIG KDATIVDVAT ESNGDVKLTF SDGTVVVTIP
 ARKGDVDEGE KDGVDGATVVS TATDANGVIN ITFSDGSLV VANGKDGNDG SDGDGADGE
 NKGKDGNGAN ATIVDQIAND DGSITIVFSD GSEVTIPAPA KGATDELAQC LLNPKMLLLA
 AIPAAAGIAN AVAPAI PRVV EDVRAQFNLP SLNPFQDQWL NYATKCIDAG LLISGATGLA
 VLSVLADDFC GDIDADDNAD GDVAAEKPTG SSGLSGSEQS EKVDGDDDSV IDTETDADLE
 VEEDGELVNA G

> RXA00274 (1-2610, translated) 870 residues
 LSLNLKKNNA RSITALTAVG LGLSIVPAAS AQDVADDTTN SDSTRDAICA AAPLVAGAAV
 GVGLLSQQPE FQHMVSIQIS DAQRIGQDLS NQFNNSLESIL NIGLNGVHG PQQNAVQCID
 LTEAARTMAG WNDLAAQVQG TAGPAIGAVA GTAGLIALDV YCNLEGFDAF SSGSGTDGEN
 GVDGQDGTSI TITEIRTTDD GNTIVVFSOG SEITITNGKD GAATITVNTY RDEGNTVVE
 FSDGSTIVID KGEDEKDGED GKDGEDGKDL TVPTDYINDD GDTVVVLESDG STIIVKKGTD
 KKGADGSDG ADGVSITVEN SYVDADGNTV VEFSDGSNVT INKGEKDGK DAGADGEDGA
 DGESITVVNT SNAEGNTLV ELSDGTVITI NKGDKGDAGA DGEDGSNGAD GESITVIET
 FDADGNTVVV FSNGETITIN KGEKDGKGD GEDGKDGTLT YIGPDGNWMI GENNTCTAAR
 GNDGKDGDTP RIGDNGNWWI GIVDTGVPAR QDGANGADG ANTVEILING YWINGENTGV
 KAVGNGTNG ADQDGDGNGT NGANTVEIIN GYWYINGENT GVKAQGPKEG KGTGDTGAP
 GEGSGNVDIE IRESSYPGGG QATIIILDQF EYEIPHTVIG DNGNWWIYEGK DGTIPAQGGT
 GTFEGEDGLTP HIGDNGNWWI GDTDTGVSAS PTPVGEAVAG VTDVVENTSD EPKTITATIN
 GEEDYDTLNP HSAVFFYATG SPMAVSLPNA SGLTVIGTEE TPGFTTIRFS DHSTVTIPHG
 RDGTNGTNEL TVRMVSPRTS VRTETGGSAG RTLVRQPLA VAATLVPAMT ASRSQVMILD
 SQMLLRPVQR PVQMPKVLIT KGHATTMTD

> RXA00275 (1-459, translated) 153 residues
 LDKRRPELSD DFIKAFDDFL HSFACLDKTT ITLLAQSPVR TSTGYGTFTI GIFPNEPLSE
 EPTPTIYIVH DNHTGIIHSY PARMINKLSE LGSAEMIHEA IWGSPHQQLL ISWYETYYTN
 IYGGNPPETE PHKSLIFAQ DFCLTPPEKE PFF

> RXA00276 (1-342, translated) 114 residues
 MDLSSRRQDH EAYGTYNPDN GVMPDHVIVP SPYEPYDDAA PIDPFYDEED LLDEIKEERA
 AHAVDAQVTE TTKADADVAQ LATAIDEQNR PTKSCSLRQI ARNYSPPGWIS VAQN

> RXA00279 (1-1386, translated) 462 residues
 LDTDDSPDHW LDPLTEKDT S KRTLVSIVQ ETFQPIFVA RKIWA FNVS PGRMTLMTII
 ISIAIFAAGY AMSVSSDTRQ SNLDDLITNA EPVSYNAHVL YTSLSVADTT AITGFVQAGV
 EGEVNRVKYH TAIDRAAVAA THTAASDSS NEHLMELVLE IQRQLPVYTG LVGTARTNNR
 AGNPFVGVAY SEASAMMRNE ILPMASELYN LTRSAVSDQQ RSVTPQWPFV LSGLLAALAM
 LIVAQWLMLR TIRINKRG ALATVMMMTA TLWVSAANWA TWQAGTKFE EASGGLNSMT
 TARIYAQQTR TTETLSLVRR QSIQSGSTGF TATINQIKRA LDEYETTAQS QTEPHQQLIT

AIRNAIAAWT ADHDEFTVLL ASGDYNGAVN AVLNKDEEGQ TSFDELDTAL AELIADSRSS
 MRSYIQSGLQ ATELVSMVM ILSVSVLAL WVGIRPRLQE YL

> RXA00282 (1-789, translated) 263 residues
 MSRDDQTNNN GEGDDTSREQ SWDQSWQNLN KDSQYGPTSH PEDAPGGFQG NGQGNSSRGNA
 QGNGQGNGQG FGPGNASGYG GYGQPYPTQ YQNSYQGYGA TSPQNDVALE ASNGKVDIMR
 AIRFGFKATF ANPAVWILGT VGLGLAFMIV SGLLGYLSFL IDPNAGTTTS GFVSSETLLN
 VAIGIITFAI TICVMRGALL SGDGHKVRFG DFFKPINVGQ TVILMVGLGI FGIIIGTFTT
 FLTQNLVSNF DAAGTVEVNN SGL

> RXA00283 (1-1128, translated) 376 residues
 LALAFPLAYE ALIMAFVAMW TVGFMTWRAR YRRGFRDRIG FALVDMLLLV WPIGFVAVW
 TGASNLTTGE LFAQFTSTDG NAALIAASCG GAIGFQALFE ASVRTELISF ALLLVAVVAV
 FFAYRRRDPE PIIPALIGS VVFFQIITYS LGSTFGLLRF FLTALPLTII LLFQIIPPRH
 RFPFLRPAGC YRDRVTGKYV PKTITGVVLV AIFGGTGITL YGMSANWAP QEYAIQELVF
 NMGSPSQDAV HTLNTFSTEM DVADEFVDSL LGDGEVLLST TYGFVAVLTG NQKQFIIPS
 DEDFTITLNE PAEHGVKYIL ALPREGRGAT DFINLRYFDM YETGSHIATM EIEFINQGGQ
 QPNWRLYRVL TPPEGS

> RXA00285 (1-513, translated) 171 residues
 GTELGALLLR VLNRREEMDR FARELGFFVD KQLEEVERIN CHHNYTVQEE HYGETIWLTR
 KGAVLADEGT PALIPGSMGT ASYVSGSGKN AEALRSAPHG AGRRMYRNGA KRFSTADLD
 SRMAGIVYRP GKEWIDEIPD AYKIDIDQVMA DAADLVITRH KLRQIVNVKG T

> RXA00286 (1-564, translated) 188 residues
 VLKIPRLLLR RVLPVLITLA LLCGLVLAWF IYPAKAEPKK DDVVLVLGAS SDGRHEYGAE
 LVEEGYASNY VVSNFSGSKD KVGVAHCAGK SRPKNAESFC MDPYPVITAS NQKQFIELAK
 KEGWESVLV TSRTHTQVRV TMFDQCYTGD STVLNVNSLG RTGLHNAVH EIGGFIKFWI
 TAPCADTN

> RXA00294 (1-429, translated) 143 residues
 MSISNAILRG VSGAYILQSG YGKGLPLNEA AAGIQGLAAT GIPAVADMDS DTFGKFVAYS
 ELGIGGALLA PIPISRLAGL GLGAFSTGLL AIYFRNPAMT QDDGIRPSQD GTGLSKDLFL
 AAIAGALVFA PAKKRKKAKN KSK

> RXA00297 (1-912, translated) 304 residues
 MGFTVVVIVI GIGWILGRRD TLGTHAQKPL SLFVYYVATP ALLFDVTVKS DTSTIFSLNF
 VVIALSALIV GFLFLLMRV VIKRTAAVSV IGMLAASYAN AGNLGIPLAA YILDDFTVVI
 PVILQVAFY APIMTIMEM LTNKKSTNLV RNLLVTPLTN TMVLAAIAGI AVSLTSMSPV
 VVIAQPVEML ANASVPLALV VFGLSLSKSK ILEKGVSRR DVFTAALFKN VLHPIVAGLL
 ALAFMGEMTA LLSAVILGAL PTAQNVYTYA LRFRTAESMA RDTGVVTTLI SFVVLVAVSI
 IFGS

> RXA00318 (1-210, translated) 70 residues
 VSDVTVGDIL RLDEAYPPA LAESWDKVVV ICDVPTESVK RVGLALDCTQ ALADKAVDMG
 LDMLIIHHPH

> RXA00320 (1-180, translated) 60 residues
 MAKEDLKWFY DLATQKVFQG KVSGETRMR PYDTEEAHH AISIAAARTK AAEIWDKDED

> RXA00321 (1-1815, translated) 605 residues
 MGQHLEVEVK FSVSESTQIP QLEATAEVDH IDRTEIHQLS AVYFDTVDLR LTRAKITLRR
 RTGGNDAGWH IKFPTIGIRR EVQAPLDGEG ATETLPPREL LGHIRALIQQ RETLPQAQVD
 NERHMSYLAD EDGAVIAEFC DDHVSTVSHL PGVVRKQWRE WEFELADGTL AEAISVLLQ
 SAQSVLTAAG AFSVNSPSKL VSAIDESVNH APKPPQMAQL DKNDPARGVL AAIANASKI
 AEYDPRVRAD YDSVHQMRV ATRELRLSHL TFEIGLGED YLNLEKELKV LANILGRAD
 AEVVEERLSN LINTEVGDSI EEETKKELLE DLGAERYRREH ERVVRALDND RYTDLLQALE
 NLLVDPLIIT EVEEPEATEA PESAEETSET DVSEATEEAD AEAESEVEET QEESADAPE
 SADLDALDEE YSPGSAQVPE EPKEPKKVDA ALVLEHLDK AHVKLVKLEK KARSQWDDL
 IPMLEREENF HNLRAAKKLL RYSAEAVGKA TTVETKKLYK ACSGLQSVLG DYQDAITSRN
 ELLRRAQVAR RQGRDTFAYG ILYQHEQTLS REYLTYGSDA FKSVEKAYAK LAEDTAKRSK

KNKRK

> RXA00322 (1-1104, translated) 368 residues
 MTLSHFSNVN TDAQDSYRQI LEESIISHLG FCALRGWTPA DLRHEFSADI DPLLHFALPE
 IAYSCSDEMY TLWVNGTRAA ETSHPVMTL EKILTELPKL STLPDWAMLA ELHALDNQDT
 SPMTPAQAKA HHRITALLKK AESTNFEEEA EALILKAETL RQQYRIESLL INSYDQDVQA
 RSSTIRASRV YLEAPWIRHQ YKLLNAIARV HSSEALLITK SGICTLFGEQ DDVAHIDLF
 NSLNRQRAHF MKTSAGARIA QLNGETSSYR RSFMISYASQ ISRLLSIAKE DAFNELAQQA
 FLAHSAPVVP LENRSVRSKE ALKETFPNMR TMTFKSTNRR GIIDGFNAAN ESHLGGESAS
 LEDSTFMF

> RXA00325 (1-645, translated) 215 residues
 MTSIIANSND LSEALRTHTA QAHEEAHST FMNDLLTGKL DAQAFIKLQE QSWLFYTALE
 AAARACAEDS RAAGLLDPRL ERKETLEADL DKLHENTTWR DNVTTATAATA SYVERLESIE
 AAKDFPRLVA HHYVRYLGD LSGGQVIARLV NREYGVSEEA LSFYCFEDLG KLPKYKDNRYR
 AELDALELTA EERAAALLDEA SDAFRFNQVQ FQALA

> RXA00326 (1-480, translated) 160 residues
 MAIKLSIDL S DATFAELSAV IGYAHLQVD ADEKLTFFGT VLNIIEFDGDL QFDDVFDAFD
 EAEIELDNPR EDGPIYADDL IDEDEDYRAQ TKSQINDEVI NEIRDGISSF VDIGVNLGLQ
 GRRGGRYGDF GGPRGPRGPR NDGPFPGFPGF FGEGYRGPRF

> RXA00334 (1-336, translated) 112 residues
 MAKLLDDNVQI ETVNVSFEAG GRTNWHHTPV GQNIIVLSGL GIYEAEGEPA RLLEPGDVVF
 AAAGVRRWHVG AVSGAPMFHV VVNLKGIDGE TVDWEEFVDE EHYRSVSDEL QR

> RXA00336 (1-471, translated) 157 residues
 MAKPPRSWLD GPEIPADFDD PDAPGRWPG KLGLPQEGAG SLSSVARRIG GVCVDWGVSW
 VTAIVLSNFT DVLGDVATST LIIEFVILGW TGWIFARTPG HAVFGMGLAR VDAAERVGWV
 RALVRPLLTI LILPAVMVDA DGRGLHDKAT GTAVIRG

> RXA00337 (1-525, translated) 175 residues
 DVEGGVEKHS LSTADIAARA HAHMKSHDVL GRQTTPPQPE GGVAARLGGI AWTMIHKQML
 SRDTKGLDIT VLSITPEGVG LGENSAMDVA LALALYRENI EAPTKARIA DICSQSAMF
 SETSVLRAH TEALRGETGH ISVVDYADGS VTQAPHPVSR SAGLSAFVAA AQET

> RXA00338 (1-783, translated) 261 residues
 VGITAGRPPIA TRLLGGMDKW GVHVLPKDA VYKMLFDFAG AGAIGDYREC AFEIEGTGQF
 RPVEGANPAE GDVOKLFKSL ELRIEFVAPR NLRARLTSLV REAHPYEEPA FDIEMHSAE
 SLENATGLGR VGELPEPMRL ADFVQVANN LPVTEWGVRA TGDPEQMVS R VAVSSGSGDS
 FLNDVIKLG VDYVTSDLRH HPVDEYLRG GPAVIDTAHW ASEFPWTSQA QEILQDKAPQ
 VEVDVISIRT DEWTMSARAV N

> RXA00339 (1-717, translated) 239 residues
 MKLDPSLHKT LLQLATTLRT QNANSAPKTT PEQEAVDKAV AELSRNRDAA SAGQMAVDDM
 ENELIRIQSD ERKLRRKKD QGDALGAETD EERRDLNHD VYTAKSRIAD LMSELQEAHN
 EIHALLNRND LAQSRVKDTE RQVADARAAA EAAAAATPEG EDPVAVIAHL EKPLPSEALA
 EFHAQRLNG VGAAFLNGRS CSGCAMVLP TGISDIRNTP KDEVPQCPEC GSYLITDIS

> RXA00342 (1-429, translated) 143 residues
 VADAPGAVKQ QAQDYAQLLG IQSGHIVQEI GWEDSDTLI SESIEDAIGE ELLDEETDEL
 CDVLLWRE DGDLDVGLV DSIRSLAENG RIWVLTGPGIG KEGALAPGVI SESAQLAGLV
 QTKAERLGNW QGSCILVQRGN KKP

> RXA00344 (1-579, translated) 193 residues
 MSFGLGLSVL FHLVYGRSS TAFSLLTGQI VGVSSSSLMI LVAVTVIVVS AVVIFWRPLL
 FASADPINAQ ASGVNVRFA VAFVVLGLT TSQSVQIVGA LLVMALLITP GAAAVAVTAN
 PVKAVVLAVI FAEVSAVGL LLSLAPGLPV SVFVTITISF IYLCRLIGW LRGRGQRDE
 DAYRRRQHDH HPH

> RXA00349 (1-1059, translated) 353 residues

EKILDELEQS PASYGFPVAL LGWPMGGAV AVLLGGGCV SLIAFITFT I IATTSFLGK
KGLPTFFQNV VGGFIATLPA SIAYSLALQF GLEIKPSQII ASGIVVLLAG LTLVQSLQDG
ITGAPVVTASA RFFETLLFTG GIVAGVGLGI QLSEILHVML PAMESAAAPN YSSTFARTIIA
GGVTAFAAFV GCYAEWSSVI IAGLTALMGS AFYFLFVVYL GPVSAIAIAA TVAGTGGLL
ARRFLIPFLI VAIAGITPML PGLAIYRGM ATLNQDTLMG FTNIAVALAT ASSLAAGVVL
GEWIARRLR PRPNFYRAF TKANEFSEQE EAEQNQRQR KRPKTNQRF NKR

> RXA00353 (1-693, translated) 231 residues
VGRSFTNRTF DPLPFMVVYP DGVDQHWDA RLGLDENTRH LGIDVDGVFFV KLATHLNGNTY
GIKRIFIVGY SNGGQMVLR L MHEVPKMLSG AATIASNMPV AENTLPOVKT FKTHPVPYLA
MAGTADTFSP YEGGDAGIGR EHRRGVGMSA FDSAAYIAAR NGLTEHRHDV IDDVVSIDTW
DGENPVFEWT LINGIHLVPS GRTYPEFLGP STTSVIAAEE IKGFFDGVRR R

> RXA00355 (1-126, translated) 42 residues
IAFGRAAHM KQQGQSGAFT VLEVAPYLLS PENLDDLIAR DV

> RXA00362 (1-960, translated) 320 residues
DEKTGTWATER SATLVAGNSG LGVALPPNST MFIIALALPA AASSASQVYI ALACGGAYAV
LYRLAVVYFV TRKDKIPATP DDQVSVFGEA MKTGWRSPLI FLGILIPVIL TIGPLSEWLK
THGVGESGVK SMSIIVWVPI LITAIALIEG KRRIANNMHA FRVQISKDL P QFATVGISLF
SALAANIME ELGVGPQLSN WLDSDMLPKS VMVIIVCIME IVVATPLSST ATAAAGAPA
VAALAAVGID PTVAIVILL CTSTEGASPP VGAPIYLSAA IADANPTKMF VPLITYFVVP
MILLAWLVGM GFLPVIVPTG

> RXA00373 (1-339, translated) 113 residues
MDIQQLDAET TAWKDSLLRA AQEAGHFHEP PKLFEDFETM VEYKQQAAS DPDIWDVDIQ
QMWGIVVGEY LREKMGMEWV VITDDYGTDL AILATAPNGD HVSXCPPIV GKR

> RXA00375 (1-501, translated) 167 residues
MFSPATGKG DINRRPLNEP NADATTIPTA LKVVFWMFLA TAAFMIFTGL VMYTAGYTG P
DDVDSEYKAV VYNNQEFIGG INAFAGVIA ALTSQLPKGG KNPRLLLLAI MLLVLLTDL
SFATRAGGFA LAIIAVLLAL EALLMFRPAV NDHIDRNHMA RVMNREK

> RXA00380 (1-621, translated) 207 residues
VRLTKLAATI GCVTLISGLAL VACSSDSTAG TDAVAVGGTF QFHSPDGKME IFYDEADRQ
LPDIGDGLM EEGTQINLSD FENQVILNA WGQWCAPCRS ESDDLQIHE ELQAAGNGDT
PGGTVLGINR ROYSRDIAQD FVTNGLDLP SIYDPPMTA ASLGGVPASV IPTTIVLDKQ
HRPAAVFLRE LTKWDLVDA LPLVDEA

> RXA00387 (1-813, translated) 271 residues
QNDPETWDE ELRVNHLRI EGDVYVLQGH GFAPTFTVTW PNGETRTQT V QWRPDDPTFF
LSSGVVRFDP PAGMYPDLYE RRQNLAIQG LFAPTAEWEG DNNELLTSSY PAMRDPAVAI
DIYRGDGLD TGIGQSLFSL DSSLMHSGVL QKIERVNLQI GDTVTLLDDGT TVSFQDASEF
ANYQISRDP T QNWVLVTVI SLVSLVGLSL IRRRIWVRF YPQENGTRV ETGGLARTDR
AGWGGEYEFK HRELLGLKEE DEDEEYFDHD D

> RXA00390 (1-405, translated) 135 residues
MSTTREIAFL IARILLGVIL IAHGWDFKAI TGLEGVTFGF DSLGIPAAGI AGAIAAVVEL
LGGILILGV FTRIVAAFAV IDMLFAALFA HVSSGIGVTN NGWELPGAIG AAALLIIVAG
ASAWSIDGV L AKRKA

> RXA00392 (1-864, translated) 288 residues
MMVGYAVRQI ASVFITLLRM LPLAARNRVA RGRIPETGDV VISLTHHGKR INYVHTIES
IARGHVHAPI VLWLDKPDFD APWPATIKRL VARGLQVRCS DGFYGPHTKY WNQFREIHT
GVRVATVDD MYPPEWFLQR LLFIGDLRMD AVVAYRAHRI ELRDDRMLPY VKWSAADTSK
ASFHLFATG SGVLYPVFI DYVVSQGDV LENCRRADDV WLHACALRD HPIRQVYAQF
RHFAVVPITQ GALVVGNTL MGGNDEQIAK VYTDVAKL VAASKNED

> RXA00394 (1-333, translated) 111 residues
VSESSTPNLQ THQAPELNPE LQKAARKNVL IYGLARLLLF VVLTLLIHS L ALLISAPVPL
VMSAMLALIV AFPLSMLVFS KLRMNATQAV SQWDAQRKAH KEWVRSELAD R

> RXA00395 (1-300, translated) 100 residues
VGRLLLIILV IVAIVLLWKA FKPSTWKRNA EINQGGAPRA VKGPDDEEF LWNIEKNRFX
QRRADAAQL EEEERLKRAR ERYAKPESE EGPEKPTEDS

> RXA00396 (1-471, translated) 157 residues
VTEIAENLQR LGIELPDLPA POYSYVFPNR QGNTLYVSGQ ISRTAAGDIL AGRVGEDATL
EEGIIHAEVA TINLLARIHQ SIGLDNVAQI LKLNWVWNS DDFIQPPQVA DGASQLLEAV
LGEAGKHART ALPTNTLPQG ALVELDAVVA VTEAAEV

> RXA00397 (1-540, translated) 180 residues
NLHSSNRMLF PGPPVDFPIN AETRCIQLDA GVAVKKDGTV LGTSDMARSL PRTAAGQEAY
EYFFKVVRG IIGQLRPGVI CADVHEATLD YLSPQLPRMI DIGMLGADTD FNTIYKRRNV
GHLMGKQESF ANELRPGYKH ILHHSYGAA EIPWRYNGVA IGTEDLWYIG ADKTYILSQR

> RXA00398 (1-681, translated) 227 residues
YLPEFTVDY YVARVEGLEV AGGAIVSGSF QAFDQGYLKD ALAVLPGYV GTQIPADTS
DQELDLDKA GVKAVRLNLK RCGSAGLDDL ETLARRVHDL AGWHTELYVD ARELDELEST
LASLPAVSID HLGHLRDLGL ALLRLVENG I KVKATFGGRV ELDPTEVIQA IMAVDPITALM
IGTDLPTSTR KRPFEDADLD LIAETVGEDH VDNVFWNNAA AFYLGQD

> RXA00399 (1-315, translated) 105 residues
MSHNDSPNFA RRALNWLRLQ YPTGVPRHDT FALFYVLERE LTEEDLNELA ELLIAEGENN
GLHNDPITRE KIGKLITHVH SQPPEDEDID RIQKKLQAEQ FPTRN

> RXA00408 (1-447, translated) 149 residues
MNPVSPKLT RYLTRIPWL LISAIIVFGL GVFFVSWFYA GVIVVAVILI WQLWLIPQOV
KRLGWLETS ELLITKGLW HTFTVVPYGR IQFVDVTAGP LERAFGMKQV QLHTASASSD
STIQCLPVAE ADALRERLAI KARERMSGL

> RXA00409 (1-1413, translated) 471 residues
MSSLEGFRKV HRATPFRLIW TIIIVAVLAA AFNSGASVLS FIWGVVTGEY GFAVLPILLT
VGGAVIVVAL AWITIGIWK AVGFRTTNEE VQLQRGVISK DLRTARFDRI QAVDLVESFI
ARIFRLAEVR IETAGGSDSA ISIGFLRKSE AEALKRELLD ASQHSVATTP AGVPAEPGVG
ETVVVESAGD VLVQPIPVQR TLASTALSLA TIITAIGIVI LLFVPPGVSI AVFFVGMVMP
AVWNLDKSW QFTATQRNDV LHVSYGLANR RKQSIPLGRI HAVKLKQPLL WRLVGWWTVT
VPVVGYGDTT QGGTSKILPV GSKELALKVL EAVGPLNSAD IAESADPSHM SRPQYTPPVA
ARLLTPVDRT RQGVTLIGVA GAPGAVVHHE GRFMPRMSVI DTSHIQELTL KHSIQIRILG
LSTVVFNLVQ GPVGMAASDL SAADGKELIN ILNRKLPAL ESAPLQNSL D

> RXA00411 (1-675, translated) 225 residues
NMNEMILAAD NRLGPTFQTA IIDTLLMVII TMVVAGLLGL VVGLLLYTRT AGGILKNKVI
YTIILNVLNV VRPIPFIIIL AAIKPLTVAV MGTSGIRGDG IFVMVVAIF SVARIVEQNL
VSIDPGVIEA ARSMGASPMR IATATVIIPEA LGPLVLGYTF LFIAIVDMSA MVGYIGGGGL
GDFAIVYVGR AFDNEVMHYA VLVIVIIVQA AQLLGNWLSK KIMRR

> RXA00416 (1-327, translated) 109 residues
TSHYANPLGE FGNNRAFIED LAIRSWNELA DPQQFSDALN TSPWTIPEVF IFRGSIDDDP
AGWKYDVAED LYPNPNVRF RGVYENFESF DQMWQTKQVG FVVVVTHNE

> RXA00418 (1-1065, translated) 355 residues
LASYLSPAL VVAVLAIFLS ATRLYLDGIS VDQGFRTQFL TRMADDIGLS DMNYIDMPTF
YPAGWFWLGG RLANLLGLPG WEAFQPAIV SMAVAASVLV FVWQRTIGSL FVATGIALVT
TCIIILAMNS EPYAAIVAMG IPAMLVLASR IAKGDKFALA GGIIYLGVSA FTYTLEGTAI
ALSAAVAVCI VAAIVQRSIK PLLWLAVLGG GSIVIALISW GPYLLASING AERSGDSATH
YLPLEGTQFP VPFLASSVVG LCLVLGLIYL VVRFHNNEVR AMWVGIAVY AWMGMSMAIT
LGLNTLLGFR LDTVLVLIFA TAGVLGIADF RLASVYQLYP TQITERTATH LTNLI

> RXA00422 (1-423, translated) 141 residues
MPTNYARDNV ISLASAREQR SGKPEPKPEL TLIVRATNVQ ADGEVHRQIG LNSAMSLDEL
HNVLNIVFVG GGEQSPWRFE DQFHQPSAPD TNLGELLPEP GDFLFYFWGL WQFNLCQVEM

YPRDNGTPRA LCIGSGGLG D

> RXA00423 (1-453, translated) 151 residues
 MTPYPLSVLD NSGDHNIWH VQTYPAALPT GAWIADEQQL TOLLKDTVVF LTPGSTAPEN
 APVATIEGVR VDVDKQVAEY NKHGIRLPSL GARTVEAQYR GEPEEAAWR TAMELVEIAG
 GWLEIEAKRR ARKALAEAFG AEVQPLPLDT E

> RXA00424 (1-471, translated) 157 residues
 LQVAAGSALI GAGVAVNDYV QSPVRAISY GALALSGATV IAMQDPTGE RSIIAKDSAT
 MYDQIRQEIG DLGVTGPES DVDAITERGE LVTWLLLAVF VVAFFTLAYF SMRMDVAVMR
 RIAKFFFEKRG ASRPFTCTGM VYAAFIYAIC ELEARTK

> RXA00425 (1-225, translated) 75 residues
 MFERFKAKA PEVHIAAERT NLPLNDFMTR LFAQELPLLD STSRSEVYRL LREYDGPTIS
 SQEEIPAEIR ELMDL

> RXA00428 (1-633, translated) 211 residues
 MPGLVLSTNV AHIGQDPGGD DRISGINKLP VATGIDVFIIP GPNYGDGSGV VGDAIGDSLH
 HGGAHKAIYA YSREELDFD PTYRNGYFGE NLTTSGIVLE DLLINQVRI GTTLLLEVSI
 RRPCTRFHW LDIKGWLKTF TQRGLPGSYF RVIEEGHINP GDPIEVLQAP DHDITMSMAF
 RAKMGKNOLA RRVVAANCLP ARYHEELLKL I

> RXA00429 (1-402, translated) 134 residues
 MKTFNPMTIA GLIGVLYFVL LTLFISIQDM ELAAEIAFGI VTIVGLIAVW DNFRDRNNST
 WKTWTGLVGG LLIAVPGICL LVGNLVLAV DGNPSTMVNT LLSVAGIGAI FLLPIGIIMC
 LIAGFNRYYA ALKV

> RXA00430 (1-411, translated) 137 residues
 MSLKTAQAFR ILTGGLSAIV DLGLSLLQL VFGLPVPVAR TISFIAGTTT AYMINRRWTF
 QAESSTSRFL AVVALYGVTF LINIGLQTLIC SALFENWGWV EAVAMVAVFV IAQGTGRNGHQ
 LHRPKNHHPF SEVRYP

> RXA00433 (1-525, translated) 175 residues
 MDVLKIAIIA AAMIGVPLV VFLIVFAVHK LAKEVPRSGR RPIGIGLLLL GFVAGLIWVF
 VWLSWGQYIE NEFQMGQGPY RFWQVACGV TMVAVTVILG LWTWRWASGP FYSALGGASG
 FSAWADDAI PQDETGLSAF GLVMVIVGVG AGLNVVATIT SIGATIWNRR LPSNA

> RXA00447 (1-300, translated) 100 residues
 MLGSLWRFAV RTAAGAVLW VVIKLIDGIS LSFPTTPLYQ DGQHDNLLTF LAVAAIIVVL
 NATVKPVLKL LGPLTLIITL GLFSLVINAV IMLLAEYVSD

> RXA00451 (1-492, translated) 164 residues
 MNTEEDGLSF AVTATLVEGK WQVREFEDHF SKLSTINAV RSLRSEGPAP ALLCVDDEYF
 VMVRETPSRV FLFLSDAPMA VDDDFAAAVM DELDADLPDI NPDDLDDIDP WPEGDFDILA
 DLGLSEEVLS VICDDMDLDP SEQLLRIAEE LGFDNDLARV VGFD

> RXA00455 (1-618, translated) 206 residues
 ILLALFVAVF LISNITATKG VEIGPLVTDG AFFLFPISYV LGDVLAECYG FKSTRRAILT
 GFGITMLAAL SFYISIWLPF ASFWEGQEF ATGLGLVPOI IVASLAGYIV GQLLNKVLV
 ATKKRTGEKS LWARLIGSTV VGEFVDTLFL CAIAAPVIGI ATAPDFINYV VGVFVWKTLL
 EVIILPITYA VIRWVKRREG YETFDA

> RXA00457 (1-1080, translated) 360 residues
 MTIALEHPVL HSTAIAPAR FQASYTTRLV AVGVDRKPSD FWLETAGTFQ AGDVVIARVT
 AINNHRKVRP PESRKAILFE GVLVMLAYGH RYAADQFLAH VPEDLGPCHL VAAGGIAGTV
 TALHDRVDEP TEIEPLGLLT NARGTVNVRD FAADFNPFLKV EAPNKRAQVI AVLGTSMNSG
 KSTTLACLNV GALAAGQKVA AGKITGTGAG NDRMIYHDAG AHSVIDFTDF GYPTTFKFLN
 AEIRALSVNM INVLDAGAD TVIVEIADGI YQGETSRLLR DQVFQEAVDH VVFSAVDALG
 AKAGVQELQA AGLHVAAASG VMTASPLATA EAAAVLEVVP VPTFDLTNPE IVTAVLTDHA

> RXA00462 (1-1380, translated) 460 residues

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MEAIAILFVI GAILVVAVIV LGIFFLTSRT WIKVAAADEA LIVSAKKKGE SQVIVHGKAV
VMFIQTTHQK ISLRSRQVNM QVTQSSDDNV TLNVEAVALV KIGSEAEFIR RAAQRFASSD
KEIVRFTQDQ LEGVLGRVVA QQTVTSMLRE RKKFSEQIAE TVIPELEKQG LILDSFQIRG
ITDDVGYIKS GAPEIQAKK QAAEIAETEA ARAIAKSRIA NQEADLVEQT QLDANKAAAD
AQVGEARAAQ MQAERLGADEK ARLEVLRRQA ENKQIELEAE VNKVADAERY RNKQVEADT
FEQTRRAQAQ VIEIAEATA AKVRAMAEAE AVRLKGQAEF DAIKAKAEAY RENQEALLAQ
QAMEILPELM SNFASGYANI GSMTVLSGGE GSENSVGSRF AGEQALGLKS IIESVKQTTG
IDLAEIIGQR AAGHAQGSQA GAAIAEALSR DETVEDRSEK

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> RXA00463 (1-822, translated) 274 residues
MQTTTGETSI SNETSFNASR ETSLTALGFL DYLDDEQRRA LLGEGLDIST LTWANQVLTAL
RVLESLEFNEH AYLVSVAIQ HVAQEPGDNF HHFLKFSPEP STENSWELTL DQPTVGLKVT
FDPDGQITFK DAHLGLSPA E VVSVEALDT SYSESQIKKA AEQLVGSLLN TGQAALQSGG
LRGAQLTEEQ KTLFLKMTSN WIDLANGDSG SEQQEIEADT FSDTYIIWNE QKDGSAFFQM
KGPELDFSYK ESVPENAEIS ARGVPNIQTS EQSP

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> RXA00468 (1-819, translated) 273 residues
VKVVDQVVM GPTHAMSGAA VGLAVAQILP AEWGGVTTAT EAFIYAGLAA GAALLPDLDS
PQATVSRSGF PITQVISRFT ENICQTFVNV TRGRKDKHCN NGHRTLTHIV WSAATAGAGA
TALIGAYGPK AVIGLLFFFL GLAIRGLMPE WSKNADWLIV TGASAAALAVG WVMYAPESFF
GIVLGSIAITV GSLTHLAGDM ATKAGIPAPA PVIPLKGRKW WNLKLPKFLS IRANGPADKFK
LLFVFSVAVI IQIGLVSSGN MSTIMMNLFS PAL

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> RXA00469 (1-1176, translated) 392 residues
MSTFEQPHHN QGFIPFAQPG YEAPTHPLAT GTFQOMWQTR PARIPAKQGG HAKVAGVCEG
IGVRYIQIDPV LIRLFFVVTG VFGAGVAAYL IAWLCMERYS VPVSPIALNW TPCHTKDRNH
GWWLVIAFFM FSGVLSSGAG GISGPAIAIT YLCLLAMWWA LHKKQLPFRP GLTTFEFTVS
EDATMKNEEL YRPQPDLSI ITPVEGYAP FAQQTPEAPH WDLPAQNQIN TWDVQVPPKQ
PQKKRRHWVFP VGGGVGTGV VMSALAGLFI SNIDPIYFED DPGIGQVNLII PTNDELLSSY
TSGVGEMNLD FSNLTQLDQE QNVQITSGIG EVMVTLPDDV FVSLSCSAGV GTARCDDVDDL
AAHNADLEGP MLNLVNVNSGI GDVKEVFAFD NM

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> RXA00472 (1-861, translated) 287 residues
VSSVATKTKTS TLPEMNSAVS ADGVTITIDS AFTTDSVEME SLDSPSGDIO PEMSREDGIF
VVVETTIKNE SGAOMDITCA STGSTVYAEI STNQEAIVYQ IRDLFLIPGN PECHNMLGSG
FDAPMTWVQF IPKDATAERF GFTHSELGDG KLTWIALNLD SNSEPAETSE MRDEAAIDPS
TPQQTFFVQET VISQNTIETP VAPAPAVPAY GASCPSVMDQ QPSQAADGSA LVCIYAGTPN
PIWVYGEPEPL GVGATATPGGA CEGYEAGGQD ASGNIMMCSG GQWVYGP

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> RXA00473 (1-765, translated) 255 residues
LWGDGTPVSL PDLGSLSRAE RIDALSRMS TMGAAPVKFE PSVEESAEBQK QDSLAKEQDI
VAVPFAFSDL FPGDGLPRRA VTQLVEQPLV VVDFLAHIA QGGHAAVIGW KDLAYAGVID
SGGVGCENIIA INPGEPEPLN VAAVLCEGLD VVVYKGPETS LSPTRARPLL GKLRQGTAAAL
VMVGTKVSSP ALSVDAEITD YVGIGAGSGR IRGVMQVRA VSKTHGVRSG KVLISRPQDA
ALLEPEQPTT LRAVP

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> RXA00474 (1-1578, translated) 526 residues
MALWFPDWPV QAVHLEDEDAP AHNKFPVAIAA HYRIQVCGVA ARKRGRVRRGM KVRQAQAVCP
ELEVVDDADP RDRAMFEGIV ASLGEVASSV EVLRPGLVAV DAGAAARYYG SEDIAAQMLI
DAALRQGI DV FAGVADEITT AVIAARANGS TVVKREASRS FLQQQPLGLV AAEALGCEA
EVVRALADLG MRTLGEALAE PVEAVATRFN NAGLRCHNIA RARHDKRVAP PITHADWEVS
HVPEEPLILRV DAASFVARNL ASRLHQLLSK GGVVCCQLLV TADFSTGDTV SRIWRTGEPL
TEQATDARVR WQLDGLWTAR GVHSDDDPNEH DGITALWLIP LECVPPDMAS GGLWDTGRSQ
QHVARQVIER VQSSLGVDAY LQPVPAAGRG VEERIHFVPY GEKRDIAIRN AGSWPGKIPG
PLPARLGGGI NHPASQVTMI DTEGQRIYVT AEALLSSSPY ALSWGPARYL ITGWAGWPVW
DDRWEKNGT KYARLQVVR AVSEERQLNA WLLMWKDNKW RIEATY

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> RXA00475 (1-660, translated) 220 residues
VTQGYGVCMY VQPTSHSKHR ARLKTLAIVG ASALTLAGCG TSNSTNDAS SVTQMTSATA
DGAQLSNEAS TGPTALGEAD VAMKTLRPDA PAQLMVDIVR IGSHSFGDVR VFDLTGSTGP
GWFIIDYTSNP TQQSGGNTIN FTGDTALNVN IDGTVYFFDL GLEDPEIGTV DSGSGIVTVQ

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VSAGTFEGRS QFVIGLNGKH RYSVTELDQP HRLVVDVLAQ

> RXA00476 (1-861, translated) 287 residues
 MTLRCSQDVNV EPLPGTAKTG SGFVLEEHAG SWSRDVLDGG TFDPELTDQL KRHLKASGMG
 LQLIRKPGRE GNRVEKHNL FVFAEASIIIE HLVDVADAPVD LDLDLSGPGK NNAQRMDPDM
 LLICTHSTKRD VCCAIGKRPL AAAEVQFGP LHVWEASHTK GHRFAPSMLL MPWNYSYGLL
 DEAETVQLFQ GALDNKFLFP GNRGRGTLDA RGQVAEIAVA EAFGEAIVAS SLQVEFEDDS
 VLVTHPDGRT WVVELERIEV DGVVSSCGDQ PKTGKAWVAR QVTELG

> RXA00481 (1-585, translated) 195 residues
 MLNMQEPDKI HPAEPTLARI YDVKTSDPKS ELVRSQMS EDAIAQIGRLM KSLASLRDVE
 RSIGEASARY MELSAPDMRA LHYLIVAGNA GEVVTGPMGL AHLKLSPASV TKTLNRLEKG
 GHIVRNVHPV DRRAFALMVT DATRGEAMRT LGKHQARRFD AAKRLTPQER EVVIRFLQDM
 AQELSLNNAF WLNTE

> RXA00485 (1-2043, translated) 681 residues
 LPQGPGEIAV TTAPGAPEVG EHVSIIRLSQN TEDTEVLVVG VVEPAQOETL GGAPFVVASP
 DALMEWNSSG VRGEFRVATS DPASLEAASF SDATVVVASA EGHVDKLADS LQGRDRYFL
 LLAFAFVAAA AVAFVLFVESA YSVLTGERVR EFLIRISVGA STPQILGSVI FEAGILGVVA
 AGFCAPAGLM AARLLADNAA RFGIRVPIDV IDLPSSTMWL IAGVGVVMSV IALPAVFSV
 CRKSAVESLS TPAISRTSPW FGALWLLAG IVGAGGMWAY EATSDYRGMR SVALSIAAGS
 ALVCALLIAT AVLVPWLLHV FSRIVGGTVP TLQGLAFAP KQKRSRAALI AVLAGSALS
 SAVLHGQAHG GTHLVAVAKG MGGTDMMVTA LDGEIPAGML EISSIDGVK TAIAPATTAV
 ELEDSGNFVS LMLAEEDGAS VMRAGDTGAP AGGLVLGRNS PDQDAYPAGQ AANIIVAOTPY
 TQAEIFHSDN YFSMIDPALA TGPSTTRNV ILLDGDSNQA PDNATAQAVR KTISLFDGRY
 SITEGFSARQ NTFELVSRIT TMSTLLAIVA LAIAAVGLIN TVALTISERA RDRYLLRTIG
 LTSTGQILVM ATEMIASLAP AAIVGAVSGG FLGRFVASSA TNTAATAPLQ VDILGGTVLA
 MVAGSVLCAL IVLANKRRRV V

> RXA00486 (1-702, translated) 234 residues
 HAIMAAVDHRA RAAVLDSLSE VSGTLKVTSF QSLFLTAPK AIARLTKYEP HLQVEISQLE
 VTAALAEELRA RVDVVALGEE YPVEVPLVEA SIHREVLFEF PMLLVTPASG PYSGLITLPEL
 RDIPAIADIP DLPAGWEVHR LCRAGFEPR VTFTSDPML QAHLVRSGLA VTFSTPLTLP
 MLESVHQPL PGNPRTLYT AVREGRGHP AIKAFRRALA HVAKESYLEA RLVE

> RXA00490 (1-903, translated) 301 residues
 MNKQSAAVLM VMGSALSQF GAAIGTLQFP LNGPWAIVTS RLFIAGLIMC LVIRPRLRSW
 TKKQWIAVLL LGLSLGGMNS LFYASIELIP LGTAVTIEFL GPLIFSAVLA RTLKNGLCVA
 LAFGLMALLG IDSLSGETLD PLGVIFAAVA GTFVVCYILA SKKIGQLIP TSGALVALII
 GAVAVFPGA THMGPIQTP TLLILALGTA LLGSLIPYSL ELSALRRLPA PIFSILLSLE
 PAFAAAVGWI LLDQPTTALK WAAIILVIAA SIGVTWEPKK MLDVAPLHSA CNAKRRVHTP
 S

> RXA00491 (1-420, translated) 140 residues
 VYVLIATSAN RVEDVNFDM MPRDPFADDP NDRASFITDD DPYDHPLEPS EERIIVHSQD
 LRLVMEFKVK LGRPIEGVF FMCEDCEEHF YVDWIDMAAN MRATLAGELS FVHEPSAQFN
 IDAYVPWDYIC IGYLDGLEAK

> RXA00493 (1-324, translated) 108 residues
 FEGDQKGVGR ALATALGKPA YWIASNAGLD GSVVVRTAA LPNGEFENAA TLEYGNLIND
 GVIDPVKVTH SAVVNATSVA RMVLTEASV VEKFAEEAAD AHAGHHHH

> RXA00496 (1-402, translated) 134 residues
 MTRRLHGGEG DQGEHVKGQL KQLFDDDAFL TDLRGVDPS EGGDALAGLL LDLTKEAQEP
 PATMPDWSTL LPEGLDQDQD LPVESTSDTT VMQASNPATQ EFAPVSISDT PNTATNSADA
 DESATVVFLA ARRE

> RXA00504 (1-246, translated) 82 residues
 MTYGFVLVNTD LTHRAIDFDL ENAAKFLGGA DGRVAVAFQ EDGTLVAAAL SASAKDEGAA
 ANPVASLGRN AAATGDGSFF SD

> RXA00505 (1-252, translated) 84 residues
DLIHMDAYRL LGEDSEDADP IGALDSDLDD TDLDLAVVVA EWGGGLVEQI ADSYLLITID
RETAVQEDPE SEARIFHWEW REGR

> RXA00506 (1-1341, translated) 447 residues
VLDFLANPL IALVVILAVG LAIGQIRVFG LSLGAAAVLF VALVVSTANT DIVIPMIVYQ
LGLAMFVYVI GLSAGPAFFS EFARKGWKLT IFMLLLLATL IGLAWVLKIS LGLDAAIGTG
MTGALTSTP GMAAVVELIE GIDPSLASEP VIGYSLAYPG AVLGSIVVAA VGAKLLKVNH
REDARKEGMI TAPLVWKGVO LKPGITGRVG DLPLRAGESI IATRIDDDPH TRILADPDLPL
ITEGMELLIN GTEEAVDRAI KALGEERETK IEDTELIYTR LTVSSPEVAG RTVAELDTVA
HGFMRIARIQ GDSEVVPKPD TVINYSRIR VVAVPGRVAE VRRFLGDSEK SLADVNLLPL
AIGLSLGLLL GAIPPLPGG TTMSLGFGGG PIAGLILGA LKHTGPLTWQ MPFHANRTIS
TLGLALFLAG VGTSGAGFR AALTDSS

> RXA00507 (1-855, translated) 285 residues
VAENLNKHLIS KLSKRGPFRV LVGDMNYAGI PGKIYTPAEG DGIPGVAFGH DWMKSIKYYH
QTLRHLSWAG IAAVAPDTER GFMPDHKGFA SDLESSIQIL GGVKLGSGNV TVNPACLGVV
GHGMGAGAAV LSAANRDLVR AVGAIYPAKT SPSAIDAAFA VKAPGLVIGS SSGLGFESGE
PAKLAANWAG DVCYRESEK NQQGFSFEDM FKLVAIGISF QTGAQETVRG LLTGFLHLQL
AGEKHYKAFS EPDEAKKVV SYFGQELQEH AFPKDTSPFA FLNEK

> RXA00509 (1-177, translated) 59 residues
LVDVLSAAL LDPPELPELA VLELEPPEEA AAEVAPPDE PPEAALHNGF GSVSQTCTFP

> RXA00510 (1-531, translated) 177 residues
VEKPEKTEPE KPVEKPEVEQ ECEKEPDPDP EXMQXKEPVE CEPTPKPETE PEPKXDTTHAX
XPGTPTPIPX ARXLRIXXX XQGXXGTDGX XXXXSESEEC APELNDVPPE SDLIQGLVKG
ATIGIGIVVG VGLVWNFLEQ CVFVIEEVPV PEPEPIPEPA PQPEPTSVKP PESELDK

> RXA00515 (1-480, translated) 160 residues
IESYIAQDDN APTAAELQVR LDAIESGEG LAMLLPDDPTL ADPNAEESFK TEYTYDEAKD
IISGFSSDPA SDVLSQLQQA ATTGTRTAEI RAEVFADRTD DYNESQTALK EDFQNCIDAI
DDARPIPLQY ILIGGATIALA VIVLGIRAWT NSRKQSKHSQ

> RXA00519 (1-513, translated) 171 residues
MAGGGFLFETG AGGSAPKHVQ VQREENHLRW DSLGEFLALA ESRFHELNNN GNTKAGVLAD
ALDKATEKLL NEEKSPSRKV GEIDNRGSHF WLTKFWAEL AAQTEDADLA ATFAFVAEAL
QNEIADIDAA LLAQGGGATD LGGYYSFNEE KLTNIMRPVA QFNEIADAL K

> RXA00520 (1-198, translated) 66 residues
MRFSRVLPAL LITTAVS IPT ASAATLTGDT DKELCIASNT DDSAVVTFWN SIEDSVREQR
LDELDA

> RXA00527 (1-1764, translated) 588 residues
VIATSDVREI SSEGIVARVS VNGNIEAART TTIYTSITVP VANLPVAVGD RVAADQVLAE
LDASALQRL DETDANNARA AMANRNSIAQ SQQAYEQSRE LLDSEGLSPEI NSARSLRAS
SQAYQDQRL FEAKQRVDVG GLDSTMVAQS DALKAAREQA DAAEIERLRA DFGLLNNDRS
NLNDVIGLLE ERESLSAAS ELAQARAAGD LEAVAAAEAK VAGLEQSIAS KTSWTPSQDQ
TYLQSYTALE EAERRVASTT EALEIAERIY IDSLGKVDSE LAAQRAVAE AHSQAQDAAL
GLETAQLSTQ HQLEAQSSAI DAALGLASVD NEAATRSTSQ LRMDINNTTV RSPYSYVSS
VQAQGGQPA GALLSVADDS ELKITANVKE AEISNVITGS RVTFTTPTSTG TKEFAGRVSK
VSPIAAAAAS PATGEGAAAG ATTTNTDVTF PIEISVTGDR EGLNLGGSAR VRVVEIAPH
VLTVELAVY KNDGDKDAVL IISDNDKVEE VEVKTAESDD FDIASVAGGI SEDARVLTQP
GNRYGLIGET VKLHADTVEQ AAAPFSPAAP FDPAPAVSA KQTVGQVI

> RXA00528 (1-1089, translated) 363 residues
MSTSTIRVAI AGVGNCATSL IQGVEYRNA DPSETVPGLM HVKFGDYHVG DIEFVAADFV
DAEKVGLDIA DATEASQNT IKIADVPTG INVLRGPTLD GLGDHYRATI DESTAEPVDV
VQALIDAKAD VLSYSLPVGS EADKFFYAQA AIDAGCAFN ALPVFIASDP EWAKKFTDAG
FPIVGGDICS QIGATTITRV LARLFEERG VVDRTMQLNV GGNMDFKNML DRNRLESKKV
SKTQAVTSNI PDGFLSKVE DRNVHIGPSD HVQWLDDRWK AYYRLEGTF GGVPLNLEYK

LEVWDSNPNSA GIIIDAVRAA KIALDRGIGG PIMPASSYLM KSPFEQLPDD VACERLEAFI
IEA

> RXA00529 (1-543, translated) 181 residues
MKLKWIAPIL PVLALAGCGN YVNVESQGKS GISHDEGNI SVHMYICGDN AVDELILSGG
FYDGGPPGNN PALGMLKTSN PESGYVVVNI ADPAPEVVE PINLPTEQKG YIIANPRLVD
KGWPIFFAKE KYMPSVSTSV GMLEGIDPGL VMRDMYTEST HVFGTAEDFV EAGQWCEDY
F

> RXA00530 (1-1281, translated) 427 residues
MSIGFDRDLV IKMQSQHINE RREQIGGKLY LEMGGKLFPD MHASRVLPGF TPDNKIAMLT
ELKDELEILV AINAKDLERK KTRADLDISY EEDVLRLLIDV FRELGLAEH VVLTQLEDND
YQALAFKQRL ERLGLKVAVH RVIPGYPTDA RRIVSEEGFG INEYVETTRN LVVVAPGPG
SGKLATCLSC IYGDHQRGIK SGYAKFETFP IWNLPLEHPV NLAYEAATAD LDDINIIDPF
HLAAAYDTKAT SYNRDVEVFP LLKTMLEMLS GSSPYKSPTD MGVNMVGSAL IDDAACQAA
RQEIIVRRYFK ALVDERREEQ DDTISARIAI VMSKAGCTVE DRRVVARALD VEESTGAPGC
AIELNDGRLV TGTSELGCG SAAMVLNALK ELAGIDRSVD LLSPESTIEPI QSLKTHLGS
RNPSPA

> RXA00535 (1-717, translated) 239 residues
MWWAGMTAM LAYFLQTVL GFGTLLVQPV VLVLSLMFTL PLSARFNGYR LRRTEIFWAT
LLTVAGGIMI VLGRPLPGNP HPPLDRWIPV LLGVAVVMGG MWLLAEYVLK KDKALILGLV
TGALFEGYVAV MSAKAVDLFV HQGITGLILN WEGYGLILTA LLGTIVQQYS FNAGELQKSL
PAMTIAEFIV AFSGLYVLVG EKFGVVDWEW IAGIALLVW IVSTIALSRT STMPAGSKR

> RXA00540 (1-243, translated) 81 residues
VARVVNVMP KAEILDPOQG AVHRALGRIG VSGVSDVRQG KRFELEVDDS VTEADLKKA
ETLLANTVIE DFDVVGVEVA K

> RXA00546 (1-690, translated) 230 residues
PVLGGIFQWI CGIITRFLYP VVDVIPFHTL PESGLYFIYT ALALAFFVLV VIRMMVELTG
NRVWDTVLVA ASPLVAVHAF TNWDTPAIAA VIGAMLAVKR GNPLVAGVLI GAGTAFKLP
LYLLGAYLVL AVKNKNLKPF ITMAAAAAVT WLNVNVPVMI AYPKAWNEFL RLNRERGAEW
TTIYQIDRNL LFINLNDPVL LNVLSFGLFG ASVCGHDFPW AQGAHSPSR

> RXA00547 (1-414, translated) 138 residues
VAILILGLKV QRTPRVAELA FLIVAAFLFF NKVWSPQYSL WLVLAVLAF PQWKVLFPPW
VTDAMVWPII MWHMLGTDNK GLPHEMLDLI VISRDFAIVV MISRCNPADA RTTCKSGDGC
ARRARIVGRA LRRKRSVE

> RXA00549 (1-396, translated) 132 residues
LTENGETPYE GIILGQYESR PLDMASAMAT IANEGVWHRP HFVSKVETVS GEVLYEFEDG
DGERRVSEKV ALNLLKAMGP IAAYSNGNAL ADGQVSASKT GTQLGDGTGA NKDAMWLGAA
PQLATAVWVG TA

> RXA00550 (1-321, translated) 107 residues
MYGNSNPATI WKQTMNDNALE NSPLETWDAI PALGYGNPFV FEYVWTFSPN IATNDFEGAT
ECAPVEDPNA VIDTPAVDPT APAEETGNQG VEILPGLTIP GDLGLIG

> RXA00552 (1-717, translated) 239 residues
FKWSEGGAEF FPKLSVKVRD EIVAFGAPDE LKVDENGUVG GGVHLKPQVQ NELVEARGDE
VVFDFGRNAM EAQIGKFKDA VVPDVETTHD FIABIESGKY DDLKDKPVVT YCTGGIRCEI
LSSLMINRGF KEVYQIDGGI VRYGEQFGNK GLWEGSLYVF DKRMHMEFGE DYKEVGHCHH
CDTPNKKFEH CLNEDDCREL VLMCPDCFAN VETRHCKRER CAAIAADFAE QGIDPLVTS

> RXA00553 (1-321, translated) 107 residues
MSIVKINAI VPEGAGEELE KRFAARQNAV DSAPGFEFGV LLRPVSGEDR YFVVTQWAE
DSYNARDAE KAKGGHGGA HGSOKKPVAS GASLLEFVTV LGSTGAK

> RXA00554 (1-471, translated) 157 residues
MNTQPEHPEN DLVDEADFSN RPRIYSDDDP SLADAPDPAE EHEKNKSSR QALIYLLQVP

LVTFVSAYVL AWWSRQGGP ICDAGEAVWI CSRAAELWWP ITTSVIAFGG MLGSAWILYD
KRYNRLRWPR WMGVLWILIP FSLMLWGTSVL TLSILGH

> RXA00555 (1-891, translated) 297 residues

SGGKRSEQND AVFEFAAWLA RTSINVRGI TTFIRWPSS SISKLGKKYH KWKYNLDSYY
RSRTIKGLKE AGVEKSQWDD DVSFVVDGFS ESTLLTHAAE EFEADLILLG SDATAPKGRF
LASSTADALL HSSPVPLGLV PRGVKLSKKG VTRVNYAFTN ESDDFFQGLR SSALATNWN
VPLRLAFSP TGITSAPTSRL SLDISTELSS EWRELTLMAL DRARDGVLT DHPNLSVSET
GSGWGWSGAI DALRWKKGDL LCMGSHRTDT LSRVVFVGSET MEIIRNSPVP TIIYPGL

> RXA00560 (1-237, translated) 79 residues

MRIDPLETRQ AVLAVKDWIE GEGDVKKPGR AALAAATRLS VRLLAQHAPG NSVEVRVPPE
VAVQCIEGPK HTRGTPPNV

> RXA00563 (1-2739, translated) 913 residues

FYKDLYARSA RGTAALWIVA ANLSSYSID IAINWVGSEQ TTTVNGASKL VKPALVPTLL
FPFAAPRVSG SMADAGPOAE SQMRLLLSV ERLIAGLAPL GSSINVGHR LHVIPGSPNR
GRFGGDGAYG ESKAALDAV TRWNAEQAAW GAHTSLVHAH IGWVRGTGLM GGNDPLVKAA
EAGVETYST QEIAEKLLSQ ATSTVREQAA SAPITVDFTG GLGESDLNLA EMARAEAAKA
ANAPVVVEAPR TVAALPTPYR PVVQTTDPFA GQVTONLDEM VVIVAGELG PLGSAARTRFD
AELNGSLSA GVELAWTMG LIHWDEDFPK GWYDSDDAV AEEDIFDRYH DEVMARVGRV
KYNDMPEYGM IDNFAPELTT VYLDQDLTFN VGSREALTY VDSEPELTFA SFDEAAGEWK
VTRKAGSAIR VERRMAMTRF VGGQVPKDFD PAVWGIPADM VDNLDTVLAL NIVCTVDAFL
SAGFTPAELL ASVHPARVSS TQGTGMGME SLRGIYVDRI LAEPRANDVL QEALPNVVA
HVMQSYVGGY GGMHPVAAC ATAAVSVEEA LDKIRIGKSD FVVGAGFDAL SVEGITGGFD
MAATADSAM EKGKIEHRFF SRANDRRRG PIESEGGTGV LLRAGSLAAD LGLPVLGIG
FAESPADGAH TSIAPAGLGA LGAAARDGVES RLAVALRSVG VSADEISIIS KHDSTNAND
PNESDLHERI ASAGRADGN PMYVISQKSL TGHAKGGAAV FQMIGLTQVL RSGFLPANRA
LDCVDPLVSK HSHLVWLKRP LDLRAKAPKA GLVTSGLFGH VSAVAIVHP DAPYEAARVA
RGAEAAVDWR ASAIAREEAG LRTIVAGMHG GVLIERPVER NLGVHGDAAK EVEAAVLDS
RARLVDGVLR AEG

> RXA00564 (1-405, translated) 135 residues

MKYNVDVSRE SEDWLATVTN LEGVSTWATT FANLDRNGRE AIALAEDLPE GAESSLTISW
SVPTDSHPFL DTAQIAQQR RYLVAQAQDL EPKVRSAISA LTQAALLGMT AGRVSPTHNP
GSRALSLDQV SGVLN

> RXA00573 (1-651, translated) 217 residues

MLVRPCGEQA VIIDLLAEDA EAVQGSILDA VLALNRSVLG MQVPGIIDI PAQAQLLTTF
DTKQITNRF AEIVDSIALT PAAGAAELT DTIEIPVVD GPDLTVAQH TGLSVSEVIA
THSGVTWTA FGGFAPGFY LIPQTLWDI PRLESPTKI PAGSVAVAGE FSAVYQQQS
GGWQLLGTE IMPMVDVRWQ PSLLKPGDSV RFVQVKK

> RXA00574 (1-879, translated) 293 residues

MSKFVISTGP QAIFQDRGRF GFASAGVGS GSPDRLSAAR ANHALGNDPN ATVVEILLGG
FEVEALHTS IVFTGTAEAV MVRTAGGQSD NANTNTIIDV AAGERIRVEP ATYGMRAYFA
ARGGFVAVKT LGSASTDLIS HMGPCPIEPG DVIDVATDIA DSQWPKLGR LPTLWKRMP
ETLTVIRGPR DKWETQESLN NEFTQVETVS NDSNRIGLRM HSSEPTQHRV EGBLSEGMV
RGSIIQPPGG NPVVFGPDHP VTGGYPVIAV LTRSRCDSRA QLLPGDKVRF KLL

> RXA00576 (1-672, translated) 224 residues

MLTLSFTITG EPGKWFRFR DRTHHGGLT LDDSDALGLM LAGQAQLAT RLPDARIDAS
LHVVTLYQE QGVAFPKDFF LSAAEGAVDL ADLGEIINW SMPDSGEVDA AAVRDALQIV
AANVGVIAPR REFLKVLSSK LVEHRDIKGG TETSIALVWK KDEDSEEIQD FVGIARGRTR
NSSRQQTAVK SARCKTLAKQ ARRQGEKPKT PKRPQARKRP GKRR

> RXA00577 (1-348, translated) 116 residues

MKPQTAACKL GLFLPATPEE FQTGALTHQE FKNLQENPPE WLQTLRRREG HPRPVVAQKL
GITIAALKKN DMDKPLTTAE IKALLENQPE WLRTARTQLA EGRETAKKET EETTED

> RXA00578 (1-723, translated) 241 residues

MTYLVWDGAT LVEGALESTP TVVDSYLAKD HRVVRWDLHE QRFATSVSDVD PWDFLHAVRE
AIPRQGSWFP KVEWHGDDLF AVNIRPAPT RKATSLWLSE DPDPRTQPTI KGPDLVLVAH
LRSRANDNGC DDALLISADG FILEAANATV VFWADPQTVI VPRGDVLPV TLAATIPLWE
KAGITILRYQN IRHIGFPWC GSSLHGWTVP VSWGRGLGKI AAKAPSVPK WNEKLRTPTIF
L

> RXA00582 (1-519, translated) 173 residues
MSDYIVAFES AYGSTKQYAE SLAQRLGVDA LNFEQACAE ANPNTAAIVV LSFVHGPHSH
GAKFITDDTL SGHRVALCTV GMTLDDVVKD KDGAAARSLGN KADDVTRFYL PGLRNIYSELS
TAHRTTMTWI VNMLKAKPLK NDNKMMINT FDTDVDVRVDE SRLDAVEEWA RGL

> RXA00585 (1-318, translated) 106 residues
VIDLSPVNT AAGVYNDTNA IILAQQQQGG PLGPEFGKAS PVGLLLIVAM LVAILVLGWA
FHRHWSRMNR RRIFAERNGL DPFIDIEGVRK AMAEAGLNEK SKKGFL

> RXA00586 (1-882, translated) 294 residues
MKHVSGLRML AIHAHPDDES SKGAATMARY AAEGNQVMVV TCTGGERGDI LNPAMDKPGI
LDNIFAVRQE EMAKAMEILG TEHRWLGYED SGLPQGDPLP PLPEGCFALD DSKVTDQLV
KILREFFPHV IITYDENOGY PHPDHLKVHE VSLMAWEKSG DAAYAPELGA PWEPLKLYYT
HGFIRQRMEM FHDLLIEQGG PSPYTPMLER WKANEADVMA RVTTQVPCER FFDQKDDALR
AHATQIDPAG AFFGTPEVEQ RRLWPTTEFE LAKTRVKTISI PEDDLFAGIT PDAE

> RXA00587 (1-483, translated) 161 residues
MSTNSNSPSN ASGASNIPNT QRPASRYNSP RPEAAAGRNI SGKIIAIVIG LLVIAIVIG
ANFLNRAKFE SATLAKAGSFE RIDDDTFRFE VDVTRDDPSQ VAYCIVTAKD YSHAEVGRRE
VLVEPSDHST VRISTLIPTRE EPARVSGGVYG CSTVIPSHMN L

> RXA00589 (1-363, translated) 121 residues
MTTLRSKEFFV SATTALAAVA LVACSPNEID SELKVPTATG VSLPSKNVSA TSTATTTEDA
PGYIDCVAAP TQQAPEISLN CAMDIDRLTD ISWSEWDTDS ATGTGTTRIVT AANGQETETE
D

> RXA00595 (1-330, translated) 110 residues
RNIAAWIAIA AIIIASLGAL LSMIRVWREV FWGGAMHQRG VSPQLRISPA KIAPALSII
LSVGMFIFAG PLIDATLTAT DGLLNTDAYQ QAVLGENAIG VPSPSYQGGN

> RXA00597 (1-270, translated) 90 residues
MTAFGIIVTV GICMFASFLL SALVLILRKT DFLTRVVLSD MVFYSMAIY LIWVLNNPTS
IAFEIALLAA VLGGVLTPLS MARIISKGR

> RXA00598 (1-318, translated) 106 residues
MTIPEIIVSI LVILAGLFSL GTATLALWRAP DPLTRANLLG TTVGVSIPLL IIALLIHTWS
VDGFNPNNFI RAIIAIIGVW VIGSVGSYYM GRAIYGVTVV DNRRSK

> RXA00601 (1-291, translated) 97 residues
MRFKSVAAIA LSTAMIRGGT ASVANAQVVS PSSTIEIPQE FVHTVQNFVP GMTYGDAGSA
IQSTAGSVAL NSTAGIILPI VLPFLGLGAV GSAALSA

> RXA00602 (1-753, translated) 251 residues
VQKTEIHSS LEVSPSKAAL EPDDKGYRRY EIAQGLKTSI AAGLGMYPIG IAFGLLVQY
GYEWNAAPLF SGLIFAGSTE MLVIALVGA APLGAIALTL LLVNFHRYEY AFSFPLHVVK
NPIARFYSVF ALIDEAYAVT AARPAGWSAW RLISMQIAFH SYWVFGGLTG VAIAELPFEE
IKGLEFALCS FLVTLTLDSC RTRKQIPSL LAGLSFTIAL VVIPGQALFA ALLIELGLLT
IRYFFLGKAA K

> RXA00604 (1-291, translated) 97 residues
MRMKIAAIA IATAALAGGT GVASAQEAGS TAGSSNLSSG IQLPQEATDL LSFLPAQAQA
QVEGAIQSTA GFFAVGLGST AIGSTAVTLG IADLLSS

> RXA00610 (1-864, translated) 288 residues
MEPKPVPYTK ELAHEYSRRT FNKLFTKITG FVYLNKDLIN DPNLVTQALL KRCPEGVLRG

YAALKQRGYQ LLDDQWPMPII SVSGDLNRDR CSRGELLRRI EPENTLLSGN IRFVNDVQAI
QDVFDLHSLN DFEDQVALID HLIRQRPELF QELIQEPKLG KHTQYANPFA ESPQESRLRV
RLHSLGYHGF IPQIHVEYDG QSYFLDLADP LWQVALEYNG GWHYTSEQRE KDSHRKNALNK
SAGWVDVLEVT SKTLQNPNSW NNLIQQINSS LRRKQARRRR RLPMTQVGE

> RXA00611 (1-1476, translated) 492 residues
MSAAASRSRN ILTALLLLVP LTAGTIYASA MGLDVSRAWS SADEVGTGAPA ASVATNNQEL
IEARARAGEA GAQAGFLTSG TEELTSGTQE LIDGAAPLEE GVSAAADGAA QLHDLGLIQLQ
AGTGMGTGA TEIADQVQNA VEQLGGLVVV QQQLLGALE ADKQLASSKI FEAECLRKQI
TEVRGHLENF GISVEMTDQL DQLRSGTRDL ANQLAVPGYG FHDGIYSATN GAAELISAGLG
ELEAGVGYAF EGFTALDEGA NRLDSMATLN EEKTSAVQRA LPVPQVPFAGT IEGTADEERT
SALAEMPIAVL ISALPMLAGA ALGWATLKNK WLMAFAVIGV TALGGIILFT VALGISIGAL
FGALGILLLA TVVAGILSRI LLDVLGTGA TVSVVLGWVA QAAVIGHVWS VTAVSDIALV
WRVVAGMPL HYPTFAVTSI GNGGSAAATV MSVAVLLAMG AIGAVALKRP KAVAVEVEEA
VDADADQAAS ES

> RXA00613 (1-453, translated) 151 residues
MSELKDKIRL DLTAMKARD KDTTGTLRML LSALTQEETS GTKHELNDEE VLKVIAREIK
KRRESAEVYT ENGQELADV ELKEAAILEG YQPEQLDDQ LNALIDEAIA EVGGEADMKK
MGQIMKAATA KAAGRADGKR LSTAVKSRLS N

> RXA00614 (1-915, translated) 305 residues
VNVKSTIAKT LTFSSAALLG AGIATAAWGY SELKKFELKT VELPILKPGT LRGKKFEFRL
HISDLHMPIG QETKKAWVSA LDSLSPDLVI NTGDNLSDEK AVPDVLRALG PLMNRPGFAGV
FGTNDYWAPR PVNPFGLYLF KKEVSHIDL PWRAMRAAFI EHGWDQANQK RLEFQVGSVR
LAISGVDDPH HDLDDYTEIA GAPNVADLS TALLHAPERP VLAQFEADGY QLSLSGHTHG
GQLCLPGSKP IVTNCGIDRK RATGLNKFGE MWMHVSNGLG TSKFVFPFRIF CRPSATLIKI
TEQAL

> RXA00616 (1-345, translated) 115 residues
MKSLEPFLAP ILTALLLVV AIGGSALANN RATPNVESEF ATVNQRSTPT TSAYEPPEATE
SPEEPTTIQI ESPVQPFVPA PAQIPQAPQV FLNYQYDDDD WDDDDDDDD DWD

> RXA00617 (1-1083, translated) 361 residues
MTAVVFLTLA SVVIITRSVL LSEVTNTANS AVEQEIEEFP RFAAEGIDPT TAQPFESGHR
LMEVYLSRQI PDENEAIVGI FPGELIQVDY SQLSGAHLPL LEHSDPLISE IRTPTLNSGV
FSDLERGTTH WGVKNFOTAS GEADGEFVVA FFADNLKQDV NGQIQILLIL GTGGILIASIL
IAWLIAGTII APIRKLSSVS AKISNSDLTW RVPVEGRDEI AQLARTFNAM LDRIEIAVND
QRQFVDDAGH ELRTPITVVR GQLELLATTP PEEQARSIEL ATTELDRMSR MVDNLLTAV
ADSGTFIHAA PTDVTDLTID IEDKARTISD RILLVDAEAG LVSLDEQVRT EAVLELFNGA
L

> RXA00628 (1-408, translated) 136 residues
MASVFTKIIN GELPGRFVYR SENVAVFLSI EPLTYGHTLV VPAVEVDRT DLPQNIWSEV
NEASQLIGNA IRTAFDAPRC GYIIAGFDVP RTHIHLFPTD KMADYDFRNA MAADATDPAK
MDEAAEKIRE ALDGLV

> RXA00631 (1-1455, translated) 485 residues
MENPVVAALD DENQEVGVKK EAEKEPEIGP IRAAGRAIPL RTRIIILIVGV IAGLGLLVNA
IAVSSLMRVE SYTRMDQELE TSMGTWAHNV ELNFQDGVQ GPSPDYVYAK VFPDGSIIIF
NDAQSAPDLA ETTITGPHF VOAASGSASN TPWRVMAEKN GDIIITVVGKS MGRETNLLYR
LVMVQMIIGA LILVAILITS LFLVRRSLRP LREVEETATR IAGGDLDRRV PQWPMTEVEG
QLSNALNIML EQQLQASILTA QQKEAQMRFR VGDASHLRT PLTSVKGFFE LYSSGATDDA
NWMVMKIGGE AQRMSSVLVED LLSLTRAEGQ QMEKHRVDVL ELALAVRGSMS RAAWPDRTVN
VSNKAESIPV VKGDPTRLHQ VLTNLVANGL NHGGPDAEVS TEINTDQNV RILVADNGVG
MSEEDAQHIF ERFYRADSSR SRASGGSGLG LAITKSLVEG HGGTIVTVDSV QGEGTVFTIT
LPAVS

> RXA00637 (1-753, translated) 251 residues
MTDRITGEAA ELLGVTTRTL RHWDSIGLQ PSWRTTIDYR LYTEDDVERA LQILYRAAG
IGLKDIAEVL DQPDANQHL RRQRELVEQ IGQLHRMVRA VDEILKDAI SVKEKIEIFG

EDLPKYQEEA FORWGDTPWE KESQKIQEKM TKEDFQRAKD EHEGFVEKLI DASLRGIAPG
 SAEGNELALA HRASIGQWYT VSAKQVILA RMYVEDERFN ETYKGHASYL LTLEIALAQV
 EGVDLNVEN E

> RXA00646 (1-441, translated) 147 residues
 MQRRARREVG LFEVLDRLEP QPKKRGRIPF TRADLNDNAE LAEFETLEAI AAGDTLITGA
 VFTGTLEGVA WEVQVDVLVR NPDGSYMPV VSNHRVARPD PHKTMQGIATV TRGLGLQPLE
 LKATLRHHTI DGYRLTLALM GLEEAGA

> RXA00647 (1-633, translated) 211 residues
 MGIFFAIRAA RAKTKAEIKA ABAKVKTAK AKAKLDLKR KLLVQOEKLN LKVEEKGLKK
 RNKHELKMAK NILEQKQGR LNKDKVKRWA GTARVLTLPL LPITYRLSTE ARDQVVKGRA
 RRAGVTAEL SQFAGHAAAL KARIQGVRET AKNSSLPAGF VRDVEERLNE LEAANNSEF
 MSPQQRNRAH QTSIRDLNQV SDQIQDRLLD K

> RXA00649 (1-456, translated) 152 residues
 MSTDFIAALE YESTIFARHR NQYTGQAAGT AGVLDSSGYN LLTLLQLRGP STIGELSAIT
 GLDASTLNRQ TKALLTKGFV ERIPDPDGGI ARKFHPTDLG NELLNEERTS SQEKYAEELS
 DWPEEDLRTF VKLEKLKNA VETRVGKHWP RP

> RXA00652 (1-549, translated) 183 residues
 MRRTLPTILA ASIMLTACTP AEPEATPETT TEAAPEVIPT GLPIDAMPV ERTAQTAQPY
 LGTDWVADTN GQRVTGYGTD ERFSTPSCVF YSYPEEPQLT VIVRDMATD DAIAVVDWAA
 PDSTEPAEE PAGWSGGRG GNDTSGALYA VQNGPTAVIV FTNQDQSLKA QLIAEEVIQNV
 LGL

> RXA00653 (1-765, translated) 255 residues
 VSVSQVGEI LITVIGILALL FAYYEAYWTN VESGKLQESA GQKLDDEWNE ARVNPRQKLT
 PELGEAFARM YVPAFGSDFN FAVIEGTDEE DLLAGPGRV DSQMPGEAGN FAVAGHRVGK
 GAPFNDLGNL EVCAIVVET YNSWDVYRVM PMSTNGADRA AEAADCFNEN QVSRMAEGDY
 VNVSGRSITT PDRIDATYPT PGVFDATAVR GSEALLTLIT CHPFQFSAER MIVHAMLVEE
 IDKSSGERPA ALEEN

> RXA00654 (1-1266, translated) 422 residues
 VLDILIYPVS GVMKLWHLLE HNVAGLDDSL AWFFSLFGLV ITIRAIAPF TWQMYKSGRT
 AAHIRPHRAA LREEYKGYD EASIRELQKR QNDLNKEYGI NPLAGCVPLG IQPIVVLGLY
 WALLRMARPE GGLENPVFQS IGFLTPEEVE SFLAGRVSNV PLPAYVSMPET EQKYLSTTQ
 AEVLSEVLPL FITAAILTAI NMAMSMYRSF QTNDYASGFS NGMLKFMIVM SILAPIFPLS
 LGLTGPFPTA IALYVSNL WTLQLTIIM VILERKYPLT DDFKVHHEQ RDYIRAKQKE
 KRIFLWTRRK NRALMILTPW NASTLHATNV ELTKRRTAEI NEAKQARKEI ANKRRETQRE
 MNRAAMQRLK QRRAEVKAKK KGLIDASPNE DTPSENEETK LSSPQVEPTT TAEPNREPSQ
 ED

> RXA00656 (1-261, translated) 87 residues
 MLALGWITWI IIGGLAGWIA SKIKGTDAQG GILLNIVVGI IGGLLGGWLL GIFGVDVAGG
 GLIFSFTITCL IGAVILLTIV QFFTRKK

> RXA00657 (1-903, translated) 301 residues
 MSTEDIIVVVA VDGSASKQA VRWAANTAST RGIPRLASS YTMFPQFLYAE GMVPPQELFD
 DLQAEALEKI NEARDIAHEV APEIKIGHTI AEGSPIDMLL EMSPDATMIV MGSRLGLGSL
 GMVMSGSVGA NVSHAKCPVV VVREDSAVNE DSKYGPVVVG VDGSEVSQQA TEYAFAEAEA
 RGAEIVAVHT WMDMOVQASL AGLAAQQQW DEVERQQTDM LIERLAPLVE KYPSVTVKKI
 ITRDRFVRAL AEASENAQLL VVGSHRGGF KGMMLGSTSR ALLQSAPFCM MVVRPEPIK
 K

> RXA00661 (1-690, translated) 230 residues
 MNPIFELDLA TLWIGGPVIL WREIIGNVFG LFSAWAGMRR IVWAWPIGII GNALLFTVFM
 GGLFHTPNQL DLYGQAGRQI MFIIVSYGYG YQWSAAKRRR LTPENAVAVV PRWASTKERA
 GIVIAAVVGT LSFQWIFQAL GSWGFWADAW IFVGSILATY GMARGWTEFW LIWIAVDIVG
 VPLLLTAGYY PSAVLYLVYG AFVSWGFVVV LRVQKADKAR ALEAQESVTV

> RXA00662 (1-1269, translated) 423 residues
VSTIPLNRLA VIAAIIGVGT GLFVAALNWS AIGVERLVYG ADHLHNYNPV ANVSPRLRSI
TVIVLSVVAS WAMFFVHRTG PKEVSVIGAI RGEKMPILET IASAFILQVTT VAAGAPVGAEE
NAPRIAGALV GERFSRWLQL DIDAKRILVA SAAGAGLGAS FHLPLAGVLF ALEVLVLEAS
TRTVVIAIIT TTAAVATTGF EVQTPDVFST VPLTESPFWML LAAMVTGVVA GMCGHWFSA
AHKMAQASPK GVKILWQMPL GFVVIAAVY FFPETLANPR WLADSM LGDG LILSTILLVL
VLR TAMFLLA FRVGMVGGNL IPAFALGSMV GGUVGAVLEP ITNVPIAAFA LLGAAAFIST
TMAAPLFGLI AAVEFTDMEA QGYLPIFLAV ASAVLAVRVW SVIAKHELRA IPITYASWTG
ELK

> RXA00666 (1-387, translated) 129 residues
MTAGEATAHS VRAAQIAEEH NYARFWVAEH HNSEGLASSA TLLMCHIAG HTSRIRVSGS
GIMMNFNAHS HVAAELGTLE AIYPGRIEAG LGRAPGTDFM TARELGRASS LVDDVLTSTV
SLQNYLDTF

> RXA00667 (1-585, translated) 195 residues
MIALKSMNR VVQKPKMKAP LPIRDGLNPS RVRLPLDAAP IRAIDFVEYL ISTQRHRNPA
DNAELQARF DADLVVNHYG EPYAPDTMVQ PDDDIWFYRM PAARERPIPYK IHHVHEDDDI
LVIDKPPYLA TMPRGRHITE TALVKMRVLT GNNDLTPAHR LDRLTSGVLV MVKKPELRGA
YQTLFARREA SKTYE

> RXA00668 (1-792, translated) 264 residues
MLTTLWIAVL VETVPGLVVS WVSGLKVPWA IAASIPATFG IYGLSAWLLG LWEMRFDLHS
VVISTLVFAA VALVWRRLFV GGLWLVRRKA RIRQTLADE ERAENAESVA GEPAESSNTE
AAESESSETE RRGIRWVIFD YMRDGGILDH RWLLPAAGAI TGAWLLIDRA VDLLLSTEHG
LGDIVQGDV HWHASTVRFI DETGIASSTM MGQLRNIEQD QDLFYPSAWH AGAWVLSVDV
NLITVEATNL TGIVLSGLLL PLAV

> RXA00674 (1-750, translated) 250 residues
IFAAALAFMG MFQLHPAPST IVMVLLLWW LLKLVLVVPSP KVKGWKAGIG IRLKDVIGILA
ITGIGVLFM LPQIVSGSEQ TEDVLSYSAE EQVTRSESWL VSIFMETRHV VDFGNIDIVP
VLVFAATGGV VALVWRGNLW APVFYFASVA LTANSLKPEF EPWGDWLVNIV GGLHYSTGHR
LIMPVAMFTF AAAGIGAAAV IRLICLGPBK KFTTVSGVVS VVMALVVAVP LQTKAKDFE
EGSETTILAP

> RXA00676 (1-747, translated) 249 residues
MAKNSRIRYS ASIKRAAAAI LTAAATSVAL IAVPATASAQ DLATGSSSIQ TDAREGAWAT
RNTIQDQLAS IGPAALPVRA AVDNAINGMF PGLVDEKVAA EQEAAAREAE REAAAAAREAE
AARVAEEEEA RFRDGRSCPAI ADVCDVIDGG RTWLQENGQV TYGAVPVSSG GVQGETPRGT
FYINKRVKDE ISYEFNGNAP PYAMYFTYNG HAFHQGNVAT TSAGCVRLNT QDAIYYFNNT
GIGDMVYIY

> RXA00678 (1-735, translated) 245 residues
MTRSNLPFAWE QADPSVHASD PRAITFAEDF GIRPIPAVGF IDTTAICATP SNGFEQLWKA
IEPETERRAN DIHLPIVVAY AERLCDAYPL ADRELVLVAH ILHDTGWAHV DESRIIEGFI
SGNWRKAARF FEHETEGCTV ARRVLPSLGY TVDFVEHVCD IIDGHTRQV AYSLEDALVR
DCDRLWRFRD AGITASSSWF GMPVSDYVDR LHREILPELI TEAAHQMATA DLNRAKALLR
TDAIR

> RXA00691 (1-930, translated) 310 residues
MVEGNTIGCA DAGNGVQYTL LDAGFDVETT VQFPEFLCRI NDFPGPDVDD CMTASFAEAY
WSYWHAPLGG DEWEYSNLGA FLYYPKPGTV EAWYWGDTDR PGAIPVSKSQ AELGLDSADP
DYKIDDFEND FITTTPTSES PIADLGGDEE PTETTEAPIA GAGAGSARGQ AAEPTVEVNP
ENPNEVLVYQ DSEGNISITKG QYENLVAAAA AKTTAAVQAP AGAGEANSQP QATAVAEAPE
VDPMTTQVLM APAGQGDGVM AEGSTQQTYA TGTVDSSAQ WIIGLTLAVI SLVSASAVAA
WAIRRESEVQG

> RXA00692 (1-1134, translated) 378 residues
VALATGVSLI APQVVAAQDA SSDIQLATQF IEKEFATNGL IPGPVGTDPDI GLNQDLLLLSL
NALAPDSPEI DAAYAAIAPE LEGYVSVDY IFSRLAKTV AFQDALGVDR ADFIAQLVSA
VQENGQIKNL DNGEATTAIN NFSQAWGLA LHRVGTEAA ERATEFLKTQ VCSDDGVQLA

SAIEPTCKTT DSDVTAMAAQ ALTLANGAQD PTTQATLDYL VTTMDETTGGV KNTWTGVNSN
STGIIVGSAFA IAGDEENYLK AREYLASVQF GEDADPSIQG GFAFTWKAKE INTAISDQIR
RATGQAAALGF AGGNYANDKL ITIANPVDPT PDPEIPTPPA DSEGSTGGIG GAGIIIALA
ILAAIAGVMG FMMAANLQF

> RXA00693 (1-483, translated) 161 residues
MKKEALEEFG SGPIHSGSYF ENYLPIIDYSE AGFHHYLYKER TDAADPSVPP PEGFVHCYSYF
WIVDDDDVLV GFLALRHLELN QHLELVAGHI GYGVRSARR KGAATAALKL GVHEAQAALGI
DKVLLCVAGD NEASRNVIK CGGVYESTIR GMRRYWIATD S

> RXA00701 (1-375, translated) 125 residues
LVGEPRSDSC GEQRGCEQSG VAEDESEAGS EGSSAEDEDK EDCFKACCAG TEWSDYGNHG
GEDAEHGYGF NVESVFTDFG DDSGQHEGND DRDVEGRGLF VGQEGFRVDD QRPEENHDAQ
NRKEA

> RXA00704 (1-513, translated) 171 residues
LTITFSRVAL TTLAVTATTL SLSTAANAQS SLDKTLDAR QCIDADNVWV SVDYGADSEK
EPEGACATEF TDGVVALESA GFKLTFDESE MGKMYMTGING VVPDWVETGT WYSYSGEVA
DDYSVDYTTY EVGASNSEPE GGTVEAWVVG TGEETPALET LSETSAATGS S

> RXA00707 (1-972, translated) 324 residues
MNVQRKLLAI VGAFMAGSLA LGTPTAQAQS IGSSASQRTS VLRGLTSSAG IPDATAPEGG
AKVVVFGDSH ASGTNAPFDV DERGCLKGNQ SWPDQLQAQ GLQQGLIDLD SCNGASINP
GFHFSDEVRH AEALGAIGPN TENIFIQFGK NDQWGHSPIN LRYSVINCLF DAANGCSEKA
VAAGTMQDPS SVTGENYAQR MKPVIDYLYK YAPNAQITLL GYQEYTPRSG SEICVRVGGT
ELRKPDAATNL VSYMNNLESA IFEASEILDV QHANLREATA GHSSCSAEPW VNGVLDMRVN
AVGGTWHFSP KSGDEVTAGLL GTLM

> RXA00712 (1-549, translated) 183 residues
AAEPTTRTTV QSATEASTTA PVQCNLDPRP SDFGPYLAQS RTPVGLAGS ADSVVQVPDW
FYHFQMGDNG YDSCSKLSYV VLNGSNGDAE RSTGTGAATA DVVULFDHG MVARPAPEFM
KTVESVTRVS DSEIQVYVGH AGRSTAEGVT DYFTTFNFVD NGVLSGRGDL PEHIDTHMRL
YLL

> RXA00713 (1-963, translated) 321 residues
MTKVAELDQE WSEVDDAELD AQSAGTSDSS STDDFADAEN TSENLGPIGP EPLPEPDGDV
PASGFQVQLD NFEQFPDILL QLITKKKLDV TEVALAQVTD EFIAVTRKLG ETSDLDETTE
FLVVAATLLD LKTAARLLPRG EVDDDDLEL LEIKDLLFAR LLQYRAYQV AEMFAQWQD
ARRRYPRAVS LETQFANLLP PVSGLHSLKS FSELAADVFR FKPPETVKTD HVHQVAVSVP
EQAGRIINTL KLAGIDHYLS FQLLTRDCTA SMEVIGRFLA LLELYKARAI ETQEEPLGE
LKVSMTGIDV DPAVVAASDW E

> RXA00714 (1-561, translated) 187 residues
MATITRTDRL ILVPLTVELE DEAHQIYSDS RIWEHRPQAR HTNVVRVTRDI IKRTNESWGK
KDLGPWGVYL RDRPSEFVGW GGVELIDGKV WDLKYRLRPD LWNGYATEI SNAATLATKR
IDDSLPLTAR VTTNHPASFR ILEKLGLTPV WEGRRVGTED DPNEPQVRIY SDRPLSDEIL
EMLKQRP

> RXA00716 (1-513, translated) 171 residues
MESILLVVDV PVSARTLAGV LGIDVPATEA ILKEMAFELS ERGSGIDLRE TAEGWRYRTR
PENADIVEQF LLDGNQTRL SRAALETIAV AYRQPVTRSQ ISAVRGVND GVMRTLQLRG
LVKEVDVDES TGAHRYGTTE LLELLGIDS LDKLPDLAPL LPDVIDSIDED F

> RXA00719 (1-1629, translated) 543 residues
VIDKHTMPGE EDDTVFVYHT HKGEMDVEGA FADEEELAPH GGWASADAPD AEFGYEDSD
DFDAEDFDET EFSNPFDEGD YSDEDWEEIE TAFGFDPDSL EALCTVAIV GRPNVGKSTL
VNRFIGRREA VVEFDPGVTR DRISYISDWG GHRFWQDTG GWPDPNVKGIH ASIAQQAQVA
MSTADVIVFV VDTKVGITET DSVMAAKLRV SEVPVILVAN KFDSDSQWAD MAEFYSLGLG
DPYPVSAQHG RGGADVLDKV LELFPPEPRS KSIVEGPRRV ALVGKPNVKG SSLLNKFADE
TRSVVDNVAG TTVDPVDSL I QLDQKLWKFV DTAGLRKKVK TASGHEYYAS LRTHAGIDAA
ELCVLLIDSS EPITEQDQRV LAMITDAGKA LVIAFNKWDL MDEDRIIDLD RELDLQLAHV

PKAKRINISA KTGRALQRLE PAMLEALDNW DRRISTGQLN TWLREAIAN PPPMRGGRLP
 RVLFATQAST QPPVIVLFTT GFLEAGYRRY LERKFRERFG FEGTPVRIAV RVRERRRGKG
 NKQ

> RXA00720 (1-666, translated) 222 residues
 MASPRRRQVA APRIKELRLT GLDNADPQDI ESNEQIESCR FNEAELSERD LSGAGFIECE
 FLGLEAHETE LRRQAFVETR IERANAPSEFK AARSINRNAT ISDSRFGAVE MYEATVQALK
 ISDSKLSFVN LRGA SLRDVL FENCVIDELD LGQARAERIA FKCTVHSLT FDHAVLSNVD
 LRGLDIERIS GVESMSGTVI SSLQAADLSG AFARHLGITV ND

> RXA00722 (1-504, translated) 168 residues
 LLPNGLLTKR ELVSIERSSH AFEQSVVILP TATLVAGLAA VSVHEPAQPL AVDSYAMAEA
 AGSMRTATIR AATSAALTQA GACSKGDLSS FIGPEIALVS EELNDALSRV ALRLLDGSSE
 QTLLLIQADR QSAFDEVDVR RGLGTHTDVE ITVPATGME NLVEIGVE

> RXA00724 (1-648, translated) 216 residues
 IGEEVLGRQY AYVVCPIREG EGGVLEIHAY LSEQVYPGLN VGMHLGRMDT DLKDSVMQEF
 AQGEIDILVA TTVIEVGIDV ANATVMLIRE AERFGVSQIH QLRGRVGRGVE HDSLCLLHAT
 FDEDSPPQGR LAIASTTTDG FQLSELDLQV RQEGDVLGRV QSGSDTKLRH LSFISDQKII
 ERALIDATEL VAASRSRALE LVSDIAMINQ EYLEKS

> RXA00726 (1-141, translated) 47 residues
 HEMGFAHEVA DQVVFMAAGV VVEAGTPEQV LDNPKEQRTK DFLSSLL

> RXA00729 (1-642, translated) 214 residues
 TVVEDYQEF TGLFLGMVAV SILVPLGMD MRDAKKRLAI VIPLFIICAM LGFFGTSFTS
 APRTPDSLIF VFICAAIAVC ALVLPVGSVS FFLAVGMYA PIMESLSNRD LSVIGVFLGG
 ALTGVLIVFK VLSVYLEHHR TITLTIMAGL MLGSLRALNP WQGDANLLA PGDNAVMIFF
 IIILGGAIVA ALMFAERVSS KNIDSETVAE EHPR

> RXA00730 (1-333, translated) 111 residues
 HFVVFPQQLQ QADPNAEYDL DVLAFDIARV ANLLRWAAVT DLLLPAEARW FQDQLGIAAA
 VSFSGWEEYG ERYVRGLQKN FKGGNKFYIE GERWLNTEAE SPWKTKQWIS A

> RXA00731 (1-2472, translated) 824 residues
 LLFGLRWLGR SRFAPLSLL MIVVMRGLRE VFGAEDPANS SLVDNGLTLT PWSLNDPHFL
 TAGFSASTTT AALMSTLWII VFVAPSERIL GSKLFAITAA LIHITSIPLG IGHAIHIEEA
 DLNRWGNMML ADVLLTPDFW VFGVAAFASA SMPLLWRRRT RLFLFTITLT LLLYGTGLAD
 VTMLTATIIG TVAGELNRHR KTFPGRRVLPG SLTVREARM TAILVAVAA GPVLAALNPL
 THGPFSSATK LIWQPLVTEE HMHLCHTDS TSDACQGALD QLQHGVSPTS VANLPIPLLT
 VVLAMGLSRG RRLAWILAVL AQLISTAVLM FQLTKLSADS TDLLSVNAF SVIVPWLVAL
 AVLVSRRRAF QVKIDTTRIS KSLGALMVTV LATAALWILA TFLFLHAFHP HPTLGLAFKE
 LPFRYLPPTI ETVLSHQLFP RSPAGWAVE WTGTLFWLVV AATLYHLLMG VPSNAHEDQ
 ENAATLLRSQ SGDSLWSMTI WGGNTYWWAP ENAGYVAYRV KRGIAITLGE PILPGDSVS
 KAELAAQFEE FASNQGWIVA WYSVCEEFSK ERINAGHHTL RVAAEAVLS ANADFKGKHF
 QNVRTARNRA AKEGVSSIWT TWADLSAEMO HKIITLSEEW VSDKALPEMG FTGLGTVNELS
 DPDTYLLLAI DEEHLHGVV SWLPVYEKGR IVGYTLDMVR RDPOGFKFVS EFLISEAVVI
 ARDHOLEWMS MSGAPLSTPP GVADDGTIGQ ILELLGRAME PFYGFSLAA SKNKFHPEHH
 GWYLCYRDEL SLPSIGLAVA ACYNNEPFLP NWLKKTATSA PSHS

> RXA00738 (1-288, translated) 96 residues
 LLNDATTQVS HILGNAFTRS GLNAEYANLY GQALVGMVSM TAQWWDERT PPKEEVAHHI
 VNLGNWGLTG MSADPKLTPI SSAEGAIFGQ EKESEA

> RXA00739 (1-816, translated) 272 residues
 VTATVLEFPQ VQLSEQDQVA EIARMEKHN RHKTWRRRTM AVVMTLLISV GLSFGAFGNK
 EREANAFASA IIAQVVGAMG EVAFEAICPS DGDTEMLLKC ITENLGMEMI IEKCLEADV
 LKCFYDAKNE EQRKEQNLDK APDYSMYRMA SAMASFYNG RAATAGVEEG GPNEFLDSED
 AGLKYWEGIL SKAANGGNVL GYADAKHNED SGWFFGNGVA NNKTYSYDS LADHAFQGPY
 HFALFGATLS GLGFDSSKAE DSQTDFAQRK GM

> RXA00740 (1-579, translated) 193 residues
MLKNKTLALL AVSTLMFGLS ACSSDADGPD SSGASSSSSTG SSSASADTDD SAAVVKDAQQL
DTFMRSAAVAD GSSAAVAVDN AVGKGFDPKAD AQAAAERLGD GFQFAADYQA VGYLESWYFG
GARSEKLDEV RSDVIAHLSE LGFTDLAEAS SASRITLGDY CDGVPEYCEL FFDGESPDLY
DMGTELDYSK PTE

> RXA00741 (1-933, translated) 311 residues
MTDSLVLVISR KGLIEERPLT ELLRACIFLG SDTNSDSLQE WAKNELNGYG SIDGIPEYRK
LKGPVPVFAKI QAGNSIMSNM VLGPHNVPER ARKYFPEELH FDQPIQTLIE WSTRQDGINL
SPPNLLRVDR LHNQYAPLN QILNLYVDL NSYFSGIVDR IRLTMSMIA DLTHATPLDE
LPSSSKVYVAT VMKHIENNYE TTITQANGAV AIGNSAKAVQ KGLSVDDLK IMQITINPEKF
DLGEARAEAE ESQISIADEL KKESPNKGFI QNAFEKLKEL SIKAGDKAFT TMLNLVGKQI
IENIPQLVSG G

> RXA00742 (1-1650, translated) 550 residues
VNVQIKGRKV NAKAADLNSY PVSVDLGRF VTLAGLLFFV VDIKKSNNK YPKYVLLKPF
YIHLDSLKAK PGQKTSIVRL KRLPSDEDRM EAIIALALAS RQEKIVENPS NYLYENMESI
TVKSAEPLNR DKLAVYDGSS PDHSIIIRTG DGIEQFVNAT VEIIPNNQF HQANYNVSCN
GVVYDNLVLR NIDDEHIELK IGKGITLRLQ KLAIADPGSV TVEFQDSLPE RLKDIIEFFLG
VLQANTFFIN EEPVVLKINS NRTVADLKDE AGVLRQLVEI ANHFNIDPSL IRIGEITEKQ
FVQLDIIYVRT AVKGEYVKNL EVKDETRLIL QPFGRWNIAL IAHPGDVAGE WTYHEVISKR
HHFAMTPTSD RSDSSIERTV PYELIDNRWL PSVLNLHLDK LVDFYSALEE TVDVONLATW
MVLRLIKAAD SEQSRKTAFL TAAQALNDWL VERDREESPI YRLNGWQILY RQTGLLDSQR
TEIRSFRHLN DQTMHPDNYS EIMIGCALLL DDREANFLL TQLSVDRRAV FNEWPIAQLM
TGALKEEIEK

> RXA00743 (1-423, translated) 141 residues
VQHLVLADVK YRELSALSVK IEEPSDRPEF KLGVTVNDKS KDEEGVPRII EVSLRVSIEV
PDGKITVEPE AIYLI PENKV YLTESDAMVD FYNNHAIFTL VPYARQAVSD LGRAFHTQI
LMPALGPGDL VFSKSTASRE W

> RXA00745 (1-534, translated) 178 residues
VAYLYGSADG MLNTDGFNMF PRASYTILGP MDADAVGVVQ QLLNSTIPMD LARLVTHNS
GASYLRRGAT NVVFETNLAL GVNPMYKRRR ATEAQRGKKR FKRDShyGGG TVTGTGADLD
VVMQARAEH REERLGEKST RKKEELAAVE AKELAAKKGP QTVEEGLAAV EKKHLAKR

> RXA00746 (1-1191, translated) 397 residues
LVHTDRVSIH RAKNGVRRTR KHIKTICIKH PIGRSVQISH SPTALSDAEN NAELTTAQIL
HIDPVTGVAI PRQNILGLED FQTMASFSQ IRHGWGITQL IGQDPNNRNP IRSADTWTVT
GSTGLTGENT ATHNTDDTDA TAAYTMPASD PAVGLCALES NKDAPVDDEF DLSLALRTA
TVMSSSGSAG ITMHDPMVMS TTGALEARAY VDGEGINQHD LDLSRLDQLGI TTDSADTTTPA
LPADPLAALG LSTPTTSALV PGLAELDCLN TDQARTWHRD DNSIGTGKPA ILAVINAEIA
DDYTLQLILKN STATPTDSTD SSDTAERFVA QLPAAETAFVL IDPDIGAVTD LFFINSINQD
LPAPTTQINS VAVDQRDPNI IYATFANDDR VYQLMLG

> RXA00747 (1-588, translated) 196 residues
MTFLHRSASF HPRTHDLSE LGLDPYKLSQ DIPTVIYEVQ PHSVFILKFN TADVRVYQEH
SOLFVRHAVL VDPEQRKHEH DQLLKEILD DAPRVNDIS GRITTVLHDK TVTVHSGGFI
AIIPHNPDA SAAASANKHK QSVMTTSRHP YAQMSLSDML KQGFTELITPLE FYCAVADDDP
SSRHTMHVIN VRDHTV

> RXA00748 (1-444, translated) 148 residues
MTYFALVARN YAEFGVSVEF HEVDDADNS NGPNNTSNLP LKLLRDHSFD ATVVYGDVLV
HTSAHLRDTA IANSNRPVR VTTAQKFDDY IRLATRHGAI HDMINNAAPT GTDIVVITAT
NDALISDESE YDELFHILE SAQGVILK

> RXA00749 (1-699, translated) 233 residues
MLRKTIVTGGI VALIATATLM NSVSSAAEEVS GDVSAVDLAF AEFERTTAED VANGVPEAIA
NAEKISINFTL SELEGFKSLI ASDAVLSRVS GEEILPDNVE VVQTDNVGDE DPNVISPAAW
QGSDFIEGCL TMTLYGIEVL KVCTGGTYSY NVGIATSVSN PRSYVKNYSA PLAVATTSNP
RGGIEGGLAA FYGDVNLVAF PNIPWVGPIIS SSAGTHRVA RSEFNSVVLN VVY

> RXA00750 (1-438, translated) 146 residues
MDWSIIINVL AVATVVTILT IIAAALYRGF TRNKIKKLEA IREAAQHERD NPTIRIADLR
GIMDTHYIY TDVVMTAHE LMITAPAFD VTLPEAVLYE DTKRAAHADAL NGYKDDTVAS
AEKIMLVDAV TAAWTLYSTK ANTGST

> RXA00751 (1-828, translated) 276 residues
MLVRSRTLVT AALSCSLFLG ATVNGTGVAI AYENVSMMAQ YEPYRESLET RLGSSGVFPK
SVEQSVENLA ELPEETRFLD EGDSEFSIID DGLLAGRLDP NTGEIRHRTL ASGISYTTGE
MKRSYTDRTV KVVVYPDGSF DRVTPH3VVY VADSIYYGIE STGYPKVRNG QTVKIPLAVT
DGGTGAVGGV PQGSKVVRDR YGSIENAEML GAILIDEXT GDLTFTAPDD RTGQLWFRTE
VTFPGDSDE VQYVIEVDQ PEPVDVIRPA GSSLSS

> RXA00752 (1-429, translated) 143 residues
MYSDDLILLF LSEQDSSYEC CVGLLDGSDG LDYIEKLLKG RKLKNHFLEW EDINKADVAR
EEIYKQLVH LVFVTALSTP GEISFVFPQG SLMSATLEED FAALVLEER TSFRPELSHL
WSPVGVWVAP GLEGFVERNS EAA

> RXA00757 (1-1254, translated) 418 residues
VSFGVVKRPD ACYALFAILI KRNQATAVSA PMARQQRQWV HARRGHFERV TRSEVELSAL
LGGVEKLSDF LAEYFQLVEI GAGIRIYLDG DGGFWTCFGH FQALEVEFVG CGERLDERRQ
NFSGWKSHKD KDNLPKAIIG LLHCEAMRRR IPSVLGVSLA AFLVACTPS PPNNAALAQM
YQDALFDSQA MSEAEPELAT LRSQHADELL AEIRRICGFD EGQVPESCQV TVPAITAILPT
DDPEKYVND5 QALILDNLDD IPEDSVALVY EQYIAQAEFA EGSEVSVVPD LETTEALAA
AKDLADREFS AAWSLGVALA QLPETDREEV ETAISNHHDR ASQLQIITSG TLPAPGYVTE
LPDPTDETSA RSNIETVENN VTQAWHAAS AATTDARWF CAHIAGDTAR ELTLIDVS

> RXA00763 (1-783, translated) 261 residues
VEKSKRLVLT IAASTIGAVA VAGGAFWVD ASIAAHAERN LSKAVASAD LENDPRVFLG
SSIYSTAFFT GKLDVSIDM LDVEIPGVGM VNARTEVESV EVSRDQILSG DLDGTATFTF
TRTLRMDGVA IGAQLGITDL DISHPIDISP SGGITSEALL TGTPPDMEDP VSVLVTLRV
GSEFQMLPYE LIDAPSGLTL DDVAPDFTWK IDTLQLPLAD RAMAVYLSGG SVHFQSEARN
VQLTTRRELSP LAAPPEENSDE S

> RXA00765 (1-687, translated) 229 residues
MSENSTPNNP VVPGAGADGP SLSDSASISG SDAVNLAEEQ SKSTAHRNIP GLGDLFIPDD
TANLREGPNL HDGLLALLPL VGVWRGEGQA DTAEDGQYAF GQGITFAHDC ENYLSFESRM
WKLDEEGNPT GVDQRESGFV RINKLDEIEF VCTHAGGVVE IYYGQPLNER AWQLESASTM
VTATGPFSTLG PGKRLYGLLP TNELGWDER LVGDALKPRM SAQLTRVIG

> RXA00767 (1-714, translated) 238 residues
VGTIEDVANE QIEVANNTDQ IPAGYKSPLL SRSGAAEAQG AAAQAGTEGV AWHYGSPLVE
QRIFETGTGL VDRSNRKVIK VEGPDAPTEL NNILSQKVD5 VENGFTAGAL DLDAGRIQH
TMQVTVVDVG FYLDTSAAEF DTLIGFLTKM IFWSEVTQGE ADLAIITLLG QEIALPDAVF
ARRVDWNGPS RIDVAIRREN LEEGVDKLLE AGAKLTGLMA YTARAREGVG ARCGRGFG

> RXA00768 (1-444, translated) 148 residues
VKALEPAAVG DLDDKTIPHE IPHWIGRGEH LGAVHLTKGC YRGQETVARV DNLGRSPRVL
VLLHLDGSAF LDPVTGAIEK AGARTVGRLG TVVHDADYGP IALGLVKRSA LDKEHLHIDDV
SVNVDRDLLP AESEQRGCR AINKLKGL

> RXA00769 (1-213, translated) 71 residues
MGRGRAKAKQ TKVARQLKYS SPDMDLDSLQ RELANQSPPR SYSSTDPEDED QYAEYADWDE
DDTDNRAYGT N

> RXA00771 (1-678, translated) 226 residues
MNPYPYAFIP LKHRTGIEPE HTFWEWENKR VHIARRRREA PVRVIVVHGL GTHSGALWPL
VAAIEGADLA AIDLKPTPLY DDWLRLLESF ISSEDDGRPL ILICAGTGGL LCAEAAHRTG
LVAHVIAIATCL LNPSDQPTRR ALFRF5PLTR LIQGRLENRE IPVTRVLNFS KISRSPALSK
LCAADEFNGA FKITWGLFAS YVQHAKLGA VPLTLMFPHD DLFD5R

> RXA00781 (1-288, translated) 96 residues
 MSENKNIEIV HNEGQKRFVI SVDGTPAGFA SYLDGDPDIRN FNHTVIKPEF RQGLSAPLI
 KFDALDARES GIRIHDACSA VAGFIQKNPE YKDLKN

> RXA00785 (1-621, translated) 207 residues
 IATLGVTLT VEARGLFLTV ASIPILFGIF TPLTSWVVSQ QGVAAVNSPG VSVTEILTAV
 YPLAQLFPTL IMVTLVAAAL AVVRILLRR NQESRQVSGE LTRRAQREAE EANQNAARRA
 RAQSTRVQSS KTRNRRAQPT GDTGSQVTV ELIRRSQERR QTVAQRQTER GVFFPTPTGP
 VVAPKPRPSA PEAPAPTDVG ERRQAAP

> RXA00788 (1-225, translated) 75 residues
 MASSINIGVF NLGNAVAAML AGATITTSLG LTSAGLVGGL MTSGLGLVLA VAVVLRRAQ
 GTQATISVVE HQPAQ

> RXA00795 (1-528, translated) 176 residues
 MIISLVSAI IMLVAVGFTG MCSFNTGSPE NGQVPEVDAS TFMSMEARAM TDHATRLPET
 PEGWTTNSAR RTMVDTPAS VVGVTADG YIQLTQTGET VEDAVAGYDT RWRDLSEYAW
 LDGHVDGIYT SQESDVRDLR VMDLGDARVM VSGAATDEEF NDLLRAVANS EPLPTN

> RXA00804 (1-444, translated) 148 residues
 MKIRSAREIA EWFVWAGDEL DAEVSPKLKQ KLYYSQGEH IAATGRKLFS DKILAWQHGP
 VTPGVYSDTK SYGRNPIDP EFVSDEFNWD DYSDVSDELV TVWRKYGIYS AWALREKTHS
 ESPWLDAAWQ QONTEITDAA LKDFFLVH

> RXA00805 (1-882, translated) 294 residues
 MAESFIEVSA GHADRRIDKF LRAQLKGVP SLIFRQMRKG DIRVNGRKVD PNYRLQEGDR
 IRMWQMLLA DLPPPVVDKH IFKAVADSVL FEDAELLVIN KPAGIPVHGG TGHGGGVIEA
 LRQKFPQER LELVHRDLR TSGLLLVSKT TSVLRLEQEI LRDRREEIEFR GYLLKVEGAW
 PGDLRQIDVP LKRTETTVVP HSDGLRARTY FEVVKRLPGA TLVKAQLATG RKHQIRVHAQ
 YAGHPFVGDV RYSGRGGRAA TMHLHAAELV APRGAGKRQK FTAPLPKEWG MGRV

> RXA00808 (1-678, translated) 226 residues
 AGFNEMMRGL RERQVRDLF GRYVGAEVAK RALEERPTLG GEDRKVAVLV VDVIGSTTFA
 VNHTPEEVVE ALNEFFFEHV EVVHRNKVGI NKFQGDAAAL IFGAPLPLSD ATGHALAAAR
 ELRAELKDLQ LKAGIGVAAG HVVAGHIGGH ARFEYTVIGD AVNQAARLTE IAKTTPGRTV
 TNASTLREAN EAEQARWTLN KSVLELRGSRQ MTQIARPIRP TLADRS

> RXA00812 (1-1059, translated) 353 residues
 MNTIITHQAIL IAVEDPVLHP EAMHVAATG RPVIETTINM DISRHFHRTS AVLIDASMAS
 QLSPGKRRDR VFLLDSDPGP SDWKATMKIH AEQAMLLPAQ AGELLSALGR DDKQLPVASG
 HVIGVAGVWG GTGASTFAAA LAKRRAESVT TVLIDAPSS GGIDLLLGIE DVPGARWPDV
 GLRRGTVQAA DVLKALPSTP DEVVVLSTAR SNILDPFALS ESDVSAADIC FLSADRSVDV
 VVDLPHARVH PDIAERLSHL VLVIPAEVRA VAAARARCLE LQQLHVSITC VLRHGRWSGL
 DVAEVEIILG ADIAEVSIGI QRLAKSVEMH GLTGSLPRVL SSACDAVLGE VAA

> RXA00814 (1-774, translated) 258 residues
 MVALGLLSV AVLISGSRGP GARTRPPTPG NGVHLFALIA LFCLATVLFI VVDAYTMIA
 IIAITTLFWY LRQTHAAAR TKQSLQLASF LSLCAGNLRA GVTMVDAMYD ALDNTTPKFK
 LSPTLQTAAR QARSGGSGPR VLIDASLPDL QRLGHLWETS ERHGIPLVAL IDQMRSRISS
 KQRHGESTRA ALQGFQATV ILTVLPIAGM IMGATMANP LGLLTGGGIG GFLLVIGVGL
 DAAGFVLTHK ILQASAPS

> RXA00815 (1-573, translated) 191 residues
 MITALVLAAV AMFLGSPNPG VRGGLISPKS GKSLRIRAGP KKLGNADPVD VSADIELFSA
 CLDAGLNRD AAQVVAHVAA ITHRELWTHV VALLSIGVSA QQVAFMAGV DGLDELANLA
 TVSHRSGSAL SDGCRNISTS LLASAGDKRT AAAERAGVFI ALPALCLFLP AFMIVGLAPV
 VLSLGTQLIN F

> RXA00816 (1-297, translated) 99 residues
 MTIASAGVAS ILISLLVLA WQAGNLVARE QAQVAADVSA VAGAYAFARG ELPDAACATA
 KHTAEANNAQ LENCATEGED LTLTVTVRQG EAHAKAGPL

> RXA00826 (1-531, translated) 177 residues
MITVLIIDQGS GAGKTTTAGE LAARTGFQLV HLDIFYPGWT GLEAASEIVA RHVLADNPNP
FFTWDWHNNC QGDWIKLEPG RSLIIEGSGS ITAATKRKAS LLGELVTVRI TGPPEARLRQR
ALNRDPDYAP FWKVWAQQE Q RHFSLGVEVD HEIVLGSDEA SGRPEEIYDS LGTAQSS

> RXA00830 (1-723, translated) 241 residues
MENPGDLGAM PQYGFHISM LITAVVLAIL VVPIARRRNF APAFGWVLLI ATLLSNLWNF
MPGYTTLDDQS WFFHFSDALR IIAAIALINR ARWAVSVTIL WGTINLMSL LTPDVQYLQV
PWLEFLMYWF MHISVFLAAI ILIFAFGEKP GLSGVMSVA VAISWGIMCL MYNAFLGNTY
GYLSTEPESA SILDLLGGWF FYIVAELVLL CAVWALWSYL IDKLPIITYR AYRPKTRKAA
A

> RXA00831 (1-702, translated) 234 residues
MSALETTLQWQ DWSSVLIVVA HPDDPEYGLS AAVKEWTDAG VEVSYLLLTH GEAGIQGLDLP
KETGSLRAAE QRAACDVVGVR RNLTILNHPD SMLVYNLVL RDIAREIRIR KPNAAVVSNF
DVEAYGLNQ ADHRVAGLAA IDATRDAAFP WAQPELLQED LQPWGAEVII IAGHPEPTHT
MDLAKDSVDA GVASLQAHKE YLAALPDPPK PEEFIPAFLE VEGGYAAAFR VFGR

> RXA00835 (1-690, translated) 230 residues
FAPWALTPIIL MLGGSYLCFE GAELIWHSLH RRIKGEQHS EPKSQESPKS EDQLVKSAIT
TDLLLSAEIM VISLNQIADQ TIWMQAQAVL VVGIGITALV YGVVGVLVKM DDVGLTLSEK
DSAGIQKFGR GLVKAMPVL QVISVVGVA MLWVGGHIMV VGTEELGWEL PYHLVHGLS
WANGIGGSAL GWVNTFGSL VFGLIWGAI TVVSVIKFF IPQRAQNSSH

> RXA00836 (1-1671, translated) 557 residues
MYTHSTGTPQ LDFDGIYPL HLFFSAQTAQ HFALEVRNWH VLRAIVKPEQ GELIVEALLA
PIESATKIGV WYQDEFLGVI AESQFLNLSQ LSRIASFAGHL ISSQLLLTPS KGSLASVLLP
NLKFLGLISND PPRADSHLLP LGRMWRVEPT VHALFEDFSL GSTILFGLRL DLEALIVSYN
GIEGGILNFD DASALSSAVK FSNANGLTPT VLGHVRENG ETSFEDLVLP LELWSKKQHR
LEVLKIPRLI PKEADSQNYV KATALLSDEI LRPTLSKKA LSLSDTAVKY SPHVACGVGM
FSLFAPVIFD KLSHDSAMLL AVISLMLFVL ALVILFKRIQ STNTQRWNL SSVGLLATLP
IIIFLVADTL IPOGSLNHA QPDVQVTTLA NRRPSSPTSL DSLGALNSPS SPNSSSSML
QNSEMFASPP IASQSPVST FRSLWDRSL PLTRENSASE SAVTALGPSI VQPAESIT
PAQTSQSRHA IDGDSDSKTS TGRPAPTNS PIALLPPTWI IGPEDPESTD PTAPTEPTPT
SEPVADEPS ETSQTS

> RXA00840 (1-714, translated) 238 residues
VTKTLPRLLT VAAALATIALP ATPVASAVTP VEQAFNASSN LSSGLPVDQW GRPNEQFRQQ
IEQAVNPQWV PQEIKNIVSQ AMGFITGDGS EGGDIEIPDN APRIAQFEWP TRNSCINCNG
SAVGSFAFV QGPADLPLPG AGVGQTSFVF TALGTGLAE QQTAMTQWV ANLSNTHGT
TTLNNTGINP DGPSTISGVA DTGRGIIVAS MSGGLTSTSE NGSANCFIP TAVVFDVR

> RXA00841 (1-537, translated) 179 residues
MTDLHPVQKE IFNTAESINT DPKGFLREVD TFKVTFDGLY MARGANHPKF GYLESWLLPE
LGLRANIFHF RKGVDERQDY YIDVAEIRVE DNIWTRDLY VDLISVCGEP VTVMIDELA
AATSAGLITA DDAERAIDAT LNAVEGITRH GDDFMQWLSR KGIELTWADA SQVELVPAP

> RXA00846 (1-387, translated) 129 residues
MLKNDLSCAR VVAVHAHPDD EAITTGGLVA DLAAAGADVT VITCTLGEGQ EVIGETFAQL
VNGDADQLGG FRIHELAYSIL EILGVRGIHL GGAGCWRDSG MVGDPANEHP RAFIHSGDRA
VEQLKELLA

> RXA00853 (1-603, translated) 201 residues
MPTSSSPATP TPLKKQSSRK QLQDIALIAV FAALIIVLAF VSIPVGTAGV PIVLQNASIV
LAGLILGGRR GLFLALLFLA LGLIGLPVLA GERTTLAALA GPTAGYIVGY LISPLVAGII
AYLAPKKRGA GMFIVLGLAG LAGLITQYAC GIVGLVLRAG LSLSEATIAQ GAFVLPDLAK
ITVMVIAAG VHAAFPDIRK K

> RXA00854 (1-213, translated) 71 residues
MRLSEFRQLI EDEFGEAKGE WIAHSHVIGA LGVTADVAVD TGVDLRDVWE QLCIDFSVPE

ERRLGKDEPG F

> RXA00855 (1-285, translated) 95 residues
 MTFYFAVLTY NPDSEKVAEV RTVHREFIAN LHAEGKIVGS GPFVDGDGGA LIVIKLEEGS
 NLVDAETLMN NDPFHVENVL DNRVIRSWNP VTKDF

> RXA00861 (1-426, translated) 142 residues
 MAPHKVMLIT TGTQGEPMMA LSRMARREHR QITVRDGLI ILSSSLVPGN EEAVFGVINM
 LAQIGATVVT GRDAKVHTSG HGYSGELLFL YNAARPKNAM PVHGWEHRHLR ANKELAISTG
 VNRDNVVLQA NGVVVDMVNG RA

> RXA00862 (1-564, translated) 188 residues
 VTETETANPV TTTTRIPSDAA PSPTTSEPTG SESNSPSPT ALPPLGSPSM DQKQQAQVGD
 SDMSIAGIRV AEHETFRRVV FDIAGNGQPG WWVDWATDPI QQASGLPVEM AGDSFLNVNI
 QGTGYPDQVV VPGIDTGSYP GAGIVEDINF TSIFEARSQV LIGVSGQPRN YSVSLLEQPT
 RLVVDIVH

> RXA00869 (1-792, translated) 264 residues
 LPFIVAADHPA RGALAVGDNE PAMANNRYELL ERMAIALSRP GVDGVLGTPD IIDDLAALGL
 LDDKIVVGSM NRGGLRGASF EMDDRYTGYN VSSMVDORGVD FAKTLVRINL SDAGTAPTLE
 ATAHAVNEAA AAQLPIMLEP FMSNWVNGKV VNDLSTDAVI QSVAILAAGLG NDSSTYWMKL
 PVVEEMERVN ESTMTPTLL GEGGNDPDA TFASWEHALT LPGAIVGLTVG RTLLYPQDGD
 VAAAVDTAAR LVHTDIQQT SQSI

> RXA00874 (1-1089, translated) 363 residues
 MSIGQHIIIE RFYGAKSHTI DNVDIVLSRE CGENTLAVVR INNALYQLLV NDDGKDVND
 HVVEEVGASFG AWTGSSAFPI GFPTPLGTEQ SNSSFITADN KAIVKYFRKL ESGQNPDEL
 ISKISSCPNI APILGFSSAE ISGANYTLVM AQQYVPLDG WSHALTTTSG SFAEDAERIG
 EATRNVHTAL ASAFTRVVP VEALADALT RLNELISQAP EIAKFKEAAI DLYQSLGEA
 HIQRHGDHL LGQLIKTPER YILIDFEGEP ARPLNQRRPL DSPKDLGAI IRSIDYAAFY
 DGEHTQWANE ATALFLDGYG SIEDQELLNA YILDKALYEV AYEINNRPDW VKIPLAVER
 LLD

> RXA00876 (1-1755, translated) 585 residues
 MTLKIDPSSI SSAVSRNLNEL QHQAITASQV GMKSTILSAF SPVSGLDQLG SGHGNVINGG
 AGAANSVLNS YAEQIEWLSA ALQASGAALT QDELFAARM DVADTGGRRV EESVMFPARP
 APRFESFVN PPAVSPSLSL DALCSQFSGT NSGAVLEAOG SWGSMASAI NVASLSSIA
 GEILAENSEG TFEQAAARIN EVAAGATFA ANAKMMGASV GTLNRIYMGH RMQVMAATS
 IKAILDVPQR LAARAFLAS FQATFQADVL TGMPPVSNLM QMKGANGSAG EIALGMDEIA
 GSGQAWSAAG LTPSCAAQGG VANAGSIAPD AAVGGAAGQS GVGSFTGTVT QLDGNIIGDM
 LTSASAGQS LANGLAMPTS TPNSASGAIP SSMSAASPLG AFGSGAGLGA QGGSIGSSAP
 GAISSRAQS AGGSVPGMTG GPGAPGITS SLMGARTHGA SSAGAVAPMM GGAGMSGGV
 VGAGTGSQS KYARQTSSV GSSSQSGSL GMVSGSGKPG SINSFGRGMM PMMPMPMPGG
 AGGGKNTGK VKTIVTSAVEE DRNLALALGD RGPVVPVIG DWVRG

> RXA00881 (1-378, translated) 126 residues
 MSNTETQFWD DGSWTTRTEV GEAPTRFAVG VMEDFAYIAA TGTGDGDEEFF TLGSNPGLTF
 GDPEWLFQD NPQYVVEICG QQGTEPAALK VVDKYLRLS DEESRGEPTL ILNELVSAME
 LPALFW

> RXA00882 (1-678, translated) 226 residues
 MSSTTAQLRH RELTQEIYNI GDEVAEYIEH IMEAVSDWDL ELVEDCLAEF DEIITEARDD
 SRTVVAELSG LRHALTTGIR QGTVSARATV EVDVDKPERL TASELDRDID IDAGLVDRD
 LSTALNARTD AVVKRELATV EWLAEATDKV ANDLDSLSP LLYGRVAIVI ESATSAWINA
 VGTANPAYVR TMRGNSPPRF LLERARIDAV VARVADKLAQ KRNVA

> RXA00883 (1-519, translated) 173 residues
 VQGMKRKQVA AALATALLFG AAPAHASELV EPTTVAESVA LDPNKAINIL TPDLMEDIA
 KPGDHIHPIY QSTRNYEDLT VEVAKPFEDF QILVGLDNI VIAPVKNLSG AASVAPVFTV
 SDKNGEIDSF TIKVSVEPRR QSDEEKRSL FDISELAYR MPHLPFVSEL LKY

> RXA00887 (1-723, translated) 241 residues
 MSLPVFISDS AAGPGETIEL AGPEGRHAVT VKRIQVGEKI SLIDGRGTAR TCTVTALQGK
 DRLNAVVDLV EIPAPNPQV TIVQAIKPE RSELTIDLTL QAGADRIWAV QASRCVAKWG
 GKEAKSLAKW QVAEAAAKQ SRRRTIPEIL GVGVEEGVEK LIDESDLAI LHEEATAAIR
 ELEFSGNVVV IIGPEGGVAP SEISRFDVAG AHTVKLGPEV LRTASAGMVA LAAGVLSDR
 W

> RXA00889 (1-588, translated) 196 residues
 MSIEVFNEGS YDGVNEEMLI DVLSEFALGEM DIHPDAEASI HIVDVTIAD LHKWLDLEG
 PTDVMSFPM D EITPGYSRPD GATPGPAMLG DIVLCPEFAA KQATKAGHDL AHELALLTVH
 GSLHLLGYDH VDPAEEREMF ALQNELLDW YDNVEARGVT YQKPSGAGA FPTAADRLEL
 DEKMEADDSG FGVGES

> RXA00893 (1-597, translated) 199 residues
 MVESQHIIFI PESQQTPEDF TEVVNEIPAG IKPRIVPWSG SVSAGVQAVE SILDREIIRR
 VILVGAGTGA GVALEIAKNQ PRRVERLVLD SPLVTFDEKQ LKGMSTALKM MPGFFFRKKN
 KKDLLQVQEE ARTAVPMGFS EITMPTLIIR GSAKAGIDS DLEKQIPASR ATTITIGANWL
 TTYTHGRQTG AAIAEFIAQ

> RXA00895 (1-591, translated) 197 residues
 MRGLAMILIA VAVLLAAWAL WSMQGGKDDTS TTSAGQTQST ETNAGTIAES SGSSDSEQAS
 AEPGTSEETS AEQPAADGEA ANAAGAAAG GASSANGNST PVNTLVVLNN STVPQLAARV
 ADSLSGGYQK VESGNLPDIT IPQNTVYFTA GNTAEAKAAR ELADRVSGVA MERSDALPTE
 TEGKDALVLV LVQDVAL

> RXA00903 (1-633, translated) 211 residues
 MGNPLAVIAD ADDLSAEQMA RIARWTNLSE TTFLLKPTQE GADYRVRIFT PTGELPFAGH
 PTLGTAVHVR ELHGEQGTQL VOECVAGLVA VRAIDGPASG LAFOQAPPTLK DGPLDASOLD
 AACEALGISP DFIHRAHQWD NGPGWAVVEL PSAQHVLDLE PDFSAHPTLK LGVIGAYPEG
 APHAFEVRAF AQGIGEDPVT GSLNAFTAQW L

> RXA00908 (1-558, translated) 186 residues
 MSLYTRTQNT RSTIIIEFRR EQTRNHTMEP IQSEPRIYAD CPFRARFHGQ LFRGLREEAR
 GMEWRTPNPT YAPTGNLRIS NLESEARRGG MFHNATLIN NCQGETRTTD AHMATGPVS
 ACTNLLADAG RRVEILEFHQ FDIFEATVTF IYTCNNVSRW WAMFGGTPE QSAASAMSSA
 AHLLYG

> RXA00915 (1-510, translated) 170 residues
 MSAAYSQDIT LTVFLGRGLT AEGIRQTLED FAETGLVRNL VVIDADSFHE SSSEVTHLAT
 NQDGLPELQR RPFNELVSR SRTTKLHIGVI NVIDGSEGML HAELNPLVIG IIDSVCSSHQ
 IHRSNMVIGA VAATLDEELP ILRGVYNLML APEDSHSPGT ATVTYRHGFS

> RXA00916 (1-3591, translated) 1197 residues
 MKKVLVVGGC GSGAKTLAYM MDQLKTTLDL SLPERYPNPK EAKLPGAWQF VSDVPTSP
 SPGNLNPV EAGGRYISCG SSDRYATVDT AVSNQLSSRG ALGGVSSWAL RNPDETTPI
 SKGAGQYRSI GRMLILSRLO EIQAELRKSW DVLFSGETER ELADLSRSLY QTSVSSGETS
 KEQPIIFGVS SMAGGAGASM ALDICRLLTG LEGNAVGLSS LFMVTPDIFS QLSPDQVAGT
 NPNALAMFAE LAAQMGGAAS EEDARLFNAL GVSVDGDSIP VGRIFPVGIR SGENGALLGD
 GKPDTVYRAL GRGLAALMAD EVSMDNEFQF TLGNRGGGSA DQSKYAWGA EAKNIWGSY
 GYSQLSMGRD RYAEYAAQRL ARSAVDRLLK GHFDPSNDAA SDQQLQKRLE NRPESLMGNL
 SDVLVFNAPA GDWIFHSFNQ MIENWTORMK AIKKSQIPAA NGQRGSSEWL DVQRAQSSS
 QMIDNDSRHE LYMGVADWAS ADVLQRRVVE LLRDEIAKLG VPHYGVSVIES LSATIQNQLI
 GQLSDLANNR APEAVQLDDV SRSELDNSKG RIDDSDSYIQ EIVSRSTGQL HTRAVGYIAD
 HMASVDDDFL KNFIYPLQRT IQREHHSLEK DYQLTNDVNL GISQLKTNVP ALWPDQSQT
 VPSRFSQAAE EFLVTDVASF PEQFQAHVRS STDDINEQND YSSALQEAST RVSVSGWESK
 SGSEKAPRDL IRLIDVWVAR DLTRDPGSGG SLRDPKQARF ELKIDTGEVL ERSRQYIRR
 GFSFQOFTAS SIREFITAPG LADHERRARR QOVLSKFSEA MTYALPLAQI NPQLVRALYG
 DEVRYNPNFS RPFPADELG SSLEQAVRDY PNHRPADISK PLGKALVSGQ EERSIDIFGS
 YPNYAPIVFD SLLPPIEKQW RQITGDRTEF WHGRRTPLTP AALPMTDLER NAMVKGWYIG
 RLVGVRVFFPA TLDTADTPV QIYDEKSDSW INFSTPMLTP VSRFRGSLDW LPNLLSASL
 AWARAGERPV FESVEPYIQL RQLWDDAASP SLPGRTRTGE KLLHDWLFDP NRMAGNVLIQI

PGTEAGVTPT ARFEAAKNFL QRQNEISQNY VPSDKLRQGR LFTTADRPFPG DVKDRELAAG
IPVFADLAAD VFDGTQEIID ILEKCLAAGP PSAQVFDMMV ARRDVSSGPGS LPGEGEF

> RXA00917 (1-1383, translated) 461 residues
QLNMQLVGRD GQPRILEGSA LVDLGFTRAD TGEFAPLAGQ IDISGGELSF PLDTISQLPA
IGTVEARATTI TTAGVDDLPQ TPLSPILNTT RITITQORDM QLPASVRFTA DEDVVTVDIP
ITGPGKVVWIA PGTLQSGVLP DGVGDIAASS TFDSPPNALV LGLDEQGTIP VELTVSDLRD
GLVNGSIPLQ ISNAEGANET SVDLPTTEGLT SVPINASTFA LAFILALVLS LLPLLLIYI
VRFLSAKVPIS SAMSGVRIPV EFSGEALRYA GSTMPOLASQ TTATQQVVVH GDTFNVGEHKH
LKVQRFLQNP IASPAVIVQT DPSISFDGKQ KGTQAKLPLA VQGSWFLTAS GADPSKMEI
ALTNLPLEQG QIDRMIAGIT SKAPDRAREL QKLLDDAATS QPAKVPFPRAP AAQGHVKEQA
PSFGTSGSGG FGSSNGGGFG SGSSGNDTNG FGSSSGGFGA R

> RXA00921 (1-1899, translated) 633 residues
VEGGTWSAQK TKEDLQFIAE VAPTHIETVT PFDDFISSD IDALPRRFEY RPLAGRSLIM
QSVVPAGKDAT GRPGNVFTHA VFDGDLSEPL ESVPISLYR SPDLLTPFRA AAVNAEALPL
DAGEPRIGPI TDLSLWMMI DSMFQDRROQ FYQLQDALQA GDKATVLLVN SNEAAAYLQ
ALSSSTLTFPE ARRLHFSTF ERAATLPAPD KSMEARSLFV VPGIDRELLA EHSQVVIIDP
EIPQSQPFPG QGSWSRMTEG LFSDFGDADE LVAGLIRANE NLDNSQKELA QFGDGLARFI
RNGRFSGTHP LRVLADQHMF GKVPDPKPAK VEVVAPAPNP NAIWARASEV VHNPRASES
QDWPRLRRPL DSRRIINMS EQAINSIEKL HDSPAQDLVA YLDLTKTEL ATSNASDPF
FRSSFSDFPA MDNWRHIKFT EDAHPRLEL LVDAERDARN RAPAIVLDH IVPNFSRDRS
LPDIEDWTRS DEAQQIFAGI IAGASVQTGR SHFMWDLRA YFGVALIGDE DTYRAFTLT
VDSVLSFVQL TQEGRTEDI RRFEKYGEQI AREDLPSILT NARAVQQYLG YIDQDIINKK
VSRSRDVNQI FTEMARAIR AISRNNIGKD MRS

> RXA00926 (1-363, translated) 121 residues
MDIVPLIILL AIFIVPTFLM SRRQARMTE IQKLQDSVVP GDRVITTAGQ HATVISTTAE
TVDLAIAPGM ISTFEKLAIV RVLSKANEPQ MLDEPTLFDQ PEDDQPNDFG DGRDTGHPEN
R

> RXA00930 (1-753, translated) 251 residues
MSGHSKWATT KHKKAANDAK RGKEFAKLIK NIEVAARTGG GDPSANPTLD DMKIKKAKAS
VPNDNIERAR KRSGGEEAGG ADWMNIMYEG YGPNVAMLI ECLTDNRNRA ATEVRTAMTK
NGGNLGESEGS VSYMFTRTGV VTVQKGDLE DDVLMVLEA GAEVNDNGD LFEVTCAPTD
IQAVRDALVE AGIEVEDSES DFRASVQVPL DAGARKIFK LVDALESDSD VQNVYNTIDL
SDEVLTELEN D

> RXA00932 (1-474, translated) 158 residues
MTPQKLHRFA ALLEMGWTWL LIIGMILKYB GVTDAVTPIA GGIHFGFLC FAATITVWI
NKNWTFPQGI AGLIVSVIP AALPFALWAD KGLVAGGWR FSDPSEKPHF FFDKILAQLV
RHPIRSILIL LVIIAVVFSI LLAMGPPYDP DAIAANTVD

> RXA00933 (1-462, translated) 154 residues
MTLVVLLIIV VVTATVLWAY FTAQRLNRLH IRTDSARQAL QAALDRRAAL VGALLPDAAE
ASKRAEAIPL EYSRFSQAR AEREISELIL KQKGTLPDSI VDAATRVELA HRFYNEAVSD
TRDLRTRLMV RSFRLGGTAP LPEYFELDDT DLT

> RXA00940 (1-396, translated) 132 residues
VILVLEAES MRGYQIITTI SEQTEGNWTP SPGTIYPTLS MLEDEGLISI SHEMGRKMAR
LTEEGAQEVK KMKDAWGSI EAYRNPESRE VRVFNIRSEF HKVREAAKAA PDDKAEQIIE
ILRRADDIK RL

> RXA00943 (1-507, translated) 169 residues
KPGVKWRATN ATKRGKKQLQ QALSTKSETE KFGKASDWF NDTSDKVTEY AYTAQDFVGE
NKDDWIKSAT ETAHKVADTV SDYAHKATSY LEENSGDWLE AAQANAKTAR KSAVKAAGKA
HEKANFALQV AEETSGRANK KATKSYDKLQ KQADKAIDRA QKKLKGIEL

> RXA00946 (1-774, translated) 258 residues
MTHTLQATNP LDQTAHAWH FSRNKEAISR TGAISLSATE WISATTLKDA HTFPSLPGRW
YKRGGGVVGA HLPAPAFATTG TVQLRPGELL IAEDFTLTVI ERLGQALQV FDARNPKRFE

FHSIAAFPPS EEWRIEARFF PEPDVTNTAA ADGVIVATPT AGWVHFLKGR LDYRLRVTVQ
 KNNLRALFSD NSSTLGVQYH RFVDIPRPA EGNTIIDFNR AYLPPKALNR KFLCPSPSLN
 NHLNLTV EAG EKVVVAGG

> RXA00949 (1-648, translated) 216 residues
 MKVFIIGAAG GIGNRLSSLL HARGDAVSGM HRNLEQASKI TDTGATAVLG DLIHNSTEEL
 AELFRGHDAI VFSAGAHGTG QENTTLIDGA GLRKAADAAS AANVSRFILV SAFPESSRGE
 NNTENFEHYM KVKSADVYL SHTDLWDVIV RPYGLVQDEAG DGLVPTAGLAI NYGNVARDNV
 AAFIDEALHQ PQLSKIIVEL TDGSTPVAEA VERLIK

> RXA00959 (1-327, translated) 109 residues
 MTVIGIILGS LFGVLAVLLI VVGALGWAAK LPGNPVVGIR VPEVRKSQEL WDMAHRVAGP
 LNVLSGVSVF IASLVAFVAS GWMNLVVVALG VEAIAFIGM GAGMAHTG

> RXA00963 (1-438, translated) 146 residues
 MRLATIRITNG TTIAARVESE NTATTIEGFA NVGELLQESN WRELAENAG EAVTFENKEL
 DAVVPAPKKI VCVGLNYANH IKEMGRDLPD TPTLFVKFPD ALIGPFDDVV VPWEWANKALD
 WEGEMAVIIG KRARRVRQAD AAEYIA

> RXA00969 (1-147, translated) 49 residues
 IRQERDDDA RLIVVTHSAL ESDLSTVEL LKAKPVVKAI NSVIRLERD

> RXA00971 (1-273, translated) 91 residues
 NHAEEELDE ALSPLINLR EMGFDPTEE EANSALHSC PFVVNDKRPS AFVCAIHAGF
 IQESLGENNR IQLELKLPA PGTCVKVHVS E

> RXA00973 (1-603, translated) 201 residues
 MNHSDDDRMQ KWFQIRRELK KEIVKQLQKD LPAVASDIGS MVYSSDQVPL GNATLTAYGD
 IGNRVASAAT SARNVVEELL DAIENARFAI WVPNYDNSY LSGEEGADEF QTYLIKDASR
 FLESSGNTTP ENPQYSDSKL TFASELLPFY TAFNNSTYPL LHACVQGEPT EVDLYFYELE
 QAELEKEKETA QLSSGSSFGS S

> RXA00978 (1-615, translated) 205 residues
 MSRSPLTKGL NQLEHLELDK SLTAWSAED DPLYLAGENL NGSYLIVAGR VVRSDRTIDG
 KELTVDIATP GDVIGAIOTE PQPAVDSAWA IETTCALFLP ATALATVIEQ HPSFALAMIR
 MQQQRLATAR DHEINLITTT VEQRVAIAVR TLGRKIGQRR PDGILLIQVR IRREDVAGLA
 GTTVESTSRV LARLRKEGVI DSGRE

> RXA00986 (1-342, translated) 114 residues
 MTLKDKYDTE VAVSNNQDKH QFEVSYPEDA VTAGFAAYLD KGDSRIFYHT VVGDEFGGKG
 LASILVSEAL KATKEAGLTV VPVCPFVKGF VEKNAFEGYR KPNHEDMELV KSQM

> RXA00987 (1-465, translated) 155 residues
 MPKSLTFEDS INIAAPINQV YALVSDITRT GEWSVPCEKC WWDDEGPPV GAHFTGRNVT
 PERTWETRSE VIVAEPNRCF GWSVTDGNVK WIYSMEPLEE GTVLTESWEF TPKGQRFHFD
 KFGDKSIEEI EKRRLLAATG IPEPLVAIQR ILEVE

> RXA00988 (1-423, translated) 141 residues
 MSKREESIEY GPLGKGHDPL KDPMKGIRGV MAGTLVMEAI TLGLVLTVIL RVDDGIYWT
 FNWVYSAVA IAHFVAALFQ RFSWSIPMNI VLQVLALAGF FVHPAMGFAA IIFITAWAYL
 FYLRNLLDR MKRGLLTQHS S

> RXA01005 (1-846, translated) 282 residues
 MELARAAHAR ADSFTKDHKL RROAHIKHPV FDFLFEYYPV RVAHLKTHWP GIGVFLEGT
 PHATMRDFLL VDASLHHAAG VQLDLASYMQ RRGSSVRYIH ELLSATRDNH AQDFCFLHE
 WAMVYKSNLD RHDLPLRLTP SETDRVVESH NIKTFHEDAY RFTTTPAIPL NLTVLTREDQ
 PRNDQCCGDLH ATMDLYKWSA KLGLPLVPGDL FLDAFELARD TRILDEASP YDVRGYGFGY
 VPIETAEGKA EYVSRQRELS ERAKPIRDRL VSITKQALQA SI

> RXA01007 (1-1707, translated) 569 residues
 VFKKHRRHGLG SPETKPRISIT RRFPTAAAT LAGLAVLSGC TAQPSQAEDN TLTYLEPQFF

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RTLYPPSAGF YPNGSVVNNI ADRLLYQDPE TLELKPWIAT ELPEVNE DAT EFTFNIRTDV
TYSDDTPLTA ENVVKNFDLY GLGDDRRLLT ISEQITNYDH GEVVDVETVR HFSEFAPGPF
AQATSSSFNAG LYADSTLEFA NEDFAPGNAQ NVIGSGPFVI TDDETLTNLT LAREDEYDWA
PPSRHGHQRA KLDVAVNYVLA GEESVRIGAI VAGQGDIARO IEAPVVAHLK DAGIPIISAA
TNGVNNNSNF RFKNELLSDI RVROALIHAI DREKIMRVLF SDSYPLATSV LAQNALGYKE
QVDAYVYDLD KATALLEDEAG WTLDSDGMRR KDGELELTF NEALPQPSR EVVTVMQEQL
GDLGKVMNLN PGDQAAQDAD SKDLNKIQVR HTMVGRADYD VLKSGPLYSTN RNELNMTVE
GETADIGDPH LEELLMATAS SPREEDRAAA SAAQDYITE QAYVLPFLFE PVVYGVQPYV
KGFSPEVIGR PSFYETYIDH SSDSHSEED

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> RXA01008 (1-1941, translated) 647 residues
VSTTDKQVAI VGVGPRGISI LERIAAALNT VSRPKQGLTI HLIEDAQMGA GNVWRTDQTR
TLCMNTLAGA VTFLTFPGST VSAPVVEGLP QFDWIRLLRG DEDLSGITPK AIELRTYFP
AASVAEDFKE ELAATVIQSN PSRALYGAYL RWAFDVALQL LPQWVKVEQH HAREGIREED
GDRDVITLDN SEMISADSTV LAVGWQTPAP NAEELSIAAA LEENPOLVWV KPGNPVEQDA
SLIPAGEQVL VRGLGMGFFD IMALTTIDRG GIFHEDPSTR SGLRYEASGE EPHFVISSGR
GYPYLPKSDY KSLPBGAKLA RLKAVIAAAN AQNRGVASIN YDAEVPWAVA DAYEAYEYET
LDRVSPESIR TGLDKIVEII DEVDVDKLPK ALAAHTDDVF DLHAWFEPLA GINESVEALT
ARIADGMARD IRHAFTAWDS PLKSALWSIS AARKPSSILG AEGRLTFESR RNRFPAVMAI
GQMVGSGPPL FRTRELLALV DAGLAHFAGA RPRLSVSDQG WQISSPTTGD TPIRSKVLVD
AMMHNPDVNR NADPLALSLE DADRVRFPND YSVDGTAAPT GSPEVDPATR LLVHPNGNLD
PRVHLIGIPT YQQLADTTIS PMPGTNPLML QETDKTAVHV LKQLGLI

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> RXA01011 (1-1233, translated) 411 residues
MSDLDMLVG EDLPQDRNR PQARDNAQKS FEALLEPVNP GTFSFGERYA VATYVAGLHQ
FAPAVDLYQD LLLDDAPTTL ANAVSDAIDE GLSAGPYGT Y REPGLSESE FGSVNRNDA
KLGERLAAAF DYALLLVFHP RDSRPEVLGR LSGAGWSADD TVTLAQLVSV LAFQLRVAYG
LRTLKGEDIQ VKAPRLSIPE AKWELSNNGF EISTYEELNR PEAFVNHSLG WKPWPVPAK
ADLTREEQLDS LQPERADMP YFRLLARDDA ALKARTLTDL DIFENTDGLG LKPAERELTG
TVTSRYNGCV YCASVHAGRA QEESGRADVV NALLASIDS LGSDQNVNVR DAARALSSTP
AAFNGQCITK LRGVGFSDLQ IVDLINSVAF FNWANRLMS LGFEVPPKRF L

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> RXA01016 (1-648, translated) 216 residues
LLPYAIVGLV ILLPSSWLP WAVAVLGEVS LVPVAVFGGG FLLIPSMFLI GSALVRYGVV
DRAENAPRAM GVFFAVSAAI AIPTLIIQAR DITSSGFSIV STVAGLALGG VYISLVLLAL
HTPIRALAA VFAPLGRMAL TNYIGATILM LIGGLIVDLR HSTSWTATVL LAAGILIIQE
LLSAIWLHRH TQGPLGYLWR WWTWGSRSFP LTRSAS

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> RXA01017 (1-609, translated) 203 residues
MAQKYTFWFD TTCPCWVTS RWIKEVEQVR DIEIQWVPMs LAVLNEGRDL PEDYKERMKA
AWCAPRVFAA VATDHADKLG DLYTAMGTRI HNDGRGPIEG SFNDVIAEAL EEVGDLDAALG
EVADTTWEDD ALRAFHQTAM DEVGNDVGTP VVKLGDTAFF GPVLTRIPIR EEAGEIFDAS
FKLASYPHFF EKRKSRTENP QFD

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> RXA01021 (1-522, translated) 174 residues
MSSSESSSRG GQGPAPSVQP ERRADDSTGAP AAASKEASQQ MDAAGVLEWA RTAVEQLSER
RAEINALNVF PVPDADTGSN MTYTMTAALD EALKLGLGD VARITEALV GSARGVARGNS
GVVLSQVLRA IAQAAADGVI DCHTIIQEALS IARSLVORAI TDPVEGTVVT VLRS

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> RXA01023 (1-951, translated) 317 residues
PANGGINKTP MIIALVLVSI VLVAVLFGAR VLLGPAQQQ IAMSGLPAPD AESAECAALL
EDLPGEAFGH TRAEIMDPVP PGAAAWSTSD LERVTLRCGV DMPFQYALA NTVDVDGTTW
LPVSDMTFGS SLETWYSVNR FVVAITADD ISTDSADNPV DPFFSSAVDKL EKRDDGQFFDA
PLTGLSSAGT TCTSLFDALP RQLEVGDDGD TTYERIEEDR MQAAGYSDDA VAMDTPGLEP
IVIRCGVEPS ENYAAAMQLQ QDDIPWFED TILASGTTSS TWYALGREID IAVSLPQAAS
SILITISGFI EDTVPAE

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> RXA01028 (1-624, translated) 208 residues
FYQNTLASSR GSNTFLEFSVP YIPATEGEET HPATDTSTIA TPTLSFDAYG NKAEMVPTQS
TVDKRVPSSL QYRTTFTHVR QDTQAVFDV IGANPVLIAA AKAASISPA ADSRRKKGLA
STNADEVAKH VLEIAGADVE SLRHEKDLKV TKHTGQDPAL PVVFNQTIW HNPNDVINA

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LLGAIDQDAY IDMAISSYNK SWHNIIPA

> RXA01029 (1-489, translated) 163 residues
MLQTTISFFKL NLLTTLKRKG ELVIMITRHD VPYIIAPPVY AIFASLMTTP PWFYRTTYTI
DGFDFKISWV YTITITYISLM ILIIGFYQAN MRKACPYEED PLVDIWHKVV STALFILPIV
LSIAVYSLIIT QRGFDWYVMV FILPVGLMIA YGFFKPCDDC KHR

> RXA01031 (1-666, translated) 222 residues
MKLLQYAGGA VYVDPEDSAQ SQDLDASTAR DVIDATNTAM TTITSRPTMI VHLHKVRKVI
EILCNPALGG EPVNIDQDET GKQVYTPTPT LVAYRFISDK EILLHLAQA GVQGVVEFDG
SPDMLSRWNA GRIPVLLLQP ASAGHGLNFG HGGHRLVWYN LPDNNHEHYMQ ANARLHRIGQ
KNPVTIIRII TADTYDANMP AILAGKANRQ QRLIDAVRRD PV

> RXA01032 (1-375, translated) 125 residues
MSDHAPQPTP IPKGFQWQID HQLDRLGTQR PETFAALRDI LLDPAYTAIV HDNRNRYGVVT
FDTNSAFFSG SGGDNGLADV LINCWWRMTD YRAEYVVMT HKYTKESFTY IEGDVKRGLD
IPENN

> RXA01033 (1-336, translated) 112 residues
MTQIAMYLGA PMTGPIPEYNY PTFHAAANKF RAAGYTVLSP AEDEYESQLT APLPENAEHK
YDHYLRGLIE KLLKADAVHM LQGWSQSSAGA TLEHIDIAQKL RLAIITYEEFP AS

> RXA01034 (1-354, translated) 118 residues
MDMAIIQSVE YTSDVSHERI TNVSVGVVY EGKQYVVLDN GDDIDTELDM ITLKEVIKIG
REESARQIRR GSVDAELHRK ARLWAINDNM AVGQRGIVPQ EIIDAYKEYC EKEGIPFE

> RXA01035 (1-606, translated) 202 residues
VLIRIAEHGG RLHVHSPYSK AFAARARKLN GLWSPETKTW HFSPDKQEPV RRALKDVGYY
DEFTTPELCT VQLTVPPEAV LNKHTLTIAQ VTLLSRLRRN YSVWLDGNVR IISGNFPPEAA
GSPQYPLIMG VKAQPVVIHV QEFPPVDAVST IPPRFNPIVI TAPPSIDIAA LRAEREQLTR
RISEIDKKIA RAVHPTIQTE AA

> RXA01036 (1-453, translated) 151 residues
MHTVGYKLDL DLRLKTNTDV LDLINALFGT TVTSADDEAA DFIDSDPQFA VLVELAYHDC
ARRAAMGLSR VQQLIYNDAK KSTYYRSVAA RHRKHIREHL EQTQRDGIHF DNPLSRAVIN
DLSMSMNRAR LNRIASWKSA GVQRYLNPTI S

> RXA01037 (1-528, translated) 176 residues
MTTSSPLKHS NSLNGAQTTF VRNCVADGPT EVKATIDARG GIEQLRDNEI ASLPDKLWFN
SATASNDSEF TDPENIRGLL YNMALNKASA HRYELAAWY AIVSPQPSQ SAKHRIASWH
LTQLHALVTL SRTLGVIIIP DEIDALAQSM ENARQVGTEN WSTVTMRTYV TNRKAS

> RXA01038 (1-747, translated) 249 residues
MTRDIFHEAA KLIAGLGRWD AFPALQRTDP APHAVPIRA FDLKAGAVIT DENRSNAYIY
DTLVITQPYK HELPHQNTHP FEWALEQIAT LDPAFSIKLD RSVTVPEIGL YARTLHDLNT
RHQDFLAQRN AMLLVVARRG VDPKNIADVL GLTTNQIHRH LSATPADSPT DLGVNPATMM
GDVVRFIKKR RTTMQLRGTA VRALLYHGLT PAVISRLSGM SRAGVINAAC AFPTTINHVK
KKRKQHFFV

> RXA01039 (1-576, translated) 192 residues
MAIKGAMPKN RVPGVAAGAF IAAAVIAGGS GVTELAQSGV DVNTVAVVEP QDEVKNQVVT
ETEIVTKVHD PSSSDASDAD SNTGTAEGAD SDHKEPREHD SAQEPTAPTD FTTLITGNGD
TPVSALDAVA GPARGTVHV IENGETLSSI SQDSGVFPVGL IIDRNKLVDP DLIYAGTPLA
IPTEGELAAA IQ

> RXA01040 (1-903, translated) 301 residues
MTYPTVPQPV QPAPVAEKIK ASSLKEGTQV FIKGRVNYSR IASFITGTER ENNRNDRLHP
IEFDYTSLTL SHPEIYGNP QOKTNEELFL EQRIYVGKKR PEEGPKFSID NKSNNLPQVW
VPSTNADGTY EQLEGELEGEL DAGLNVIIIL EFYKPRTOVN RGSRLNAVFL QEPRIYYTPG
YNADKLAAAG IVLNAPPKDT IQLVNEVAA QGDQSTTDAS GLPLFGQGVY APQOPYQAQF
QYQQATPAAA PQQYQAPQVQ YQQAAPQAQF APAPVAQFQQ ASASGTCAS TAASVSTTSC

R

> RXA01041 (1-153, translated) 51 residues
VPOQAPAVQAA PAVAQAPVAP VVDMTEPASP WDLPAAPSPQ AQPAQGITYP A

> RXA01042 (1-1278, translated) 426 residues
MVNPFHTLND SPFDPVQAF AFYHNPLNH LGRRRAWITS DINKRPINVO QMLTTATYGS
PVIHGARIED AATSLTLTDE LRTQIPTAAN NAFYLDVADQ GCLILDIIEKT CPPEVAATLL
TLPSTAFYTE VMSMGGRGYHL VMPIENFAA FPAVHNKPSI KHPKRWFEIL TSQWITFTRO
PIPEHVLHHS ESANTSAPVW LNDQPLTWEN VFADLAKTVA PNLKTGAGLT ITPNALMPPD
LSDAERIRSD EVIDSTCRLF AEHYSKTLAD FYDDASRFEF SQIGVIINLL LPTMRHHPHT
ISLDKPIIND HIIRLLFAVA TRVITHRSKH DEERSGVPLY MYQVISCGLDM REHPDNGDYR
VVPSSRHNRDQ HSNNSAHV V HQQPQPQPSA ADSPHHYRAL PQENTVSEHS FKIYNPPATP
PLGGGN

> RXA01043 (1-573, translated) 191 residues
MLKFRIISTV TTGSQPTPRK SWSHPDPTLL VTMVTAPSLC SAINVWNATE RIPAQKILNV
EEVHVLGECSS DAIISTSLTK KDNPHALVPD DFDQIGDVFG YAQDNVAVED VIVAALGGAG
YGLLPGLVMH HIDEHTVALV FDTDSPTGTG ILGERCVYSD IIMHTDDKSA RGVGAVIAIA
RAILIKVEQI M

> RXA01044 (1-1257, translated) 419 residues
MSLYLDDTLS RIVELDLKDT RIVPFLAGEP GIGKTSFIYG IGERAGYKVF SISVNTLADK
GDLTGARTLQ DPADGKWKQM FFPHATFVEA NDYALANPNE TVVILLDEIN RTDSVTSAS
MTISTERRVG TTDLAPNVRL AVTGNLTGNV THLDSASLTR FSLYEVKPSA ETFMNIMGGR
LNKYRTVTLT KPEYIFMKP TTATALITG DDDDDHTTNA KOMMDFNAVL GSDQDMVQFT
APRTIEGLSV WLNNAADDLFL RLLLQEKVDG LARSMILLQA TLESHTGDTA FTAEVLSEMT
NDLLSSASQA PSGPIKPFVY DRLAAAPSNT VLEQEVHTLS LNDRADVLLF ALHDTVNNAA
PSIIAHLASE GVLDELPKDR ISKIVSLGPV PTANYHALTR QDTTLTRNLG PAVLGFLES

> RXA01045 (1-1824, translated) 608 residues
MVTFSVANHA PHTFSPFDIE PPLTGNATTD EHGHEHTSVL EKLASNHLFN PINPQHPVTI
TATENGSTVD LDAAALAQHL ALAITPDSML ANHQGYNRDM MGLLSQLTNH VGFDRRFFVD
QLFISQVLKA NRLPAPANNV IYTPNDVIP SAKDILSTTA KMNNPLTVTA SAPITVDDIH
TAYEVFFASL ASVFFPYTYG AVFLNNAEFV EFVDYLINEA TTHLSASLIS NNTFNRFQSM
RNISIDNLTA EFLLRKNEAE TDDYSFPRV LVSILLHSWK LNHDARANN DAPTALAPP
SVAQWIMPET IVFINAEAAH HASSQDIEKK WKEINAALTG SIRIMSPNAI SKLSAQAHLG
MQAQMOMARA RKDHHNMOKR SSQENDFSKA LPSPQITVLS VAEVLRKLTH VRQSHNFPKY
QKKSILTRAS RHPDNPVPG TIKSKLFYPD LHVVDVTSGS ISEESYRNSV VLMLQLATKL
DINLYFSTFS HVLSEEVLLP TKGKTPQOLA ALISAIPKWS GGTDYHQIWD YIQINPQRYE
RMNLVLTDFG FMPNRAGLND HPSSIFYVPI LPDYGSSWSMV RRDMSHFANE MVDFDQYTHS
RLLGVHGK

> RXA01046 (1-1779, translated) 593 residues
MIPFPGQPOQ QSAPNDETRF IDLNERKKDD EPALFRDDVI DQTLAILISK NKPNAALLVGP
AGTGKSRIAE DIARRLANDD VSIPDQLVGH RILDVSIALL VAGAGVGVGL KKRILDLIKY
ATDPSNKVII FDEIDHQIAG QSSSHSGSQA KVAQILKPYL ARGDLRVIGA TTPQEARDFD
HDPALKKRRFS RVNVDEFDRD QTLTILHAAR DGYIKHFNNA VTVSDVDVLY VYTYSQQNP
GNTAQPDAAAL TLFDKALASL TMEKQRLINN HVIAPSLKFP VSEVRHINHT RKLAFSGQVP
ASINTDDARD KLETIFGQDH IIEPVLTAIK REQLGIFPRT KPLSWFVACS SGVKGTEMAR
ILSRINGPEYI PIINGPEYI SPESITGLIG SSDGYIGNSN KRAKPLDPLI SNRQPTIVLD
EFEKSHPHFG QLFMAALDTG TMAMANGTTL NFSQIIIIAT TNAARDKIGR DSGFGSDNS
GVLGSAQAAT DFRAGERLKS LMSKDFLLNC STVSRSISLPS TALMQAPTVR FWITISVAV
TPCCCLATPHY AAQIPADIDS DTLQDLVETI FSIIDGARPA ARTIEDHIAS LLM

> RXA01047 (1-474, translated) 158 residues
MDDTANSTNS GTLPLTLADQ AAFITGFCEA AIFTATVTID NEPIFLDEAF FLGQETYTDI
LMNQCLRTNEA IVKDCLDFEL DNYTMMNKLI VDGLCPDWEH HGHDFLLLTRD HHGAGFWDRG
YDEYGAQLTD NAEKYSENCL NFWIEPDSDP LIINFEYH

> RXA01058 (1-321, translated) 107 residues

MRKLRTASVA LLTAGALALT ATPAMAQSTT GSSASSQVGD ALGASDYERD IWGSSKDFDD
VTFPGSVAWG YTLAATAVAI SGLVYANLPA IEQAAQAGI KLEIPRY

> RXA01062 (1-496, translated) 162 residues
MNEQEREALE DAALEEAALA DELAALAEAE GVQGSVEPYD YAADLDEDE FDEDPFAQDE
PRDAGPLGEL SSDNHVSEAV AEDTGTSTEE SAQEGSHEES VDNPRDFTGT ATAVRSFRPR
LPVFNALRGL PPIRTQPAVN TDIYDGGCN TAGATAADVG AG

> RXA01063 (1-330, translated) 110 residues
MADEKKYHVR ATLRFSDSTH QRAIYWADRK GISLSAYAE AIREKIDRDN GVHVIPNSLL
DNRMNQIIDQ LSSFGRELAN NTTVVTSGFN TIIGMTRGDS YLSDDLDDLGL

> RXA01066 (1-726, translated) 242 residues
MRRDSFRDRA LUVKTYDFGE ADRIIVLLTR DHGIVRGVAK GVRRSKSRFG SRLQLFVELD
VQLYFGRKLS TISGADTVGY YASGIIEDFT RYSCASAILE IATHIAGLEN DPHLFEETTR
ALKNIQDSPE PILNLDEFML RAMNHAGWAP SLFDCAACGR PGPHNAFHPG VGGAVCLICR
PPGSAEVPPE ALHMMWLVA NQAARIPREH FEQQTTHQL TTAHLQWHIE RKLPTLAVLD
QA

> RXA01068 (1-1071, translated) 357 residues
MPTNQPTPAQ IKRRRGYLAN EQAEAAAYRD LAKRREGEER DILLALADAE HRHAAYWVEK
LGPDAENPPK ADVKTRLLGF LARRFGSVFT LALMQSAETR SPYDDDAES RQISADERIH
AEVVRGLASR GREERMSGNFR AAVFGINDGL VSNVALVMGV MATGVPAQIV LITGISGLLS
GALSMAAGEY ISVRSQTELL DASLPDPKAR EALHALDVES NELELVYRAR GMSDEARAK
ASQVFQRISD QKRISDNVLG STEIQSAGSA RSAATFSFSL FAIGAFPLIV PYVFGMEGLA
GAVVSLVLVG LSLMATGATT GLLSGKPPGI RAVRQLSIGY GAALVTYVLG LLFGMIL

> RXA01069 (1-603, translated) 201 residues
VNDLNLPLKL PFNNTWVLAT VATTVVLAGI GLVYVYPSLP DMPFVHWNGS GEADNWTFSK
VGSFSLILILI GPGIILLTSL GMQALLTMQS GVITQRGGAK SANEAHQRWE TYKATSMRMH
WYMFVLNALI LVMIILNEFR NPLPGGFIIG LIGIIAATIV LVLIGKTTI SLAKKYPMPD
QDGKTWGFY NDPDDNRILV D

> RXA01071 (1-387, translated) 129 residues
NILYALLALS VIVATIGIIN TLALNVIERR QEIGMLRAVG VKRGQVTRMI TLESVQIAIY
GAVIGIAIGL GLGWAFVTVM SGEGLDAAVS IPWQVGLML VGSADVGVIA ALWPAVKASR
TPPLDAITD

> RXA01074 (1-705, translated) 235 residues
LAEAAIGRLW AEASSAVAQV VSADAEQITT VGVETQLPTP DAAFKAGEEL ARIHLAGAPA
FGCPCPAGWAG LNYIGTGGQA CLSTPTWGVF YSQQRVLPPA RRARRRNHLT EHALWVVEAA
CDLISLEPDD VPPARIHGDL WFGNLLFGTD GPVFIDPAAH GGHPEITDLAM LDVFGAPYLD
EIREGYLSIN PLPDGWRERT PMHQLHPLAV HAASHGPSYG VELLHAAKAT KLKLD

> RXA01075 (1-411, translated) 137 residues
MDNPNVILNE QEALERLQSV SLGRVVVRRS DEMDIFPVNF IVDKGAIYIR TAEGNKLFESM
NLNHDVLFEA DEVKDGKAW S VVRATAEIV RKLDEIATAD TELEKWPQFT LKSNFARIVP
NEITGREFTL GEEPERY

> RXA01076 (1-1020, translated) 340 residues
MTPAHIFSEG PINSVLSQD EDGNFTTSYQ DTFSDFSFLG EGDVLIEVGV SSLNYKDAMA
LKGDKGVVTR VPLIPGIDVY GTVIESADPR FGRGDEVVLN GAGLGENRHH GFTQRLKVPS
EPLLIHPEFN SAQQVQALGT AGFTAALSVN ALVDQGIKPE DGEILVTGST GGVSSTIALHL
LNKLGTYTTVA VTGRRERAAE YLTSLGASDI IDRAELSEK RPLQKGRWAG VYDVSVGSHTL
VNIAIQTWKG GIVTACGMAQ GPDLPGTVLP FILRGVHLVG INSDVAPREL RRRRAWALLSE
HLDTAVIDDM TTVIDVDKVA QAGEDLMAGK LHGRTAVRVH

> RXA01078 (1-834, translated) 278 residues
MSNAVPHVNS FNFVPRAYRP EKPRTEGMEI IRAPYVSTFG TRHLQDVFDV AGQWVDGIGW
AGGSFSLVPT EQVRAFSDIA HENNAIVSSG GWIETVLRYG DDAVDHYLKE AKEVGPDVIE
ISTGFMILNT SGLQRLVEKV VKAGLKAKE LGLQIGSGGD SGEAEALAEK KKDIGDLVDR

GKKALDAGAS IIMIESEGIT ENVTEWDTGA AASIINGLGL ENVMFEAADG PVFEWYVKNY
GNECNLFVDH S QILQLEGLR QNIWGNKSTW GRVINPAP

> RXA01083 (1-276, translated) 92 residues
MFPRIPLAMC AVAAIPAVVL RFSELSASPV ATMLIFGTAV VAASEVLAWA AEAVRKDISG
ALAVALLALV AVLPEYASET VVEHTYQTS A AN

> RXA01085 (1-957, translated) 319 residues
VTDKARNRDV HNEQQLARGE IGE MRSFPMNV EVGAAILGVF VLVVMWLAWG GIGLLIQTMM
NTGSPNDKEL FDEGLVRFYY VAVEQQIGTS SAHTTCYQPL DEFGNNFGDC TRSVKPEPVW
YADYVASVFA EHGFDAPPEI DNSVGSWLLF GHVGIIIRVF VIAVAAGVYA MSRAAMMRQL
ETQNVASVDT DINQHTNDAR LAIPQEIIVRD LSLFPDVGAG SPVQPSSMIS HVMLSNKGLK
KVDVTQFAQE TIINDTGEI VSEKGEVLYD GAGQPITKSL PMIDNEFSHA IFDKSDVPNL
PELRRFFNPA KLEWNPSSGS

> RXA01088 (1-1182, translated) 394 residues
MGLWIDATAG VAGDMLLGLAL IDAGAELEKI QQVVEAVIPG DVLLRTEEVV RQQRGRIKLH
VDAQHEHHHH RHLSTIKELL VNADIPEQTK QDALGVFELI AIAEGKVHGI EPEKIHFEV
GAWDSIADIV GVCEAIRQLN PGLIAASPIA LGEGRIKAAH GDIPVPVPVAV AELVKGWPTQ
TGALMESTEP VGLATPTGV ALIRHFATQD GPFPGGIINE VGIGAGTKDT EGRPNIVRAI
LENTSRSNPD TRTLVQLEAN VDDQDPRLWP GVIEILFAAG AVDAWLTPII MKKGRPAHRV
ISAVDSSEVE AVKTAALFAAT TTFGIRSWEV EREGLDRRFE QVEVDGHTIN IKIGSRDDQV
SALQSEFEDI RSAVALGDIS EREVVARIPQ GTTE

> RXA01091 (1-471, translated) 157 residues
MVPNTVLIHD ETADLATQIQ RLEHIMACLRL DPVSGCPWDI EQTFASIAPH TIEEGYEVAD
ATAQEDWPEL RGEGLDILLQ TVFHAQMARE AGHFALVDVV KAISDKMVLRL HPHVFGAQS
AKSADQVKKI GKSSRRPSAR AKRRKAFWMA SRWDCLP

> RXA01092 (1-180, translated) 60 residues
VETAAFVAEQ LRSFGVDEIH TGIAKTGIIA LIHGREAGPV VGLRADMDAL PLTEITGVYY

> RXA01096 (1-699, translated) 233 residues
MKPRVLSALG IGAGALVVMI SSRMNWVTIE AFDDKSGSVT QSIVGATWST EIMALALALL
AAFAAALVLK RMGRRIIGGI SALIAGVGLS SPLALLTQDP DAERARTLLT SGVASQKANS
GTLLSDWAEI INTTTHPLAA VVAMIGCALA LVGGVVLAMR PAEDTAKSNQ YERKQARAOK
IHTDLAQDPD SGRVMWTHSM KTLTSPRRLR NPKKPQVKAR VWHPDFFRHV CSG

> RXA01102 (1-1245, translated) 415 residues
VAVLVAVAAA FGSWSLLLPV VPLAVLNNGG SSAVAGATTG IFMAATVITQ IFTPAALRKI
GYTPVMAFAA FMLGVPAIGY IFSVEPIPVV VVSALRGIGF GALTVAESAL VAEIVPVFRL
GKASGMLGVF IGLSQMLFLP AGLALGDQFG YNVVYVLGAV IALVAVMCL RIFQVKAAAK
QQPQVSQER SVSTWKLVLV PSLAVTSLSM TFGAVSSFLP AAVIELDPLG GAALAGIILS
ITGSSSMVFR YLSGVIADRR GVPGTMTIPA QIIGFLGVVL ITVTIFQGWS VWLLIIGAVM
FGGAFGVQVN EALLSMFRLR PRTRVSEASA IWNIAFDSGT GIGSFLGLIV AASLAYSGAF
GSGAVVILFG IVLTTADRII GRHRITEYNN TRARLRQVPV ARRVAQVGLRN RRKDR

> RXA01103 (1-225, translated) 75 residues
MNSSPIDMV TAQVNEPDA GDRWFIYGLF LIAGLFFGGA WSAYKSENKI LMVAAGLIAV
LAVAGGILWL LGEMT

> RXA01107 (1-1200, translated) 400 residues
MDFTSVNDRN VPAPTSIPF PVDLNRVTEA VDSLGYHLS SEDRIIPWQ DHRISMYFSH
ESGQMLTILG TRRLNLDMAF INDAARAVTE WNAERIGPTA LVHLGNDGEV ELKFRITICI
DEGLSTQQLR QFINLSLDTT AMAVTYILER FSELNFSDTG SPDDTNNADE LSDEQDQADL
VEKIRLYVP TPVEELIESL EDAEWEESDM ADEDAEDDYL DDDSEIEWET DDDYFEPEEV
DMDELLNGFL EDSDIPOEVT LERIRAQLHA IGVVKTSGED DFIIAWINEV FLGFFVDNPG
TFLVKGHWDP SMDPTRDFMK LFMMCNQWNE NSLTTKAFCH TDDKGLQVRV EFAVSVAEGL
NDDQLQHNIA LSIHHILQAI DSISTEATGS STVEWPEKNR

> RXA01108 (1-651, translated) 217 residues

MTYPGITSIDH NPYDGYTGDD GAGNKRNLNPN RKKINKSVGV YAGVFALTILA LYAIGGAAGW
LLRPPTYTAYV EDAETASIAV ETNTSPFAGY WFAIATGVLA AAIALFVFLR TPQHRGPVML
LWLGLVSIAG SVAFLVFGNV ASTMLHGSPY DYASAIASGF QVAPITIPGV AFGVAPFLSV
CMYWCACAVT PEEEDIQDDA QGGTSKASGS EMTGASG

> RXA01109 (1-642, translated) 214 residues
LSISLSKKVK AFAALMVTPPL LLTACGSDDS DTEAASSSAA TTTNSSSSSA ATSAEAAETT
SSESESEAT TINEEQQAQL DYVLSQELSEN PITFAEAPV ENGETASPED TAAIEALVRG
YTDNTLRS LAYTINNTCT RVLEASGADA TQLDLNTIPD IPLGGEGTGT VDSITDVVVN
GQEASAWVVA TAGGTDTSAT QRFNEGGQW KFCF

> RXA01119 (1-930, translated) 310 residues
LAGVITGFAL ILSVIGVGFL LAKLGVINDD KQRLVLNRIA FYAATPALLF NVVARSDPDA
LISPVIVVTF VATIVTAAV CVISAIFFKK DIATTATGAA ASAYVNSNNI GLPVSIVYLG
TGAYVAPILV MQMVIIFPMI LAALTSGDVK GSRGQKIWAA VKGSLSPIV LASIAGLIVC
LLEIQLPAAV MEPTIILGGA SIPLILMSFG ASLSTNVLA SKADRPVSLT ATAIVGMGP
AITWLIKAKF GLEGDYLYAA VILAALPAQ NVVNYAATVR KGEIVARDTV FLTTFLALLG
MLGIAALFGR

> RXA01121 (1-678, translated) 226 residues
MNPEFIHGAT EIETTNRGLR PHRLSKEIVE RYCDPQFSAM ERQPSGVRVW CRTTATSVTL
TTSYTRVVVL DSGRPGGKID VLIDGAPTSS TPTSGETTE VNFITGATER RLKDPQVLTV
DGLSEQKVV EFWLPHNEEI EVISLKANAA LNTVEDTRPV WINYSSISH GSVATAPTKI
WPAIVAGSKN YNLNRFGGG SAMLDPFMAR LIRDTPADLI TLEIGI

> RXA01122 (1-522, translated) 174 residues
MPFPALLPL IFWTGIALS SWAVSRALPL RADNSIEIDA PVEKVVDFIE ETRNVPEWNE
HLIVYQAPGE IEQGMKLMKM TRHPETNRLT LKFRPTIDVL RPHRELTWST KIVARWLLTV
TDTIELKPLE DGRTEVDQSM SPSGVLSPGV PFLASISRIK ENSNRQLKAL IEAE

> RXA01123 (1-447, translated) 149 residues
MRTLAAELNI KAPSLYKHVK TREDIAAHIA TKAFIQLGQS LHEHCEVED LLAEYRSMAR
ENPNYIRLLT DQSEIFRELLP EGLETWAGTF FYLVGTGHPD KQALWAFAH GMAILEIDAR
FAGPNNGSPA DQVWEIGARA FDTQVDFDQ

> RXA01127 (1-279, translated) 93 residues
GIGLAASGNI DATGTNPSMF EPVHGSAPDI AGQGIADPTA AILSAAMLLR HLGDEEDNAV
IETAIAADVA GRDNSQPST TEVGDRIVKA LQS

> RXA01128 (1-1014, translated) 338 residues
MSFTFIRTFV VLFGITLLVS CVPEPPDSYT KESTVLRYQV SDFNLNFVEL AVALGYLNNI
ELQVVGVSQG GVESIESLKK DDIDFAAVPF IGLVAGEIAT GAPIKAVAS YGISHDSSA
LVLKDSIEIH EVHDLIGKTV GINTLGLGGS AMVERHLFDA GLTEPEIVSV TQRALPGEYL
EQRLYQGGVD AIWVTDASAKH QALETGDFRI LAEDSDLVGE LNTGCMVVSQ KLIDEHPAVV
GELVDGVAQA IEFERSHSE EVREYVFNLY EAHGQSDRIS SFRYWEHSGI ATRGVGLSDR
EFSMWSHWID RQYDVPDINP ASIYTNQFNP YRKVNPSF

> RXA01129 (1-1866, translated) 622 residues
MYNLSMVELE EIRDFLAGFE PFAQLPAEEL DQLPGKMSLR YFRGEEIIP IGVPNHVMGV
IRSGAIDVLD QEGVLLDRRD AGRSFGYSTM GPERNSRYRM VAVEDSLVR LGRDDDFELA
KRNPDNLNRY SWSKRIKRAA ADQLRQESSV KVLRTKLGEF KIANFISCSF DTTIMDAIK
MHEFGVSLL VQIDGELKGI ITDHMYRSVR VAKHLDIQLF VSEVMVTDPDR CATSQGLAFE
AMLLMSLEIRI HHLPIVDGQ ISGIVTAADI MRLLRHDIPI LTADLSRKNT VEELANTFQS
AAEVASRFID RGASAEVSS LLTVAADSLA RRLVLAEKRF FGAPPVPYCF VVVSQGRKE
MGLASDQDNA LVLNDSYNDR EHGQYFAALS EFVCQGLDRA GQVLCPGDMM ASNFEWRKTA
DQWISTFHWS ITAPEPDALL HAQTFDFDRG IYGDTEMAKD VHQNANVMAR GARRMHAHLA
SLAARRDPPL GFFRGLVVER SGEYGATMDI KKGGTAGIVQ MARLYALATG SDAIGTRERL
IAASGHGQVS RKGAQDLDA FDFLAAMAFQ HQARLIKVGE KPNYHIDPKT LGKMDREHLR
DAFSIIKDMQ SALATKYPVR NI

> RXA01131 (1-867, translated) 289 residues

MPPATLFNVNL TSAGLDPHQS GDAIVVESAH FLTFTTWEDE LRAQATWVGE LSASDYVRSI
 VAINSADHAR ATPKMLDAP TGLTTVLKAD KGQLQAFVE ALPIGDGLSE AQLAGFVAAA
 FDGADILTRE FHALYPERSF QERGAMLNK LVDAISPSQT TPVRVANWFM DQGVEEVPDY
 AASGRISFEL GDTPTDVILD DPPELLKIQAV VVADRDVEAT EVLHLCNRRAN LDSDHSTIFM
 RSDGDDVDVF ATVAVPIRAG LNDFQLSQL HDGVGVGVGQ VRAVINQLH

> RXA01134 (1-459, translated) 153 residues
 SATQDTGVWK GIFALLMGRG ARDWRGQQOF DRWTFDELGC NFHQIFPTKW CKERGIDPVL
 TESVLNRTPM GRRTEVVIGD TPRSRYLSRV QSKSLMGDEE FDQMLDTHLL SAEDLHSSNT
 THFFASRRTN FIDMVEDAIG KAVIRDVNES DLT

> RXA01137 (1-360, translated) 120 residues
 VRPTFVILRI SEYFGVAEAA INAATGRLLS LSEVFIDNAA EIQDNLSSLV ALQKDLAERV
 NVEGVNEVPT VDLLELRIGS AQLAVAATAI EVRVAGGAGY VKSSSTSRFF RVEMGACTGP

> RXA01140 (1-786, translated) 262 residues
 MALDTRGEEM RFRPRALSGA PDTGKDPGLL LDGQOQLRT LYHCFSGDGY VNTVDFRSKK
 VTRKFYIDVA KAVESPVMDS EAFISVDETG KIISHFGPVI DGGITDLETA LAHGCLPVSF
 LDDNDGDTFL FDLADMAGEG AREHAKRFQS QIVKTLVSVD IPMIRLDRET AKGGIGSIFA
 QANSSGLQMD VFDLLTAVFA ADESVEFEFS LRDDWVRVER NLRQHSALDG IGSTEFLTAV
 ALLVSARKHG ASGVREDILN LT

> RXA01148 (1-600, translated) 200 residues
 MTSPPVENVKK KFRPLALSPS RAGDYQQOCL LYRFRADRL PEPKTVAQVK GTLVHAVLEY
 MHKLPREERE YPAMVKQLKP TWAQMCEEDA ELKELVPEDE LYDFLVDSRT LLRGYFEMEN
 PQGFDATECE MYVOTVLPNG VPVRGFIDRV DTAPPAKSEL STTRLARNQS RSGASKRSSR
 CCSMHWSGTA CSMKSQLSFV

> RXA01153 (1-543, translated) 181 residues
 PFLSPIVTST HAVVAYSTAR GFGEHRVRWD YAQESPLRDT RGFDFLRRYHQ APVVDPHAIG
 VANVFVNGA RFYVDHAHPE YSSPEVTNAW DAMVYDAAGD HILMQAVSDV ASFTSQNRVS
 LDGHDPCPAL KIYKNNDVGK GASYGHENY LYSRETDPDV LAQALIPPFV CRQVIIGAGR
 V

> RXA01154 (1-603, translated) 201 residues
 EGIINTRDEP HTDADHWGRL HVIIGDANMS QTANFLKFGM TSLVLDAIEA GVDFSELKLL
 NAVSEVAKVS HDLSLTHQLR LADGSELTAI DILRRYLDKV QPFAETPVEQ RVTALWGEVL
 GLENDLLST SHLLDWTAKL ALIKSFEARG LSINDPKMYL IDLQYSDIDP QKSLYHALVS
 KGRMKTLCSA QDIADAAATS P

> RXA01155 (1-1365, translated) 455 residues
 VESALTRRIM GIETEYGLTF VDGDSKKLRP DEIARMFRFP IVEKYSSSNI FIPNGSRLYL
 DVGSHPEYAT AECNLTQLI NFEKAGDVIA LAKEDIAGQV YLFKNNDVDS
 GMSYGCHEHY LVGRSMPLKA LGKRMLPFLL TRQLICAGAR IHHPNPLDKG ESFPLGYCIS
 QRSDHVWEGV SSATTRSRPI INTRDEPHAD SHSYRRLHVI VGDANMAEPS IALKVGSSTLL
 VLEMIEADFG LPSLELANDI ASIREISRDA TGSSTLLSLKD GTMTALQIQ QVVFHASKW
 LEQRPEPEFS GTSNTEMARV LDLWGRMLKA IESGDFSEVD TEIDWIKKK LIDRFIQGN
 LGLDDPKLAQ VDLTYHDIRP GRGLFSVLQS RGMKRWTTD EAILAAVDTA PDTTRAHLRG
 RILKAADTLG FVPVTVDMMRH KVNRPPEPQSV ELGDP

> RXA01156 (1-201, translated) 67 residues
 VSVVNAKQTQ IMGGGGRDED NAEDSAQASG QVQNTIEGVD SLLDEIDGLL ENNAEEFVRS
 YVQKGGE

> RXA01158 (1-942, translated) 314 residues
 MSIVEHKEF RRRLLIALAG ILVGTIIGFI WYDFSEWQIP TLGELLRDPY CSLPAESRWA
 MSDSEECRL ATGPFPDPFML RLKVAALVGM VLGSFVWLSQ LWGFITPGLM KNERRYTAIF
 VTIAVVLVFG GAVLAYFVVA YGLEFLLTIG GDTQAAALTG DKYFGFLAL LAIFGVSFEV
 PLVIGMLNIV GILPYDAIKD KRRMIMILF VFAAFMTPGQ DPETMLVLAL SLTVLVELAL
 QCFRNDKRR DKKRPEWLDG DDLASPLDT SAGGEDAPSP VETPEAVEPS RMLNPSGEAS
 ISYKPGRADE GDVL

> RXA01159 (1-315, translated) 105 residues
MSLGPEWEIGI IVLLIIVLFG AKKLPDAARS IGRSMRIFKS EVKEMNKDGD TPEQQQQPQQ
QIAPNQIEAP QPNFEQHYQG QOVQQPQNPO TPDYRQNYED PNRTS

> RXA01160 (1-975, translated) 325 residues
KSSNKISDLA RQLNLLPYFT RYKGRVTMEA ARDLGPSSQ IMEDLNRLWM CGLPGLLPGD
LVLELHDSFKE VKIHNAQGM D KPLRLTPTEA GVLLLTLESL ESLPGIAKQE QVSAANKLR
AIMGEYSSTV FDSGEDLDA EVLEIIRDA DLHQVVSFEY HSHRSNNTSL RQVSPAHIET
HEGETIYKAW EEAVNQWRTF RLDRIRSIVL LDSKAVHPAR GVSVSITDDPF EFAKSSDIAT
LLLRLDAMWL GNYNAMEVDE TVEPIRSDG FSWHTVHFPL LSRDWFVRFA IGHAEHLKVT
SPEDLRKCIK QKAFSGSLAY DHHE

> RXA01163 (1-705, translated) 235 residues
MGYTNLNDTR VLKAGSCDAW WRTMSPLVQQ GSEAVFRRIM GLSRRPDRKP GFDDVPFHGA
AVRVPLKHLG TLVNAAPLKV LGARGEPNPA SSYRFEYITG DSAGRAITAT GAVLFSTRPW
TTGPRPAIAM APSTQGVAAH CDPSTHTCAIG LNAFYDKPFD AITAYELPVI LWFLAHGLDV
VFIDYPRDPA TGVQYCDIS AAKSLLDAV LASRQLGLSP EAPLGLWGFS QGGGA

> RXA01165 (1-573, translated) 191 residues
MVGHPVPAIA IPYFIIILA FIGVMMWLG F GWALGLLVLF FVGGLLAGV ELRRISKSA
IHQASGQSSA GAIAGNIGLT AAGAILVAMP GFVSSIIIGLL FIFAPTRALF RKVLAKMRMS
AIENLGVGRG EAVNGYRTQA SYGNFGAAN GGAQQPSNEP IVIDEIDEQA WTSDLKPEDF
TKGKDESDGE K

> RXA01166 (1-483, translated) 161 residues
LTGVYAYVIA GLAVNSSEM F EEIMSVLNER GVSVDLKNIT SCAGGSLAS GYSSSRGWTH
QGTPLADILD DLPLVVAEFG KQKLGKVAPE IPVLLWGSKN DDVIPIDPIR ELRDSWADKG
TPLTWHEQA PRVPGRTGLN HFGPYFRNLE KYSGLWIDLH V

> RXA01167 (1-321, translated) 107 residues
PRQLVYKYTA DGEIYEVFFA DDALPEEWM CKNGKLGILM EGEGVESKPV KPRPTHWMDL
RERRSIEELD VLLEERIEAL RRRRRNAAL LKAQQEAEAE EKAEEV

> RXA01169 (1-567, translated) 189 residues
IPVFLAVFVG SDALGSISFG PFVEAFFLLI LIPLVAAAGT QQVARKQVQ RTIMAAAAEI
MVPIMMLTLF AVIASQVEAV SGQFTDIATV VPLYVAFMLV MIPIGGGISK LGLGLGFKEQR
AIVFSGATRN SLVVLPLALA LPAGLEIAAV VVVVTQLVEL IGMVVVYRII PLIFHEKQTY
RKLSGIGES

> RXA01170 (1-483, translated) 161 residues
VSLSNKAKGI VAVIIVAVI AMAGMVAYAS SNNADKTFTP AGALEQTVA FDRQGLQVSA
VALADIYGE YVSAAILCEG TPTATLEQSL GVDLSLNDL ESVGVPVGSVY LALSNQDGEV
VYDKIDRANV DICATPLNGA FSAYS LMPVA KVGNSWAIA A

> RXA01171 (1-693, translated) 231 residues
MSQAAGKFKP MTSTLAESTL TSLKELEDPK ILSVNERHGD DHAVNLTKLR AVAKELKKNQ
PLARELWATD DTAARLVALL ICRPKFEDQS ELDSMIHEAR TPKVLDWLIN YVVKKNPHWN
DLRLWLEDP AENVAAGWA LNTHAVITKP DALDDSEILD TIEAQMKTA EPRQWSMNEC
LAQIGIHRPE LRDRAIAGE RLEVLDKYPT PPNCTSPFPAP IWIEMVRRK K

> RXA01173 (1-615, translated) 205 residues
MHVSTLPNNK LRTRIFAGTA AVALSGLVAS CSNAEDAVDS ATDAANSATS AAGSAINDAT
GTSSASTTPE SGTSGSDSGS DSAGGDTTVE ESADGSTISI PTAVVTAAANA AGFSTPESVE
EGPNGESLVT FPEGYIVNSA EGGAQALVGM IGETWIEGG LSAAVGLPTG PEEATTNGWT
QQFTSGVLSW LDDSGGFQFAA SVEPA

> RXA01174 (1-750, translated) 250 residues
MSNMQGNDSK KSSGASRAES PLIKERTLII VIFVILIVGL ASIAVGPVVY QLIMGPGVKT
EGIQADGAAP ASTDMNGTWD VAPGSIPNTI SAGFTFAEIL PGEEKITSGS TLTGVTGEVVI
EDNSLISGLI TVNMTHITTD QEKRDINVRT KLFHTDQYPE ATFEVTDSDV LSLALPDTSI

AQVVIPGELT IHGETKAVEP TFDVLRGTGQ VIVASDIEIN RLDFGVETPE FIAAKINETG
EINVRIVLEK

> RXA01176 (1-504, translated) 168 residues
VRYFYDTEFI EDGRITIELVS IGIVAEEDGRE YYAVSTQFDS SKANAWVRAN VLDKLPNPSS
KVKWSADTIK REYVEFLTST GTPPELMAWV GAYDHVLLAQ MWGDMAGLPR EIPRFTRELRL
QYWDMAGRPT LPPELNGNHD ALIDARHNLA KEKVCMAALP LGKRDRVS

> RXA01177 (1-1986, translated) 662 residues
MHGEKLVGDT EGNLSQFQWR DMATNQTLRK ALLVLSTIAL LLTLWPSIFN VRAIESVFVF
FHIDTDVYRA GANAFLEHGN LYTQDYQVGS IQLPFTYPTI SAALFVPLAI LASSVAGIAL
TLISVTLVWW SVAIVLRRVL KGLTDADSRF VSYLILPMAL STEPVFQTLQ GQVNIILMA
LVLMDDTFFKK PNLPRGEWIG LAASIKLTPA VFGLYFLVKK DWKGAGVATA SGGVGSALAF
ILSPSSSIKY WTETLNDPSR IGNSLYIANQ SVRGTLSRMM HEQQDLVEKL WLVAVVVLCLA
AVAVAMWRVV RAGNPGYAVM LNSLIALLCS PVSWSHHWVW LIPIATGLGA SANNRQRTAP
GIAATAGVLA LLTTIPMEFIT TFWNNMPYDSE SYFPWPLILQ PSGNAYVVVV IAILIVAVN
PTVLGSGNKA VSGQAEKKSS PALLVVLAI A IFYLFANIWF KGNNQNKALI QYPLQTMGR
GLTDFGELIF EFAASSNQVL SLWIIIGALNA IALAITLWFL LQRFAGKKSS WLTYLSTVAV
ALMMFVSQDA LQFGSLTLVA LALITVDVLS VREIGRGLL TGLAAALFGW PILIVIGFLI
HRRYATATIT TVTAAVLWIL GILLNPDAFN LNLRLQWFNG RDGRDNLSEY AFLARWVSES
PA

> RXA01178 (1-450, translated) 150 residues
MMFVWFVIL GLGAWAIHRT WSHGFKDLVS ALSIALPTLV LPVELHHLV LLLPLIAVLL
RQGRVAISYL IGFIYLVSWT PQHLSYSTVF PLNDPAPEGY VAHFGWYLLV EPMVAPAAI
ILGAFIACAA TTPKTSQLVQ VDKSSAENTK

> RXA01184 (1-1473, translated) 491 residues
MGLFGFGIFL ALGLGQDHMG ILAGVVSVMG VAYCIAAFMW PSGEGQLDPT AFSTMPLSAK
QLLPFGFAIG LLQSRGIIAV ICTVATSI A AVFLPVGSGM MIVFMMAVSL VTLTLLGLLEL
GALTSGSSSR VSNDRRTVLT SVVFMVFEVVG YNMLIGADGM SRIDAIGAYT KWTFPGAGAG
ATEAFVAGVL GEAGLLTLLA FVYVAAFGWL WSQLINRALT APLDQGGQQG SAKDSAGEGK
KVLFLPFGIPW SVGGAIFRS LRYMFRDSRL LGSIMVFP LL GVLFIFQSFV VEFMIIYVGL
IMMAVFAGSV ATNDFGYDGP SLWLNIVAGV KARTLLMPRH WASMLPGSVS IYVFMIIIV
LAENKTTAVL ICFIGLGIFI SSAVALLVLT TFNPYPTSKP GTSFPWGRSG YSGAAVFGAF
AALLLGWITPT IPTIALGIFG LVTQMMMLII LAEVLAILLP VAVYIGVAKV CIRKVEKDL
EIFDKVKTHV K

> RXA01186 (1-1098, translated) 366 residues
MATFVPLVFN APKRGMPPTH FADLNDEARI EALKELGLPK FRNLQIARHY YGRLEADPLT
MTDLPEGARQ EVKDALFPTL MSPLRVVETD DDTTQKTLWK LHDGTLLESV LMRYSRSTL
CISSQSGCGM TPCQCATGGQ GLDRNLSIGE IVDQVRNAAA TMQSEGRRLS NIVFMGMEPE
LANYKRIVVA VQRIQTQSPA GFGISQSRVT VSTVGLAPAI RKLADEEMSV TLAVSLHTPD
DELDRTLVPV NNRWPFVAEL DAARYYADKS GRRVSIEYAL IRDVNDQDWR ADMLGEKHLK
ALGSRVHVNL IPLNPTPGSK WDAAPKARQD EFPVRRVIAG VPCTVRDRTG QEIAAACGQL
AAEESA

> RXA01187 (1-459, translated) 153 residues
VDFPFTFNPD LPTGLDPAYE GNSELNPLGG KNIPDEFEVT ANTPAVQEPE AYSEPETAVE
SKRQAKQNTK KSEPVVAPKQ TLAGGTWVAL IVGALLLILL LVFMQNTTQ VELNLFAWTF
QFPAGIIGFL AAITGALIMA LGGGVRMFEY RRS

> RXA01195 (1-447, translated) 149 residues
VIVAVSAVLL AAWRFFTLRS RGTTVILREL PQSGVHGWRH GSFRYNGNDL EYFKLRSLSP
MADLILNRLS VTLDRRDP ADEAVFMSQG LKILHIKSKN DQIELALDAH GEMAFATWLE
AAPDARAEHS LNPDRFNRRF ASKOTRKNR

> RXA01196 (1-690, translated) 230 residues
MRLVIARCSV DYGVRLEAHL PSADRLLMVK ADGVSVIHAD DRAYKPLNWM TPCSLVETP
ITDEDEGATG ESLVWVENKK GEQLRITVEE IHSEQNFDLG QDPQLVKDGV EDHLQELLA
HITTLGDDGT LIRREYPTAI GPVDDILCRNS DGETVAVEIK RRGGIDGVEQ LTRYLELNLN

DELLKPVHGV FAAQEIKPQA KTLAEDRGIK CVTLDYQALR GIESNELTLF

> RXA01197 (1-453, translated) 151 residues
 MSTEQSLNIP HEYVICLDHV GIAVPDLEEA IEFYRSAFGW VNNHQEINEE QGISEAMIGP
 KDIKTGEMI QLIAPLNEEDS TIAKFLEKKG PGIOQMCLRT NNIDALSEHL RRQGVRLLYP
 EPKNGTGGAR INFLHPKDAG GVLLLEITQPQ S

> RXA01198 (1-303, translated) 101 residues
 MIVAFSVAPT VTDNFDPAEMA DAVTEAIRIV RASGLNETN AMFTLIEGEW DEVMAVIKEA
 TEAISRSVSR TSLVIKADIR PGHTGQLTRK VEAVEERLAR D

> RXA01206 (1-261, translated) 87 residues
 VSAENTEND SPFEISEFDD HRRPLQRALK FGSIALIVFT LISLAIWGAT RGVPGVSAVV
 IGAAVGAGFV LLTALSVLFT TNSNVTT

> RXA01207 (1-648, translated) 216 residues
 VSRIYDCADQ DSRAAGLKAA VDAVKAGQLV VLPTDTLYGL GCDAFNNEAV ANLLATKHGR
 PDMPVPVLVG SWDTIQGLVH SYSAQAKALV EAFWPGGLSI IVPQAPSLFW NLGDRTRGTVM
 LRMPLHPVAI ELLRGTGEMA VSSANISGHT PPTTVLEARQ QLNQNVAVYL DGGECALATP
 STIVDISGPA PKILREGAIS AERVGEVLGV SAESLR

> RXA01210 (1-693, translated) 231 residues
 VFPVGIPLLL FLINGGAAE SANSFDYFVM YTLFVQFYT VLSMATTRRD ERVLKRLRTG
 EARDIDITGA ICFPGALLTL IFTVVIPLL MVLGAPAPIN LVPIVFAVLI GLLLSALAL
 MTSGFTRNAE AAQMTSMFV MLAMGGLGSI RFVFGDSIVA DILAYTPFAA ISDLVQIGWA
 GATFADSVGG VEAANFAGIF QDMLIPLGIL AAWTAAVWA ANRYMRWDSY R

> RXA01213 (1-1227, translated) 409 residues
 MTNPTTEERNA RRLNWANGLO NIGDQIVAAK TVLEWLLQAA GAGFLLALL VPPIREAGSML
 PQAAITCWVL RQTSRSKVWV IGSNGQFVSA LGIGVAALFL RGWALGITVI VLLAALSFR
 SMCSIASKDV QQGVISKGR GLVTGRATVI GGVVGLVAGL AIAIFLGSHS PTRVLAANVVI
 ASSFSWLFAS IVFARIEYAK PATPKNAPSA NPWVRRICIAA LKDDKAFRRP VLRSMMMLVT
 ALSTAFIVAL AAESGNSIDS LGFFLIASGL ASMVGGRISG IWSDDHSSKNV MAGGALFGSI
 VLILVVLSSA FAPAQINTLV FFLSFFLITL AHTAIRVARK TYVMDMAEGD QRTRYVADAN
 TLMGVVLLIV GALSGFIAIF GNEAALLFLA AIGLLGTISA RGLKEVSAG

> RXA01218 (1-429, translated) 143 residues
 MARLQDMIF INLPVSDLAA SKRFYAGLGF KENTVFSDEH TASFEVSDAI VVMLLETARF
 SDFTKRPIVE KNGSREVLNC LSVCTEDAD EFRRAQEPG GTITRELAAE GPMYGGAFDD
 PDGHGWELMY FDPALAQMM PEG

> RXA01229 (1-693, translated) 231 residues
 MIISINTAHP LHEPHVPSHH NRMNTLRAGV LGANDGIVSI AALLLGVIAT GASDTVVFGA
 GLASTIAGAV SMALGEYVSV SSQRDTERV TAKEAKELAE DPTAEHVLS EILHSYGSIP
 ETANAATEI QGGDALGAHL QLELGIDNEQ LTSPLAAAFS SAVAFLLGAL LPMVSVFIAP
 AGWDAGVVVF VTLLVLAVTG FISAQISGTS PMRACRLRVI GGALGLALTY G

> RXA01231 (1-504, translated) 168 residues
 MLGYTFVIFI LAPFLILTGI AMAPAIRSRF PWYVKLFGGH QGARSHLFIA MVLMTGFVIM
 HXRPGFLVHG DYNMVHMVFG DMNTDRAAQA YIIIVITIVX GGVLXAXQY IXXWXTXXAX
 XGXPPXSXEX XKRIFXPAA SPDEQAXXHL HGQGH LAVPL DQWPAADR

> RXA01234 (1-384, translated) 128 residues
 MWKFMKTQYV CTTYFIAAPE DEDEAYQTYR SRMNSLAALN GADVVSVDAG LRMEVDQDIW
 GSLAEQYQIE QEGLYPTGHN LYFVVTVVNL DSDSEVYDRT MEHLIMDDFY VRVDRFPSTV
 HASTQIML

> RXA01237 (1-441, translated) 147 residues
 MNVQFESDMA VQPGNTMEAT VTDIRDAKRK TTQLDSVTFP KKNCPSPRTL DTISDKWAVL
 ILLSMENGPQ RNGEIKDQVQ GITPKMLTR LGVLVEDGLV TRTSHAVVFP RVDYQLTDLG
 ASVIEPCRAM YSWAVENIKQ VEAYRSA

> RXA01246 (1-639, translated) 213 residues
MKRTITIAAL ALTSTLVLSA CADNTEGENT DTTTIIATTS PDDTTETGTAT TDPETETGAA
GEVSAEHNDAD DMFQAQMMP HHQQAQVEMSE ILLAKDDIPA EVIEFTQGGVI DAQGPPEIDRM
NTMLETWEED PVTGDMGEMD HGGMSGMMSE EDMTALEDAQ GTEAARLYLE QMTAHHEGAV
DMARDEVTDG QNPQAIALAE QVIEDQEAIE AEI

> RXA01249 (1-300, translated) 100 residues
VSGDFTLTH GLAAMDAVEI IDHLDRQKVT ERPTDLIASV RADELLLSDD DQEVVVLDLPD
NQTYVSIAPY LNSTHDCFPYH SLTTCGLDLD NEDIHVMTD

> RXA01251 (1-309, translated) 103 residues
MTQPDMSQIL AQAQMQAQL QAAQQEILAT TVVGNAGNGL VFATVTDPKV
VDPEDEVETLQ DLLLLGAFKA HNKVANVAEE KMGPLSQGMG GLF

> RXA01263 (1-912, translated) 304 residues
LTPYDPTAVN KESEKEAAKN LFGAEALTVD PDAGEVVDV DNFYPTTAKA KRDPSPNYAA
GCHQEVNETS PESCIVGDKN SDFSVALVGD SHAGHWLPAL EPFAEQGWR LEVYTKSQCP
LISTAKLGE TFYAECYEWN EKLLAKLTGP SAPNHVIVSS QRYASANPLI DSVATGTVSE
GYEMAWNSLK DAGVISVLL DTPRFQIDIP ECVASNRDNL SECSVHRSA LGTEAHPQQK
TAAQNIDVPV LDLSNWCPE EYCSAVIGNV LVYRDSHHLT ATYARSLSSA LWNELVASNG
EPFK

> RXA01266 (1-1035, translated) 345 residues
MPKVSVTGTF YNRCHELERT IESILNQYIS DFEIVFDFA STDGTASRL ELKEKYDDPR
FRFIIHEENK GFVKGLSEAI SGAKGQYIAV QSGSDVSLPR RLQLQVEFLD ANPSVGAVGG
AIYNIQEDTG TRNPFQFEKP IATFDLLTS NPFTHGEVMY RLGLYSIGG YRSGFTFAQD
RDLWLRMAKK ADLGIIPDFL YHRYTLDDGV SFVPDKTIQK RCFSEAAVRL ALMPFEEGAL
AYSRLEAEGP TAVVPIADRA VQKFPVKAAL RLCLYGAPET GLHMARYDIQ NPLRRITVVV
LISIISSRLI KPLQDILYKS IFKGVSSISK IKSSLVKFTR RIQQK

> RXA01267 (1-1314, translated) 438 residues
MYAEINGGFI PEGTVRVSGA KNSATRLAA ALLTDEVVHL GNPFKLVDV EHKIRFIEEL
GGKVHVDHDE QILVVDADKL AAREMTTDEL NIPRTTYLL AAAQIGRGEI ARVPFPGGCA
IGGGPAGGRG YDLHLMVWEQ LGCKILEKDD HIEVTAQPGF IGGVIDFPIS TVGGTENALL
CASIASGDTK IANAYITPEI TDLIELLRM GAETIVYGS RIHVKGAGRL LQGAJMDVMP
DRIEALTWIV YGIISSGRIT VEGVFFSSME VPFIHLEKAG VDLFRNSSV YITPECLSPG
SVQPFLEACG THPGVISDMQ ALFVLLGLKG AGTSRVYDVR YPERIAFVEE LTNLVSQDKL
SAEAGKITIQ GDAFRPQGY NSTDLRGSMA VVLAALCADG KSTINNVMHA LRGYNELDKK
LRLLGADLTI REGEVPSF

> RXA01268 (1-840, translated) 280 residues
VAARIARVPR IVYVAHGLRS ETVLGLKKKI LVFLEYLTQL FAHQTLAVSH SLKKAIEDAH
PRFKGRVQVL GYSGMNGVEL DRFRVPSLEE KLSARNALNL PSKSVIVGVF GRNKDKDGGD
LLAALTKEHA FTRLRLHLI IGELEDDDLR EAFIKLVNEG QVTITGWIDF PEEPLAAVDV
LLHPQREGI GMSLLEAQAM GVPVLTNAV GTVDVAVTSG GGGFADDDSV ESWVSKIDL
VSDPKLDRM GRAGRQFVSA RFNRDDVAAR FSHFVEQFKK

> RXA01271 (1-1812, translated) 604 residues
MAISIGKAGQ NLKGSVPIGK VLFLIDALAW ISALFIGVVL RYEFNLSSIN WSAFAWFGLA
AVILQFVLGL SLHLRYKGLR HLFGSFEDTL NVSISVIVVG VVLWIASLFV GQRWKISRGV
MLLVIPLALV FVLAVRYLAR MRVERFRRA ADSTPALILG GGYIGTNLIQ WMSDPKSPF
RPVGVVDNPN ELACQVRGV PVLGKFDIIA QVASDTGAEI LIVAIGDADS ALLRRVQDTA
NKNGLSVKVM PAIDRVVSKG VRGNDRLDLS IEDLLGRQPV ETNVSEITGY LTKGRVLVTG
AGGSGSQLC TEIAKYGPAE LMMLDRDETQ LQQVLINAVG NGLLDTDVAV LADIREADM
KEIFLKRKPE VVFHAAALKH LPMLEQYPDE GWKTNVLGTL NVLAAAEAVG VETFFNVISTD
KAANPTSVLG HSKRVAEKL AWYQNSISK YLSVRFGNVI GSRGSMPLTF TRLIMEDKPL
TVTHPDVTRF FMTIPEACQL VLQAGGIGRS GEVLILDMGE PVSILEIAR MIAMSKGID
IVFTGLREGE KMHEELVGDG ETEDRPFSK ISHAHAESLA PNNLDRDRFM QRAGKLASTD
SEII

> RXA01273 (1-1434, translated) 478 residues
MELREYATIL MKNWVLIVIA SILGIAAGAG FSLLATPEYQ SRTQLYVSVR SGAGTTSMDV
QGANFSRQIV NSYVDVIKGT VVLEPVVDEL GLELTANQLS SHISAASPAD TALINITASS
PSPQQAEEIA NAVGESPKNV IQTELEPDSG DGMSPINLTT TQVALEPSSP VSPNVMMNLI
LGLLVGLAIG VGIAVLRAAL DTRIHSLRDI EEVTDKPLL GIIADSEVEK HPLIIKHKPH
SPIAESFRAL RTNLQFLNVG GSSSVFVISS ANPGEGKSTT SVNLALALAE AGSRVALIEA
DLRLPRVSKY LGVEGNAGLT DILIGKAEVN DVLQRWGRTO LYLLPAGRIP PNPSELLGSA
EMDKVIAELE ESFDYVVIDA PPALAVTDAE VIGHGKAGIL IAVSAGSTKK PELEATLSTL
ENADANVGVG VATMLPPKSV AGYGYGNYG GDTSKINAPK PDNTELTSTD ASKANNEQ

> RXA01275 (1-918, translated) 306 residues
MEKIRSPAVQ SDALQVFKSA LAATVTWWIS VNLLNSQLPF LAPWVALMTM QFTVYHTFIS
GIQTATIASVI GVLGSFVIGT YLDVSVWTFG LAMVIGLIGA RVPKLRAEGI GIATTSIFLL
ASGFDDQQPL LYDRILEILL GVAVAIAINL IIFPLRDQE ANMVGVNAGRI RMGEVLQKMA
DELAEKWNID NADEWLEEIN SINNDLEKAW HSRVFRVRES RVNPRKIRIQ EGPRQPTETS
YESNLTSLDE GIAHLRLHAR TLRDTPIID DWGSSIPATV GIPYARCRSF ARRSSEGNRS
YRPPAL

> RXA01276 (1-546, translated) 182 residues
MRKTLITMLA TTAIAFSAIS PVQAQTVDTT DDAVSSELS SGTSSGSSSED SEDSDISNRD
IIFGIAAIAA VGGLIAGGVH WAVQQRMIPI PLPGIIPNPP ALAPQAPAPA PAPAAPQAV
APQVVAPQV APAAPVQTN RTYKNCTEVW NVLGRSIRQS DPGYGTHLDR DRDGLGCESE
PR

> RXA01281 (1-762, translated) 254 residues
VGLSRSHYQL AAENTKSLVR MVPMTVPQGN EPAKKLATDL NRNQVVDLS AAVSRGQLTL
EEFEDRSSKA WNAHRLDTLV ELISDVNDNP YTLGQQQFPG ASYAPAAEYTP TPAMPNVSD
PVNIYVRNRI GNPNGSKMSV SFMGGTVRKG GWHVVPNVHTS FMMGNGQID LRDAFLES DR
IQINAYTFMG GIEIIVPEGV FVICDGMGIF GGFEQSVDKA GAINPARLPS NAPTVMHKL
AFMGVSVVTT KKN

> RXA01282 (1-780, translated) 260 residues
MDELLKQEVK DFLTRRRARI TPAAAGLETQ PWSDRRVVGL REEVADLAG ISLEYIIRFE
RGNLKGASPE ILQSLAKALQ LSPIEREHL NLAYRADHPR NLPSAETPTA PLQDIVDAVT
DKPAWIRNEQ MDILATNRLC AELYAPIFKD LPDRPNATRH CFIGATASEF WVDNRQDSAE
FAAKRLLEYA RRPSPVGLKE LIDELHQKSS VFRDNWASAD VLSFGSGGTR FRHPTLGRV
YEYETFFNLNS APGYVLSIYF

> RXA01294 (1-666, translated) 222 residues
MSTIPDVFTS EVFPEISGTH EFRGLTYMFF DQFTLPTAEQ LEQAKAAGWS LITGWWNNSD
TDLEDVELED ITNCGDSLKP LTDEFAVSSL STFDLNSQGL TDVDRFPQPI EEAADLDDIF
SEEECGWGLMA INCPNWQVPA ACEWLGCMMV GEFFEMSHVL RVWNQSWGVE ALAFGGEEDD
ADLLLRVPFE SEELLKALVA ASDQVTYKH EDLGFSLASLW FD

> RXA01295 (1-975, translated) 325 residues
MTENLDNALL SMRMKPVQMA LMTLGYNHDM AVTDSGMELI VRRPGLTVNF NLDVSTLCIV
ADFMMHGCVP AKKQAEYLRA AEFNRFRTRD LQVVLDEADS KNMTVRGREF FFSVSGATVE
QSAEFVHYCM NDVATTFVSW CEQWPKFSP ERVEFNATPP DVFDFESDQ LKEGNPFGLI
DEPTFLVSLD RYQQYELMG ADQLKMGEDF VEYLHMGQRV SAWLTGNNNG SRDKTLAVSS
GTGVKIKKKK QLQELLGLCN LYSKEHVLVT VFEEIENGA RWGIFAEARI DLPAGLNDHQ
LWVFLANSSK WTAEVCLTVA HRLQN

> RXA01296 (1-1083, translated) 361 residues
MSIEQATSL SARVRELKPI IETEEATKTA LIIPFISNVL GYDVTDPREV IPEYTAADVGV
KKGEKVDFAI KTGDDFHFLI ECKKVGSPLS LDHANQLVRY FNVTDTEPAI LTNGEIIQFY
QQLDAANRMD AKPFMTLDLN NIDARQFPHL EMCTRKHFNP QALAAAEEL KYIAELKKVI
ANQFQEPDVE IVKMLAATVT TKRMTAQNLE FETHLVNTAS SQFLKDEVNR LRSQAQVFD
PVQTGGADAE TPAEDEAVIE EVVSEIVTTE EETHGHSIVR AICCSVSAQ EITMRDAKSY
CAILFQDNRR KPIARFYFDR KIPRIGIFNA EGEQEHFDLE SIEDIYNHAD LLHSRVVALN
A

> RXA01301 (1-405, translated) 135 residues
 FLRLLEGIEPK GPARAYYFGD VSDTVDLILG FVSPSPAQAES LRRGALSQSG GDIDDVVLHH
 FRDMKTMHSR HSGPFDGVER VWDEILDEVE DLGCTLPSS IGWEEYIEGP ATADTCDQLA
 SEVYVQVCQA PVKSA

> RXA01304 (1-486, translated) 162 residues
 MPAQNKNLPG SVIVVSDRIK SGERIDKAGP VAVDLLQESG VEISTFTVVE EGFEPVHQEL
 VKALARDRVR IITIGGTGVG PRNRTPEATE PHITDILLPL MTQILFSGLS NTAQAGLSRG
 LVGLSARDST AALIVNAPSS SGGVRDALGV VCPLFGSIFE RL

> RXA01306 (1-1008, translated) 336 residues
 MTEWVVLPA TILLIALSAF FVIEFALLA ARNRNLEETV ETSRSSRAAL RSLNELTLM
 AGAQLGITMV TFALGAITKP WWHYALMPLF EWARIPLVMA DVIAFILSLF IVTFLHLVIG
 EMAPKSWAIA HPETALRTIA IPARGFINLF RPLLQWINKM ANDLVRKVEG TPDVRAAAGG
 YDITDLHALI EHSRETGALD QQSAAQISGI IKLDKITVGO TLTASPFTHS ASATVAEVQA
 AAQRSGSLRV LIDAPSHLFP HVIHVRDTLG ASPDEKASKW SRPILTVAET DTLHQALEYM
 REHNEQISAV LSADGKTVLG VITWDHILKY LWPASV

> RXA01310 (1-327, translated) 109 residues
 MSSAKKKPAP ERMHYIKGYV PWAYSSPHSS LERSATWLG M GFLTALAGV GAVLFAVGAN
 SVGQQQEHFW LYSIIGVVFA VVCTVLGTVL IIGRAPYNNR YVKETGRTO

> RXA01313 (1-945, translated) 315 residues
 ALRLISQLLA PSAALNFKSE RNAVDVAKHM LASQAQQRGS ALVALDTRSE NADAATALRK
 SLLIRSWTQR GTHQLAAED VRWMTLLCSP RILSAASAKR SSLSLDSAAV QRARDALTA
 AEKSPVSRTO AYEIFRSVDV DPGEHRGQHL LRHFGGEGDI VQGPPIGTED SFVLLDSICP
 LSLALNGDEA LTEMTRRYFH SRGAATVKDL VWWFTGLTVRD VKKGIAAVS DLIHSGVEGP
 NGEEMWIPTW ADDVTDAEVS DALALELTLP AFDEYLLSYT DRSHVMDPEH LFSIGPGKNG
 VFKEPKFVQGG EALPV

> RXA01315 (1-651, translated) 217 residues
 VDIEEQPSLR ETKRQMTLEA IEDNATRLIL ERGFDNVITIE DICAEGISK RTFFNYVESK
 ESVAIGHAK LPTDEEREAF LATRHENIID TVFDLVINLF GNHDSKSGV AGDIMRRRKE
 IRVKHPELAV QHEARFHQAR EGLEHLIVEY FEKWPQSQHL DEPADREAIA IGLLLISVML
 QGSRWEHMP QGTQADFQAC CRKAIKNTFL LRGGFSE

> RXA01316 (1-303, translated) 101 residues
 MDISMLNVT SYTIWAIFAI IGICGFVGAF LAATTREDAF EVADRQKKMV WVAIIASGF
 VLTALGPSIP ILPWVAIIMI GLYWFDVRPQ IKSILEGAGG W

> RXA01317 (1-420, translated) 140 residues
 MSDAKDDSI SKWSNAASEL SGAVSGVAKK LREELSEKET FSKLKTEASE AVDQAKSGSY
 LDAGKEFARD AGSIIDKAAK TVKGAVSDSD KNDVKSAFNG AVEASRDKFD DTLEKKRAKK
 DSPPEPGDDDI IDGEVIPPQN

> RXA01318 (1-1302, translated) 434 residues
 MGKHEVAQQT VPGSPPEMEA QRRKELRKHK AIATGLLIFA AAVYFLCRFV ETRPGETAAM
 VGFVRAAEA GIMIGLADWF AVTALFRHPL WLPIPHTAII PRKKDQLGEA LSGFVGDNFI
 NAQLITEKVS QARIPERAGE WLAQEPENGE VSRVVGKLTIA NIVRAIDPSD AEAVIKSAVI
 DKLAEPFWGP PAGRLLEQLL AEGKAEPVVO ELAQWLHKKA LGSEPLIDRL LNERRPIWAP
 KFTAQLVSGK VYDEVIKFTE AVAADPNHEA RKSLLRFLNK LAQDLQHDGP MIKVEEIKR
 DIMSGAIAQ AAPTIIWASAS ESLIESAEDE SSILRRKIAE AATSWGQRLL VDDSLRHSLD
 TRITGAAPAL ADNYAPEVTG IISETIERWD AEEASEKIEL MVGKDQLYIR LNGTIVGALA
 GLAIYAISHI LFGE

> RXA01322 (1-438, translated) 146 residues
 MKLAPRMRMR SPKTFALAS LALVIGLQGV PIAQAQTEYR TASDGSGLNWG FRQSFERNYIQ
 TGVAKGSITL GDGASDNGGN FAFTPTNGT TVTSDSQGTV EFNGSVHFLG HQAEDKWILD
 TTMSDIKMFV NGSSAQLVVD LVAREF

> RXA01326 (1-294, translated) 98 residues

LRERLLQNNQ GEVIDNENND WILHPVRDSS DRKRLVRTAN DIIRETESAR EWDNFFENAI
AIANDGTGDL IILLPDDDAF YIWSHEDEPL IETELEDA

> RXA01330 (1-456, translated) 152 residues
MMKDKTEPLP EACAEGLER VVKSPHEELD YAAVLSANWN PPAETVQRFY TEAAEYALRK
NSPALYLVGY AGNRAVCSAE AFTHASVVGIT YNISTLEHKKR RRGYGGGAILT ATLHTARNAG
CDTAVLQASE DGEFVYRKLK FTDGGRFTEY SL

> RXA01331 (1-576, translated) 192 residues
NMINGDPADG NGWMYAYNGL HSWARHYAMP AAGEGSAIATM LFWWPQLLGV GTDENPDQVN
DVDQAARDLN VGYFMISFPT FWDQFIPNER QIDLLWQTPG VTPVCKKGDG VIFAVNDMFT
DAELDQMRAP GNSPEPLPEL PTLGELGLAE TEDEVQDTYY HRPTVPAVGN SEMPSAETLY
APDPFKPHTV PN

> RXA01333 (1-1005, translated) 335 residues
MPGGCGSNIV RMLPKSRIFS AILLGIGVAL VVWGLVARRF VHADGRPLD LEATTYVLHD
SDAQTTINSR PLAGVVVTPV TRLHFEVMD PASADDATIR IGDSMLRGNE DTQGFQERL
LSATSSSFRI DRTSGEVLSD IALTNQLASF TVQYSVDGIW LKFETDAQET TYNVVDPLVR
SALPADEVES TEIDGREVLH YRQVIDNVNV AEYFADANNT TLTLEDGGT TTYFYHNVV
RDFWVDQRTG LVVLAENID DFYGDGRSGQ KEQKLLFDAS LDAAVSKLV AQAESIPGDG
VSKIANVTGI VIGAVLALVG LAGCFGAFGK KRRFA

> RXA01336 (1-603, translated) 201 residues
MEPTVKAŠAR HTIHVTADTW RIRLSASAHŠ HPNDAYARRA TAIŠAIGSVL IDVPLQGERI
SESTAYDQOI NADWNAEVTG TDVNIARDII SRLAAVPDVQ VDGFLWSLSD SLAAEAAVEA
LQGAADTARN TATAIAESLG GQLGALLYAT TDTHSSTIP AREEMMAKA SIPPRTLDE
LAPSDIEVT K EIAVTFEFLA G

> RXA01337 (1-1413, translated) 471 residues
VTFRGNGTA KHAVVVGSGP NGLITAAVLA KAGWQVDVYE AAPTGGGAAR SESVLGEGTI
SDLGAAGHPF GVASPAFHYL GLEDHGLEWA YSPFAMAHL DYGRAGLLET SLPETAKKLK
PDARRWKNLH QSLTKNIDKH LANLLGPVLK WPAHPIRMKP GFPFALLPAK RLASAFAETE
EARSFLIGSA MHSVTPPHKP MTASLGLLFG ALGMSRGWV AVGGSGRIVD ALVNVVHHG
GTIHCDSDID SLSQFRDTDA IILNQTPSQV LKLKGTDLNA GLPQRMSTWK HGSSYKVYDV
LLDEPIPSWN PQVGQATTVH VGGSSSEIAP AEA EVAAGRM PERFFIILCQ QQVADPSRAR
EGRHVVWAYA HVPRGFVDKR FAL LITAQIE RFAPGFRDRI VHSVDTNAED LEAWNPNLVG
GDITAGSALL RRMPTKIGEK TIMASASNAF GGGVHGMPGW WAAQAVLADH R

> RXA01342 (1-1512, translated) 504 residues
METPTQMDV RNLWYTSQSLK LREILPTNKT FDIQISELV DPTDFIRPNS VVLSVGIAFA
ETPDGLRMDA HRLADAGVIA IGFGSGLTFP QVQALIDAS LHLGLGLEFV PREIFFISIT
SSVRDEQTRR AGRQLQELL EQLRLNSIAI SGGIEALCRA AADYLGAVT IVDSGRVAC
SITTDLDLQ PQAVSRING SQA LDTATNF GFIRHMTRYG DRHHLVSLM PTRPTDQHRA
LIRHACGLD ILLQPEAMR DREIEVRSLA MSLLGRSDD LATIHVRFAD ITDASGNTRP
ILITNTFQPS VRKALSSVAT ALYQERALA HLRLAESTEL FLRGRSRVH NVQLFGTAA
SGVRLCTGLP TRAENIDKKL IRELTATAKT LQLGTHAEPR DGTLLWLQNP ELRKILKIRS
RDTYDRLLDH DRTNNTELAP TLVSFTQHSQ HIGDTAKELG IHRHTVTRM IRIEICEID
LNDPLTRAEL LLVIATKEGD VEKQ

> RXA01348 (1-492, translated) 164 residues
VGFVWSGDS QIYPELRKME AEELLVGSVD PWGSKGATKT EYALSEKWE ALRKAWYEPV
TYGPTRPDAR LKAAYFEVGT NGDARRHLA HIAHFEQQIK QSESMIDELK AKHTPTLARR
LERSPKKEHE RIVAFKVLAY EGQTARAQAE IEWAEGKLKL LDLT

> RXA01349 (1-777, translated) 259 residues
MATSRDAEN IDQAGSEFIE SDSGHTATPE EVVATALTFF AEDGFSETKL EKIAKASGMS
KRMIHYHFGD KGLYIKAVS YALRLRPEA EAMQLDSAVP VDGVRKIVEA LYTCITKHPE
AVRLLLMENL HSQDSVDSTA AYSDES NVLL NLDKLLMLGQ DAGAFRPGIS AEDVLLIIS
LAYFRVSNKV TLKNLYSLDL ESEANIEGMK RIVVDTVLAF LTSNIQNSGN SSYLTVGGKT
AEPETDSSVY SFDTVFEN

> RXA01357 (1-303, translated) 101 residues
MSAEELNDNYE AEVELSLYRE YRDVVSQFSY VVETERRFYL ANAVQLIPHN SGNDVYYEVR
MSDAWVWDIMY RSARFVRYVR VITYKDVNIE ELDPDIIMP E

> RXA01359 (1-1182, translated) 394 residues
MIDSRLAWA YLSKVVEGPN AHLQKLLKEG HDVERIAFGI KHREEWIGEG LLKNTDSRYS
IDTAQTDLDET IAKLGGRLIT PEDDEWPMEE LDHAFGFAAS GMSDHWRTYQ DDALPHALW
IRGGNLRRLS AQSVTLVGTR AISQYGTETV REFTQNLVSH QWTIISSGAL GVDVVAHSEA
VRAQGSTIAI AACGLDRSYP SHNRDLFNQI AKSGKGALVS EYPPGTPPQR HRFLTRNRLV
AALSQGTVVV EAANRSGALN TLSWCAGLGR IMAVPGPVN TAGSLGCHER IRNGSAQMVT
SADDVRSLLG AVGAMDSQTQ YELNFAATPV QGLTRNELRV FDALDDRREG REAASIAATEA
GTLTLQTLIFL LIALNKRGI KRDGTAWSRN AEMP

> RXA01362 (1-1395, translated) 465 residues
INELILFDVH DLVKYGVHVV GAOQESINFL SAASLYHPQT VLDSFDHDGS GNLPLGKDDN
GNWDRRPHKD RIQLVNADTL TVWKSILEDE QTPYLDTRMV YTVNTEAAAA LEKLASAPRI
KELGLQFSSG WNETTDKKKK YFDVGWGYPA SWSDAILLQGP HLG VATPMIK QPNFTMKHMQ
DWSEIDFEAI PANFIPATAY QPDRQTKPTY DADYGTWTFG DKQVPVADTF RIAREMAAT
TGFRTVYPSV IPPGANHVHT VNSAASRSNL KTLVLGAQLG AILSDYFARS SGSSHIFNDI
VRKIPLPNFT SLEKQFARTY LRLNCLTSAY APLWEEITGE FWDVQVPLRN AEQRRAAQN
IDAMVALSLG ISADELCMIY RTQFPVMRY DQEDHFDANG RKVPKEIIL QQKLKDGQEL
SVEKRTWVHP QSEVSYTFEY FFRVLDREAD LRAAYAKFEN QLKEP

> RXA01364 (1-1866, translated) 622 residues
TGTHLYDSLQ LFTFLVDKGH HPTDAKAVAF DAEAGEEGLH FRNLASDLFL PAATELIDRV
GLSNEALNKV LENLILLSRV SGKDRGFISY ATLGVTQLG VYEGLSMYTG QAGSDFEEV
APHGKADKGS WMLPVSKADE VPADSFIEVD QEAPCGGVIK VRKRHRGSGF VFRQSSRDRE
RSASFYTPQV LTSFTVTQAI EELQASKRIT TANDVLSLTI CEPAMSGAF AVEAVRQLAE
LYLELRQEEEL EQQIPAEADRA KELQKVAHI ALHQVYGVLD NSTAVELAEI SLWLDTMNAE
MDAPWYGLHL RGNLSLVGAT RSLYAPSLN KKAWLATPT RYRLDDIAQA IDENKAEPFL
NHGIIHFLPL STGWTATADA KDLKDLMAE IKELKSWRTS IRASLSKTQI KQLNNLALRV
ETLWRFLVMR IRIAESQISR STTLWGQEPD EVSEVVTREQ IEQDLFGNID GAYNRLRLVM
DAWKAFLWFP LDVATAEHF ERPALPDLE WLATLTELIG IDPLPKSKNE NQIVLGPDTN
WLAINDAET DLGFSGALSF ERVSANHPWI NVARQVAKQG SFHWDLDFA HVFAKGGFDL
QVGNPPWVRP DVNFEDLLAE HD

> RXA01366 (1-390, translated) 130 residues
VSQFRRCSRQ CGCKPAVATL TYAYSDDSTAV VGPLAPAAEF HSWDLCEHHA ERITAPLGWE
MLRVNDIKVD DDEDLTALA AVREAGRTVS GLVPEDEVGG NHPVNSARI AEQKVHRRGH
LVVVPDQDES

> RXA01367 (1-402, translated) 134 residues
MPVEVPRAHS RQAFDRAVL EAYSPLYGYI QKELSNLDA VDTVPMRLS ADLAILPDEI
TADGPVPLGR VIPPAIDTKG NPTARIVIF RMPIEQRVTN AVERHELTHA VLTSLVANYL
NIDPRDIDPG FQDL

> RXA01370 (1-351, translated) 117 residues
MGAWDDAILT EEVNVDFLDE ISELDQDIL EALEDACLIV VNQDNATEDE HLNQGAAATI
AAIMFGAPYS AQQVLENYPF IRELVGEGSE ALRGAAQVL EADVEYDLE AYLEALN

> RXA01372 (1-591, translated) 197 residues
QDTFVLPTLP TAAGLSPARI VASISTLLDL LEADPSIISD RLEHLADCID EEVESLSPER
DELVNPRGKL RAYVDHARIV HTRGTDVGLA TANVIAPIT RRLGLVSAVD FPELMESLPE
LRGPEPITDD IFHDFPIDDE PGVVPFRVAV WAEPEGPID AMAQSCDGPS KGALTQALRL
LVRGQSATTY SIEEKDL

> RXA01378 (1-1278, translated) 426 residues
HWMISPGASN PIKDRLPFWT LKVAFLSSPA ALGETVSNRL KKASAPEEKR ALETLSQLNS
AITPQTSQKY QSLLSYLGD IGVKNSDTRV VIFSERVATL HWLQENLRD LKMPNSIAIV
MHGGLPQEQ MRLVDEFKKT DSPIRIMITG DVASEGVNL TLCHNVLHYD IPWSLIRIQV
RNGRLDRYQ THNPSIVTFL LDPAESKVG EVHVLRLME REHEASHLG DAASLMGKHS

ERLEETIRE VLRGAQNFND AVADPAEVL NPAGLDDIDW LLAQIAQADA KAETEAEAEET
ENQTAPDAAS NSTQHAQRRL YQESSFLYD CLLEGFNVP EDSINRGVGV FKKHNDNIVE
LTPTDLLRRR LDLPQDYVA ARKVKEDLLL ASTLMRGQER LNAARTGEDG STWPSAHYLG
PLHPVT

> RXA01379 (1-921, translated) 307 residues
LNVEEISDH YLTNDADAKA SFSKRVRERI KEWKTTE DAT QQSGLPLTRFS SNRLQLQHAL
SELDADATTA SLVASALGYG VPSARHAQRG SDTISYSSVW NAGSVEFLA ATPAESFEEN
FRSLPLEPVA VNDKPDQITA AKLVGQIFLS DTPPAFVVIT AKGWVVLARL LTRVAGVST
IDISLVVERN DTKAQQEMQ TVVALARENT ERAADGTTWW EETIEQSRH AVKVSGLERL
AVRESIELIG NDVLTRYEAK ELSTAEIDGG ELAKQSLRYL YRILFLLFAE ASPELEILPT
GTPEYDE

> RXA01380 (1-2016, translated) 672 residues
SLILGCDTKA RLEDLYLPFK KRRKTKADIA REAGLEGLVD KLIDAPSLDA AAQAAAFTE
GFEDSKKVLG GARAILIDRF ALDADLVGEV REQMYRAGSM AASVVAGKEQ EGAKFKDYFE
FSEFPDKLPS HRILALLRGE NEGVLSLND AGDDIIEGL IADRFSLDTH TSSWLAEAVR
WGWRTKLIVS SGLDVRMLK EKAEEGALDV FATNLRDVLL AAPAGQRSTI GLDPGRFNGV
KVAVVDSTGK DVATTIVYPH QPQNRWKEAV SELANLCATH GVELMAIGN TASRETEKLA
GEVADMIKAA GGTAPTPVVV SESGASVYSA SPIAAEEFDP MDVSLRGAVS IARRLQDPLA
ELVKIEPKAI GVGQYQHDVN QVALAKTLDG VVEDAVNAV VNLNTASAPL LTRVAGVST
LANNIVAYRN ENGGFSSRKE LNKVPLRGP AFQCGAGFLR ISGSTDPLDA SAVHPEAYPV
VRNIATKATG DVSLGLIGNA VLTCLKPADF ADERFCIPTV TDIIAELDKP GRDPRPEFTK
ASFKEGVEKI SDLTPGMILE GTVTNVAAF AFVDVGVHRR GLVHVSAMSD KFIISNPEHV
RSGEVVKVYV MEVDVDRKRI GLSLRLTDEP GAPAPQKRG NPAKQQRAPQ KQSAKPATGS
MADALLRAGL GG

> RXA01383 (1-1143, translated) 381 residues
MNLHSLERQ ISSGTISERK TWIFPTAARS FNQNLVHPQS IEIDAQTGVI LAMENRLQRT
EVESVEYPTD LFNPAWTGPA ISWPLKDPSI DFPDPLPHSI SELPQSDNP RHLRVSISLD
AVEGAFFPRY IGDSIRIPLV FARDTPFMSG LETTRRAWIE AATEMDIHNT WPIILTDGWN
TALSHSKPKI RHEAELKGWF FHSFLGSEMP LTLDKIERIY GGLGTFDSGA TRWELTDTD
DAYTENGSWL LEVIVDATLD GAIPPLPQO QFEASITHIV DEQLVWLQGM LPVLRCDWLE
TGKYLQGYTV PISVSHSSRL QFSEGLIHDY ENAWSLNPV RMLAEQPQVI EPVIELDVPA
PWELQESFPD GLYFLTDGKQ T

> RXA01384 (1-1716, translated) 572 residues
MRSLSQSVLD LTSKSKVATK IVVERIEKHP VHGLGMMYFP FPFHWTAST LTIERNGTSR
RASQNGVAVL HQHEQVQITG LASFYIDSKI WVNELAGLDR INISESEVAG RDVLVLPLSD
LTLSDIDAKY LTVLAEDSDS SVRAVSVEFL DQWVDEEPP AEEVPKYTET REELPPELIP
PAPSGNRNLR VLCTWGAMEG IPEWKPGDQ VSLFLSFDLD DPFPEQLKTT RRGYTEPGEI
YGNQSRKYFH ADGNWAVISA KVLPLTEENL TGYTHSSYA DTSRRTSAVI TAVYRHGKDA
IIDVTLGDGK PPRYQESLDW SSTSTCDGET IWLSDKSLVF VRGFNVSTGK LVHEISITPF
NEIALESNGR ARAAKKLWEL PDLKEATDPV PAIPAGWKHL KRFKGNFHV SADNPTWKQT
ILRIKPKFAI ELDLGYAKIS TIYQYGERIY LRSDLHQITF NQDLEILSV EHGNDPAGYV
PLSLLPFGDS PTLGFPIGSL MMFHEQQDIY AFHDPKTTKQ LTTVNLPRKQ FEVEYASQNR
IVISLKNPES RLIDKLLVWE PQTWRREQNL ES

> RXA01390 (1-657, translated) 219 residues
MFRRSLPSNK TSSASSASSA DTSYSVRLGR PEEPGYQPEF SYSEFYTSDS FAPAGAAAAA
AAVAPPIMAE QPQIVEDARR GTLDFGLLII RAVIGYVLIV RGVFTFPTLG GSAGLAGLEA
EPAGQWPEI LAILLPSIEL AAGVFLLLGL MTPVAAAVAT VATSFPTTLHQ VNTHEGGWGE
LSEPLMLALI LTIIVVGLQF TGPGKISLDS GRGQSVHW

> RXA01391 (1-690, translated) 230 residues
VAAVAFPAAYV IDGGVEEASG TPTSSESSVA ATAPASSET AAERYAMLAS LDVKGRAFGT
GYDRELFGPA WDTVSVSEYG HNGCDTRNDI LQRDLDDIQL REGTKDCIVT SGLLSDPFSG
ELIDFVGER SGDVQIDHLV PLHDAWVKA QQWDEQTRKN FANDPNLLA VKGTLNQKQG
AGDAATWLPP NTAFCRDYAK KIITVKDRYN VVVTEAEASA LERQLDTCAA

> RXA01396 (1-258, translated) 86 residues

LKAFNTNFAA TLATGKVGDI TTTVLVAGDD EDAKNALITD VNAGGLDALD AGSLKRAHEL
EAVGFLQLTL AGSEKIGWTG GFLVK

> RXA01397 (1-420, translated) 140 residues
VFMIKELLNK LFGNKKASPA MTQSETISHK ENNTMTTYTI FGRGNMGTAI AGVLTKGGAT
VEHIGSADSD IATINGDVVI LAVPYPAVES IASHKDALA GKTVIDITNP LNFETFDLSLV
VPVGSSTAAE IQAQLQPPAF

> RXA01400 (1-1500, translated) 500 residues
MAISVSMFKA ISRELERAW LEVIERHGTI RTVFSTGMGG EVQQRHIDVG PGKWIDHAVA
PGESINEALNK AVLNRQCSPY SRPSSHLCII DAHPRTVII GSDHSHVDMW SMLVIVRDLL
AALDMELPVE PPLAFESHTA ELLAAPPAPPE RIHQWRREIL EAGGGKMPQF PLPLGDAISM
PERVEVRDIF GVNGLAIFYA RARAQQVSSL ALTISVMADV TAALADLPLR AVFPVHSRFD
QRWHDSSVGWF ISNSVIEVPD SDPHTAAQAV REAVSLGSYP LAELLEPGWGG MPETPGMFAT
SWLDLRRLPV SIDDIGLQAO YVSASLRDGD VMLWFLDRS GAHLRCRYPD SLVARENVGR
WIDAIVAQMR AEAGTVNLQA GGEQLTLRHG TRADISEIAP LLARNAADPC ELVDLEHALD
LLTHESSHFL AVVRNARGKI IAAMQLTIVP EFSRGGALHL HIEGPFTIPE YRTDLDKKKL
RAWAVEHGRA RGKVKEEVVG

> RXA01401 (1-261, translated) 87 residues
MNSPLQHSAP FVPGAQSLTS YSDEHGQAVI QLHGLTSSRQ RDRLDLDDLGL RGLSGTRLLR
YDARGHGTST GRAASTDYQW DTLAGDL

> RXA01402 (1-474, translated) 158 residues
MGCAITLLKAA VLNPDPRFSGF TLMPLPTAWE SRKAQASEYL SRAEFLETHG MDAFLNAEKL
HAQPPATVGT PDTVPDISAE LLPWAYRGAA QSDLPSSKKEI AKITAPTTLI SWTDDPGHPV
STAIELTRLM PNAQLRIATT PAEVARWPQH LRDDLQLD

> RXA01403 (1-414, translated) 138 residues
PITYIDGHPY VDGAVGETGG LMLQPAIDAG FTRFFVIASR PRDYWRKEIG RPFGIKAALR
RFPTIADLTI ARPALYNSVK QQILDLKEKQ SAYVFFADNM NIQNTTEINK KLRASFDAGM
QQTRKDWPEI MSFELNQR

> RXA01405 (1-456, translated) 152 residues
MSKIVDLRYG TRRSSELSKR SAEVFDAEAE HPITVTRRDG EALVMSQRE ADGRARLLEL
AAQLITVATD HOGTLAERMA KVFPWMLALS VADREACARE ILDAARASFA TEQPHLALTE
LTSWKETAAA VAAGLSNTDL QWYDDPHLVE RP

> RXA01409 (1-816, translated) 272 residues
DFPDVTIARL YEYMLQTPHV DFGPFFRHFK ADDDLVAALK KRAKDAGVTI PALLPVQRIS
WPEETQVRVAA VRNIKRIIQL AVDLVDITLN TEFSGRPRS EDESEDAFYRS MEELLPLEK
EGIKFNIDPH PDDFVENGIE AWRVIRGLNS KQGVFVYVAP HSFHMGDQAE AILPAVGDRIL
GAVYLDSTFD HHKSHGLRYI TNPPGNVAVR HQHLKIGDGD VNEEFIFSLR RSYGYLDRED
ALLVSNVFAE DEAADEVSRV QLEKIRSLIE NA

> RXA01413 (1-600, translated) 200 residues
LTHLFLELDE RLVLGVQQDG YQWTEHLFRL PLQHLRNSPN DLQGLKIRWC ELYSTTGKDK
GVLELLPQATV VTPNNFEAST LSGLEKLETV EDLKEAARLI YEQGPQYVVV KGGMDPFGEN
AVDVLFDGSS YHVFEPIKIG EERVSGAVCT FAAVITAEAL KGAEVDPVA TAKRVVTRAV
QDAVASNAFF TSVWLAEDNK

> RXA01414 (1-507, translated) 169 residues
MAVFDFFPNPV NEYAARCTAG LVVLLSAATL FASGDLRIIL ASILTFGFAL RVAGGPRYSP
FGRLSVHVVLV PLLKKAPILT PGPPKRFAQT IGLGFSGSTL ILMAFGFNVA ASVVLVMLIA
AATLESVFEG CLGCKGFGKL MRYGVIPEDV CEQCFQKESS RTGWLVLSLK

> RXA01417 (1-597, translated) 199 residues
MTDKFDRVLA VEVCIQEWID EQNLTELEVPL MIARLQLRDV AKDITAVHEE KEYDLTDIDT
DAFVKNIKLG WNERLIKKS LFPQDPVHKQH FTETEHGIDA TVTVVSKGPD PESGPDFLVS
YVDGLWSADI RNRITKQNR EIVSKFYFTP EHIKEDGDFS AEIIFINRPN DDDSQDLVEV
WTDQDTRYCG EMIIYFKWL

> RXA01421 (1-387, translated) 129 residues
MTSKSISGKR PNLPSLTGAR WLAALAVYFL HALVFLSVYP FQQSELFATI HKFVPMQLGS
AGVTFFFLLS GFLIYWSNSQ LKGMKNVLYY CKRRITKIYP MHLIALPMFI EASAKFTTTG
ITWVLIILRE

> RXA01422 (1-783, translated) 261 residues
EGDSHTSGTN AFFRTDERGC LKGANNWADQ LQSQLGLGAG DLIDVSCSGA SINSDFHFHS
DEVVRHAEARG AIGPNTTDIF VOLGKNDQWG LSNVNLQSV QTCLTDVFAG CGDAAVAAGK
MQDPNAVTAE NYAERMKPMI DYLYKYAPNA EITLVGYQEY TARSGSQVCV RLGGTPLVKV
DAFALVGFMM KLDMAIDGAA GILGVSHVDL RSATEGHDSG SNDPFWNVGF DARAEIVGGP
WHPSVKGDSV TAGILDRDVRN A

> RXA01425 (1-885, translated) 295 residues
VLSPDSGITW ALSIMFLTFT VRMVLVKPMV NTMRSQRKMQ DMAPKMQAIR EKYKNDQQKM
MEETRKLQKE VGVNPAGCL PMLVQIPVFL GLFHVLRFSN RTGSGVGQLE MTVEQNANTP
NYIFGVDEQV SFLRADLFGA PLSSYITMPA DAFDAFLGLD VSRNLIALVA APMILIIVVA
THMNRSLSVN RQEARKAAGK QQAASSDQMA MQQMNMNM LWFMPTILF TGIWITIGLL
VYMMNNNVMT FFQQRIFYAK MDAAEEAEEE EKRAAKRTTA EKPVGKPNP KKRKK

> RXA01429 (1-618, translated) 206 residues
MLQASLFFPV QEHIDPLHPQ ARKSVFWEIA PVAAKADPV FEKEAWLSTT LLEYESCGFN
IGYRNGTPAL ASVIFCERDA APGAKALPTA PVSSDAIIS SLFIDEVFRG TGMESALLDA
SLMELIRRDY PAVEAFGYRS ENTEADAIAA RRLEIGLIIDV EALESAGFEV VADHPVLPRL
RMELPPATVL LTAKDQRL QEMGAI

> RXA01434 (1-366, translated) 122 residues
VTDGNTSTAW TSTGGDGLLV DLSTPARLDR VIITTTGSD SNVTSTVKIY AFNDASPHSL
SEGIEIGTVD YSGRSLSHSI RDSSKLPQGV ESVVILVDEV RSSQTSDTNP MQQIAEVQLV
GW

> RXA01439 (1-546, translated) 182 residues
MTRYFAVSNL QELGSLEVHK LYKLVRDIFV HEQQTYPYAEI DDTDAAPTNN HILVWERADA
TPTNLIGCAR LAPITAEELK AYTGGKISLD DATPLSQLGR VAVAQEGRS GLSGELMRNA
LRLAEQYQPD RDVVLTAQKP LVDFYAEYGF EVLGEEYLD GVPHLPMLLK ADELERFSDL
DA

> RXA01440 (1-1008, translated) 336 residues
MKTKLWLAIP FVALAVVACS DTQPPVTETV TETAPQPTSE TAAQQPQPTT PAETTTQAAE
GINLTPRYTR QNVGHFSSGY PQGVSVFSSA DGTICEFRP MEQDAPINRE PSTDWRLSFV
QGACQFDDGY VVADTNVENR PGFAEYTTAI SHVMPENYTT LPPGTYIDLH TMACFESAD
EISCKIYATN ETFRISAQGF EMLSNAQRDA ELTTQGGGLYQ AFSNIAELRF SDGNAMSCFF
DAPGSQDFWC QTLSTPGWDD GSNLIHLTVT GGKLSLMGTQ VGNPGLDYFR GRQLIEAPNS
LLDASLSVTL DGDVRFRFTA TGEEMVSSS DYGLGV

> RXA01441 (1-1029, translated) 343 residues
MARTTTAAHV LMALSSVGLL MLQACSEQEQ TPEQTAPPTL TSQAPETPQA STTSSASSTA
TPIATPIAAT ELDYLHIDPA TYDIGVQDQE TAVFTTGDGI TAQCFEATP GETSYQIKEF
DFDETAGTCA FGDQHSIVTT DENVRERFAE LSETEELPE AQATLDVGMV VHLGHMGCWA
PSVSEFSCLD FASNAQFTMN EQGFHELDPA KATEQLINSQ GOVQTLISMT NFOFTDGTST
TCVSELQAAE FLCHNSGPGG WSTSAGPANT LWWNLQADS EFEGARPTNP TQSVYKSSQI
FGPGSYLLAN GVSAEFGDGT LTLTTPQGNQ YWANTHDFAA GTH

> RXA01445 (1-993, translated) 331 residues
MIPLINVRFP VAALPLALVA TWVNLAWADH LLLTGFIVYL AVEYATSRGR FALALILGVE
WLIAYGVAL ERPLEAKDSP SLITEILLIL VAAGTGAGRW KILSERKQRA ITQEEIIKKI
RTDIAHYLHD SMARSLAIMI VQSKLTELPE DPKKIQEKLN SIAKIQGEAV ADLHQLVRHL
VVEESAEEKAT AFGAAVAVSI HDTVNSAIQL LVDAGHVVSF DSRKKNYKLD HIAQTAFLA
FNEAVCNIAK HSPPKANVTI RITEKAQSLQ LLVMNPIGW HANGESAIPG VGTGVESLTR
RIRNIKQVQC VTSLQGYWKV VISLPLKCED S

> RXA01447 (1-849, translated) 283 residues
 MRLLVLRCA PHINEFPALS TSVEIHDLPA VPTRKDLKIL DDVAFVDVLQP DPTPSLDEIA
 KQPDFVHLLS PKFAPQQPET RLRIVVIGSD AALSAVLTRL MRADNLWAEI GFVPVGPSTA
 AKNWGLPADE AAALALALTG LVNPAPLIRD DVAVAVAGSA TITNWPGCEI TGEVIVDDHV
 LIRHEAASKA PRRGVYGARL VPMLDAPGIA AVIMDTPLPG EVPSRSLFPR PSGSVIPESF
 STGRAMQAGG PSLQIRVDGI SRKRKVERVT FYRHLRLDQI VRP

> RXA01448 (1-780, translated) 260 residues
 MAIGGILLAT MFPPGDGGSI DRMIDAFIGG GVGILVIAL PSSPLDAGRH QVANVLGIAA
 SVLEDOVAASL KAKDAALKNN ALEALRRSQA SVNKLETAAS SGKEATTVSP FLWGRDRAVR
 SLYRILAPVD NVIRNARVLA RRAVVLTEON DTVSDEQIHV IEEIADIALR LSDLYEHKHE
 ISEALEIPEL VNRLRQLGSE VGEDIAEDRV LSAQVILAQS RSIIVDLLQI CGMSRESAVA
 VLVPTESESPA YPPELWDDED

> RXA01452 (1-279, translated) 93 residues
 VIRSFADRDIT ELVWLREGAK RVDPRHKVA NRKLHLLDAA TTLDALRVTP GNRLETLEGD
 RVGQYSIRVN DQWRICFRWN DSGPENVEIV DYH

> RXA01456 (1-522, translated) 174 residues
 MNDSIFSPQA LNKAMLEAVE FIHAEGWDAG PTLFALVPTE MLVDTLDEAA DDSPLTLVVQ
 DNLPDNLPLG SEALGDYVSR LAWPAELIAGA VLAQEIMFTD AAVAGSEPRP ARLFSGVLRG
 EAELFTLLQLR PTEELAERG PFAEDEIELR GPGVAVPGVI AALRYTLEAD PDEI

> RXA01457 (1-675, translated) 225 residues
 VASTPHKHVR VALGLVALIP LLAACGGGGS TETSTESTAE TTPATTEAT TTPATTASSS
 VIETTESSTA ETSKESGET STSKPRMTKD VEVAYKAFSS LAPVELFEQF ETCDDSPGVED
 SFACNGPEVG PQQFFDNASK ATSTTQLLTE LRSSRVVEDS GSKVVGWTTI GTMSIITVVD
 NDQGLVLQQM VSSDKIDPEE RIYELGLSTP KDTEESSEET SAKNN

> RXA01459 (1-810, translated) 270 residues
 MNSNGFGFSF GNNDDDDDDKN RNNDPFGLFG GNFPGGGQGG AGGPGGLGDI LNQFGQMLSG
 MGDSMNSPEA AGPVNYDLAA RIARQQIGRV APVKDSEREA VEESLRALAE WLDNATQLPT
 SGHRVEAWNPN ENWLENTLPV WKRLVSPVAE QMKNQALENL PEEAREMMGP MSSLMNSMSS
 MNFGVQLGNA LGDLAKQTLT GSDFGLPISP VGVSAPVLPN IAEASKGLNV APQEMLVYIC
 AREAANAASS STCRGLSSAS FPPLRNTPSA

> RXA01460 (1-294, translated) 98 residues
 VPWLVERLVS SVEEYAVGLE IDTSHIQEAM GNFQMDNPD P ERLQEMMNEL QGMDLSPRIG
 SRNANAVSRL ETLLALVEGW VDIIVVTQALS ERIPSPTP

> RXA01463 (1-1164, translated) 388 residues
 MEMSYFSHQD FNNPESHINF TMAQMEIQRW TLLISNPEAD ASTLVMEKLT VTGESKHFIN
 QAINAMMAL KPLILRVVVE THFHVRIPLY ARIMQAVKQA KPELDWELDH RIAEKLTPRI
 AGQALMEASA IAGLITRWIK ELDPTFTGKK RGPKSGDGLT TFRHVDGRTY ISGNIDGVTV
 KLFQKALEKV KQKGEDLARA LVTFLAGRTK VKIVSAVYTP LVGGVSWIPG VGFLSQEESR
 KLGKTSKVI DLDTIATRVE NGYTSPSELR LYVMGRDGTG RHPGCTVSAD NCQIDHVPF
 GEGGLTVAWN LQCLCAHHNN MKTDGRIQAA IDSMGRVAWI GPCNRTVVTE PVGPLAQEMP
 TGQWQGTLEA RMEKTFEKLK SSLEVLDD

> RXA01469 (1-1032, translated) 344 residues
 MAFADIVRSV ENRTNAATLN WSIKNGWKEP VTGFSGYGSG RRVRLVARLV MSNPENLLVD
 APSQSITQQA QRGWRQFFTI QVFNLPVTVT VGGKTVTSST NDNGYVDLLV EDHNLDPGWH
 TIQIQAEGST PAEARVLIVE NTAIGLISD IDDTIMVTLW PRALLAAMNS WVLHNTNRKP
 VPGMNRFYEE LLKDHDPADP FYLSTGAWNT FETLQEFINK HALPDGPMML TDWGPPTPTGL
 FRSGQEHKKV QLRNLFIIEY DMKWILVGGD GQHDPITYGE AVEEHNPRIA GVAIRELSPG
 EHVLSHGTTA SLSTITTING QGVVPHGRD GYELLQRYET KPFA

> RXA01470 (1-426, translated) 142 residues
 MTNNALTVPT RTRHQADLLT ADWFEDMGLP QLKTTIEESI DDVALPMHTA VLEISGMPKE
 LRQTVESAMV VCIPSPSELS GSNRDPPLTAR WFTAWRRDP ELGLTECREV ITGTPRELKD
 LRGVLESAD EYRFEVELRI VD

> RXA01471 (1-807, translated) 269 residues
 MQSFKTLSEW PVDNVSASVI SDGAVHFYGD VDRVFELMSV TKLLATYGFL VAIEEGVFEL
 DSPMPGEGST VRHLLSHASG VAFDKPVAEK VGGERRIYSS AGMDILADAV AAEAMPFPAE
 YLREAVFEPL GMENSELWGS AGHEARSTVA DLTKFGQELT APTLISPETL AEAFVQVFPE
 LIGTVPGYGM QKPCPWGLGF EIKGQKSPHW TGDLMPPENTA GHFGQSGTFF WTVPGSGQVG
 VVLTRDRNEFP WAKPLWTAEN DEVWAEELNS

> RXA01472 (1-456, translated) 152 residues
 MNQANLPAEI ADLSDETALW EIINEYNWDD GFAVPLAVVR HPKCDRALAL RLFWDIDETA
 QIHSDEESA IAEIYASTAE NDPAEFDRIM DYCTTLVEGL RKQTYPRGAN RFDTGFFNLE
 DPSLTDQRK TRACKTKFAL KNFEEAFLQP EL

> RXA01473 (1-765, translated) 255 residues
 MTDIGDVDQI VWEFIHFHDD SINPFFFEFIK SDCINDEAIE RKTQILGIIL GNEPCGSGVIH
 ARQNTIKPMS HTVSFGDGWI QVLEDAEATV SITDITDLALR FSPEQAENAW EFGPLLCCGPA
 NQPPAYLTAL DGHTKLPLSP QLTEFYSYAR SWTNSEALGN VIDPDYLDH LTDPRLLHQD
 LLDNEFERVG VLVDKQNRPL DPARCALFSL DALARAPYNR AYFVFAAPEP EIWAFENEHV
 HAPDLRLAYLQ ARLST

> RXA01474 (1-546, translated) 182 residues
 LVGIAYARFP DTRDDISIRG KARSALKST GLKERFARHF PAISIPVDTG DAADILVSGW
 WLSGSKKKIL TAAEIQTLFI NRIATGPLST QLETATGLKL QVVTNRERMK ITLIEPKGTS
 GHADIPQAGK GSRGGFLLDN GQEDEYDDVD TVTIPDALNV IGYILTHGTP PQEGKWKVDVL
 ER

> RXA01475 (1-426, translated) 142 residues
 MSIQCFAGSD YSACFEPRID AWVDIRGPRK PEWLAENIDN PLRHGWDNPH IPVSAKKAG
 NIYKETLRMT RASTKTPQD PLKETLRSFI ASINQLAARK NFDIAGVRED IVVALEKLCE
 AAEASPEETQ QAIVMGEEFI ED

> RXA01476 (1-342, translated) 114 residues
 MDSDFCTVVI LNRNTATATSI LRDIKALTGY GLSEIRSRIV AGLPVVIEEM FSNAWYDERA
 QLLALALTNI QNEGITFEIR EVAEDDPIEA GALISLEVRN NIIEPDNDNES RDGI

> RXA01479 (1-228, translated) 76 residues
 VIGAAAGYVL GTKAGRKRHY QIKKGEEAAI NSPATKSAVN AARKAIANKL DPQPRMKEVK
 NLRTADGHEV LEQQDQ

> RXA01484 (1-546, translated) 182 residues
 VLGTAAQYDGV PSRQFAARLR HAAKLWLRLHE IQHVYTVGGK LPGADEFTEAE VAREYLIKEG
 VDPDLIFVSA VGNDTVSSYE ALDPEKLGRV LIVTDPNHYS RAVRIARARMG FDAKPSPTY
 SPAKFPSPIVY FLTISHEWGG VVVDQVSRLL GERVPDKVKH LCAQSAVCCA LRGVHAMSNF
 GG

> RXA01485 (1-2052, translated) 684 residues
 MNFSLVHLRE NVRRVSVTV A IGAGALLISG PFFTAHTAEA TETYVLAESP EYQDNVTDY
 TQGISSDIT NIQAIAIDVK ASEQKVFV FLSSFDGVDP ETWTQALQA NGGGNVLIIYA
 LAPEREQYGI QGGTQWTDAE LDAANNAAPF ALSQEDWAGS ALALAESVGS SSSSSGSSS
 SSDFSGAWLA AAGVGTVAAG GGIWAYSRSR KKKTSAAITL DAREIDPRDT NRIMLQPMET
 LEHLAQEELT STDDSIIRRG EELAIATSEF GPERTSRFNR AMNHSTGTQL KAFEIQRLN
 DSIPESAEER QSMVLVILSS CGQADALDA EAQNFADMR LLINAGSKLD LATQKSVOLR
 TRLPKAQETL AGLRTRYSAE VLESIDNDV LASASLDEAE EVLPQAYEIE SMPAGEQGGL
 IDAIRHTEHA ITTADKLLAG VEHADENIST AKANVADLIQ EISDEINEAG QLKQSAGADG
 ARADWASLDD AVRAASAALI TASADAKEPD LGTYTELVDV DSALDTQLDT LRATADQAR
 QLRVFDQQLQ SARSOIQKAE DLISTRGRIV KSEARTHLAN AQKLYAMAQQ NRTDRTRAGI
 DYGRQAATAV QRASKSQND ITTNNRHNS GGGTTGAIVT GMVINILNS GRGGGFCGGG
 GFGGGGGGFR GGRF

> RXA01488 (1-831, translated) 277 residues
 VLLETGAVND LALLDLFGAP EVPVYLGEPH AQTKDGFVFL EISAFIHGQN GIGEVLPAS

ESKALPGAVD FLIDSVNTHG DDLVIIATGP MTNLSAAIAK DPSFASKAHV VIMGALTVP
 GNVSTWAEAN INQDPDAAND LFRSGADVDM IGLDVLQTL LTKKHTAQWR ELGTPAAIAL
 ADMTYYIKA YETTAPHLGG CGLHDLPLAVG VAVDPSLVTL LPINLKVDIE GETRGRITGD
 EVRLNDPVRT SRAAVAVDVD RFLSEFMTRI GRVAAQQ

> RXA01492 (1-804, translated) 268 residues
 VTTTLWAEAN LHAAVKANAD PIENIQPKDP SDWLIVAGDV AERTELVLIEI LARLRRRFKAK
 VIVWPGNHLE FSRADRYQG RDKYSELVEG CRKIDVLTP EDPYLTFGGVV IVPLFTLYDY
 SFRFPGETVE QAVQAARDQ VMMTDEFSA PFVDIRAWCW DRLAYSIKRL SKINGPTILI
 NHWPLVVEPT YQMRWQELAL WCGTRHTRGW AERYNAEAVI YGHLHMPGIT NVNGVKHIEV
 SLGYPREWEH WSGQHWPYP VMEVDNAG

> RXA01494 (1-996, translated) 332 residues
 VTDNSQFHAA SALVQAAHTV SVVGHLPDPA DAIGSVAATV AALQQLGKDA VGAIGQLDSM
 PENLYTIPGA SNIKFGDSL P ESDLIIVVDC GSIERTGAFE SIIVNNPKV LVVDHHAATNP
 GFGAVNLIDV EAESTTTILY DWFDMASVQI TPDIAGHLA GLITDTGCFR WGRPMVMDMA
 KELMEFGLDI RAISSALLDQ TSVDLRLVG QIVSRIELRE AGPYTLAVLV ADPDTINGRS
 RAVVEGLIEM VRAVEGADFG AVFKEYERG YTVSLRSSNL SVASLAVHLG GGGHIPAAGY
 TARGTEIAL DTLTEATVTL GESLRSSAHV DV

> RXA01497 (1-918, translated) 306 residues
 MVGKLPIMAE TNENDLPVID LAQIEGYVDV DSEDDPVL RPDGTPPIETW REDFPYEERV
 TREDYEVKVR SLQTELLKWO NWTKETGQRH IILFEGRDAA GKGGTIKREN EHLNPRGAT
 VALEKPSPRE STSNWYFQYI QHFFAAGEIV FDRSNWYNS GVERVMGFCT ESQHAFLRE
 VPMLNMLIG SGISLTKFWF SVTRKEQRTR FAIRQVDVPR QWKLSPMDLA SLDRWDDYTR
 AKEEGFRTYD TDESPWITIK SNDKKRARIN AMRYVLSKFD YTDKDYELVG EPDPKVVLRG
 RDQIGD

> RXA01501 (1-288, translated) 96 residues
 MKEVAVNEVP AGAQLIDVRE TDEYAEVRAQ GAVNIPMSEF VGRIDEIDLD RDIYVICKLG
 GRSQAQVAEYL EQRGIEAINV NGGTGWVAA GLPTEA

> RXA01504 (1-609, translated) 203 residues
 MNITWLILAG VLAIIAVVFF YLSAQKKKSE PQPPRQRQDP LKFADGSDTF NARILGPGAI
 ISRGGVYVC RGAIQFQQQ YIWHYLLDG KKGSEYLSVE YDEGQLNLWG WITRPDLAQI
 PAHDVTVGVG RYRKTESGVG TFTSEGTGV ADQGEFEYWD LAEVBGNRLI SPERYGKDSP
 FEVSLGWTVL PGLTVVPAP EAS

> RXA01505 (1-498, translated) 166 residues
 MIHKLDCMPT DVSAEALGVS WNGESPEVLV DKLIDASHPH STCHLAVIGG SHVTVVETPD
 GRFREIEISCH AQEAEDSRWP LPDSITRENY LLQTNVAVLS EEDFARAAGE ISNGDDDLWI
 ASFPGAGEHH LTALTAEFFE DVWEWFSHHL YPEELTIVST RSIYKP

> RXA01506 (1-411, translated) 137 residues
 MSSRNYRSIG FILLFLAVLC LFAAVFAKPA VGSQVSDRWP GNNGTYSCAG ESGVDEIVN
 MSTPTDRDGT PATGDTYLRV SKNLIIISGE GTPLECTIVE GLDRVNSGAF IWLGGGFGPS
 SPSSSSGGSS GSGGGVK

> RXA01507 (1-423, translated) 141 residues
 MGQYLVGVGL GTLSYFVLAA VILVVGFEVL DLITPGKLHE LVEVHHLPNA AVITVAQQVS
 IGIIIVTAVL TSSDILSEGL LETAVFGALG LVLQVVVMVAV LEAVIPGRF DLVDEPKLRS
 GAVVAIVILI VVGTVNAACL I

> RXA01518 (1-474, translated) 158 residues
 VAFMQKTSAG WLIATGGFLA AVSAIITWRV YGSMTSISIT VSITFWLLAV VCGFAGVKVQ
 GRLDEGLIG DKSQMNPTVI AYLAAMLGRAC AWGGAIFGGV YVGIGSYVIP RAGELSAASN
 DLPGVIAICAL GGIALSAGL YLERSCEAPP PQSGEALS

> RXA01519 (1-747, translated) 249 residues
 MNQDLSHEDS GDGNSVDVRGQ ILLAVLIGLA LIASVIMLLA NSDGAMKIAL LAALWAAIIG
 FFLVYRSRQK VEAAAREKET LEYAHQSELN RLEAELVQEK MEISESRRAR DQETLEEIKL

QLEEMRTQLS ELSGREWGYE PTMLRAEARR ILELESQQLS QQFQAPQPEV PEPVAVPEPM
PEPAPVPEPV PEPPEVEVAV EAEPEAPGR RRRRHAPEE TGGRRRKDER QGGLSVADLL
AARCKENN

> RXA01520 (1-384, translated) 128 residues
VASALDELGE TIVGLLVGEL GGSIVEIADD KRAQLAAALT YAGFLSTLQR DASYFLDEFL
GDPDVTSIIV MDSAQQFQAL PSLDEVIAQY DSINNPGRQR LFRDLARRQA EISRAQDIEL
WAIQKEDR

> RXA01523 (1-951, translated) 317 residues
MKNWQEEFQL VNLTKLLHSD TETSAAISNG QMIKLTHEVA INAEKYSRLP AWDKAAARAF
AVGMTVDKAV VAGQSAARLW GYQTLTVEKT VILCLPERLR SKSKSHWPSSG MRYKDRYLS
RDIREVHGIR VTGAFRTFLD IALDDGVVAA VVTIDSARRQ NPSTREKLM HSAESFPFRRH
GVKAYRQAEI LSIPNSDSAQ ETRARLILRE AKLPEIQSVK VQARFVDSHN KYFLVDNFLN
EWIIVEIDGR SKYDSPELNE VIMAERDREK FFLNQGYAVL RIDPKQLDLN QDGECEFIGI
LKNTLQKTPP EHLKQAA

> RXA01525 (1-1722, translated) 574 residues
MRSFQSILDL VNSASEVATK IVLKRFEKRI TSETDWVPYQ RFSLWSVSGP LTIERKGPDV
RVSKONTAVL QRYQRPEAEG LISYFMDPKP WITELAGLNL DDVSEDIVAG RTVLVVPVSLN
VILSDAEFIS MILTAENDIE KIHAISELL EKWRS SHYPE PHFPAVLEPP ASTGNRNLRV
LCPEFISFV NVGDOVLFLF TFDQTLPPVD QLETRRGYT DPIQLDYDHR QYRFHADGWD
AIISTVEPLH DEEELTYGFL HRLDPDSAYP TIAVVTAAHY HGTDAIDVT LDGVHPKPNQ
ETLEGISTST SGGDIFWLSL ESLPFVRGFS VSTGELLHEI SIPTFQEIVL DSANRVRVKQ
KQWPHDFSDC KGKTWELEPD KEVFEAVPSI PAGWRLLDSF GKNLHNVTRE NPLRNLFWL
QTLRLKFFK AVDDLIGRSI ITAIYPYGDRI IYLRASNHHI TFNQDLEILN VEVFGDPEVP
ESGLLYLPPG DSPTLGFPTG TLMMEHEQEG TYAFHDPETT EQITTVNLDR NFSFVAYSSR
TKIVISLKNP ESRPTNKLIV WEPQTGWREQ NLER

> RXA01527 (1-2511, translated) 837 residues
VIPNPNPNPK AKTLRLVSAL TAITVVGFS A SPVHALPIPL DPSPDPAVSEL WVNPNARADD
ELSGVDVEIS DTFMPSNLT VQVGSFKAQ VRVTNRSSST LSNITLQARR AEASFDMASA
RVAAATDNNY YFGAMVTLDD ELEPGESVET EVEISTDSLS ISQPGSYPTM LALSGQLDGV
AQHLDSQRLF PLVLSDDTDT EDTATPTTMI YPISAQTNVL GGEGTAEASE PLLVSSDAL
AGELDEGGRL QKLIDAYLQS SPAVQQAATCL AIDPQLLDVV DRMTGGYTVT DTRPSTVRQN
QRLRELWTAD NQPTNGVAGT GAENAAIFLE KLRQATATSC TVALPWANAD LNAVSGTGNQ
WLMREALQRG VTTFEEVLGV IPESNVVIPG NGFVEPSTVG DLGWAETVLR PDQAWEVQSE
ELVAALQRT QSALDNPKPT PGTVTPTPTM STVSVLVSDN TVWRITTSADR FHSALPGITG
VSYQGSALT LATLQONPET VGYSNPDSRY DYAMDSERAR NLTQQAALRL TVDNGDSDP
VLIMPSAVL AEDGAMLLT TGALLADGSA RFFSLQYQV ANAEQRNTLA TATTPPDSTA
FGAPYDDPAS LTETEILRTT QQAEEIDDLT GIMSNDPSIA LTRYGTAFEL QRLLRALS
SERRSLARHT QATSADKLL NNRDITLQKL RSSVALLPPG NVYTRTSESS PLILVAAQNL
PLPAETQLY SGNQDAHINT PGVVRIPAQG TILQMTADL PDDNLRDQT LPLASDGAT
ISEPVEITVQ PRPNLGTTLF FVAAGILAVG GLLFIRKKRN VEKRSPTGTS PKPPPTTH

> RXA01536 (1-1242, translated) 414 residues
MAFGFFSRRK KKNKDKNFNE NSAVPAHSED SPQEVFEGNG RQVGDPIEQ VDRDAKGRLT
AADFLPADL PQLNRSRANM LRRELEYRFS LQNAHINIDG NTAMIQRS DGAAHVSLRTL
AMNAAGLDF DQLEPLVESF VHGTLADATL NDLSTADLYK ALRLRLPTF EGDDDLVEHG
LDRESQIRDD SILRTFTSDM SIALVLDTEH AIRIQPLKEL EEFDDLSALE RAADRNTWQE
LYDANVDASF VDAESDSEGS SFWAFESMSY YLGSAPLFLN DLLAKWAPLD QDSGDGVIAF
PRDRLIARP VTTGEDLMNG ITAMVRIAMR PGLGNPTTSIS FRLHLLRDNO VTTSTDFRVV
SPMEAEWED SAFDAPPAGA IGIEVRPDY IMERLQGGGF GDFGDFGKPR DLDL

> RXA01539 (1-1923, translated) 641 residues
MSSSDLASII GVEQQPVAYG ESEEPETLRD VLPRRLHPS EITPSYEVAD GEQRSIFGES
APSDFDLSD VEEFDTSHWV RAGQDSDSD DRLADEAGVP PSGAQDVADN EANLSGVDEQ
LHMRVHAQS FDEIDVAKKE KKAEEKYAK PPKSDNPLYA RDAKDAARK KRNIAAHDFN
AQEMAQAAMG FLRKGVNTQT VMAACTTAAV MWCMSPRMT VNVDMKRKFN KDLEQAKDTK
LSKYVSKDFW KSKLTRDKTE KEAKSLSDAF MQQKTAIISN RERIMPPKVAS AAQTVVRLSD
QAYEAMREVD TDGQAIIVDAK DVSAQVAEDI DMVVKQGEH GLKSKDIYGA ARDIVGRME

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RDPGYAARFN  ETAFGTVRLG  EQRRGMVISK  TPTWQFPDGA  GLSKNAGWFS  VREPMGNAQN
FADNLAATLA  TEMRVAGEQY  GSDGVRDVVA  GFMTATDVSE  SGLSASAKLL  PPDFTRGRSA
SRVQRIAMAQ  RTQAAIKVLQ  DDGNQTAMTT  EQVKEVQVWA  MDQAEKVQMOR  DHPAILDKFV
RKHGQTFGQD  ADAFVKISIT  EKDTSSSEYTD  AMVRPQENRG  SGRELAARRR  VQAAQINQAA
QLDMNVHDFR  ENSLPEERPA  NPYEAYVRET  EAKTNDPQYG  Y

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> RXA01540 (1-702, translated) 234 residues
MTFAELSSSPR  TIIAFNGRAE  SGKDTAAQYL  THMHSFHRIA  FADGVRDALY  ALNPLVCVEQ
AITHTAIYID  RVATVYDTLG  WDTAKQIPDI  RALMQRIGTE  AGWRIHGEHL  WNLAIKKHIN
ELPADHAIIV  TDLRFPNEIE  WLNSLKANPM  NTIQTVKVIR  PDHESHTLAG  SFGTTTSHISE
SFNLTITDTVL  RNDGTIDDLH  SKLADFLSTS  PQVLSRNPAP  VPKHNAAPPT  TDAM

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> RXA01542 (1-5061, translated) 1687 residues
WGQKDHGKWA  PLGDHDAVRI  YRQAEALMKQ  RAANNKGLDL  NDEATYGAIM  FASFDDAFAA
DAEAHGCVHR  PQFAKVTRRN  ILNSPOYTAI  KSSYDALVQQ  DLVAQQQQAQ  ALQQAAYEQE
QAAIFQARDQ  ATFOAEQTLA  QESVRQSEGV  GLPVIDPMES  YFREYAFYEG  VEMFGTWGTH
VDAGVSQFST  SDGRAIRALV  DEHLATYEPV  EQRGSTQAFI  ASVNAAFREV  APHAAPMFSA
IAREGEGSKG  YQALRHFRKF  MVGTAIGPNG  LPEGPDLGGR  RLPISTPYDR  WMDREVVVRH
GTKLLSLDSE  SVGMIRDLDL  ATIHQLQDNV  YEGTHREDDT  KGGVRPLTQW  VNGEIAIWR
ITENDQMRLE  NIGQFMTAKE  YRAAASWLR  GLIDTADVAS  QKIDPNKVM  DEGIARSEAI
LTYLSDEGVD  FRIEFDREPG  QLKVRIEGTE  IDIRLTDTRA  NEQWGRVYVD  SGTVIKYSAE
QTAERLRAR  ERMENGOGTW  TPATDYEPS  TEVDVLVKFA  LGREVERQDG  KGLVGVPNAR
HPRALEQAQD  AYFTKNRSFA  MYREGLSIVQ  DARDSAGPG  KWFNDNEAKS  EWLGNIALT
RARVAEELG  EELTALSAQY  ADDPDFMPAF  AGEDELMAIK  QDYWAMLRGE  ETDLLNPGVN
RDDYMAAIRD  GDHEQIAAMT  SAMNAVTVED  VRQHAALVL  DDYVGTVEPD  PVTGLRFPNV
TVAQHMPASAR  SLWSNHDDII  AALRATSITG  DELRGDEFYN  DVINQQLKLF  NPETAQKMVN
NPDDLPSOLK  FGTVIAETIS  RRGADVVVIA  VDDNGVVRMT  AQRRVHGKRS  RAVDSKGGVR
GERTRHVGSE  IQQIFTRGEH  GEIVTKFNGG  ENYMFAPGTY  ASVVPQKQPE  TSLKEERTLK
KGYEQVMQEA  LYVRVREDLM  PTERSVCAT  TSINSAYKRL  VDNRFVPDFT  ERSAAEGLSD
EWRAALLETA  SLRVRYDNSI  RDGANVMEDI  RAQQRGFDAR  NDNSRDALVL  TGGRNISVLD
VDAGKGFTEF  MMTGMAANQG  SVRYLLPSAK  VGADGMITPG  DPADRVFVAA  HPESWAMGFD
PHDRQNMFFD  NIMQASAVTG  GARTAMIQLG  GWNFEDGIIV  SADFANTHVI  RPTDEMRPL
VAGDKLSDFH  GNKGVTALV  DPAMSADAR  AAGLESEVAF  FRDNPDLVV  MSPFSAISR
NGGTARELMT  NPQDVVFRNN  DGSTRVQPGA  SGDLNFIVTH  MAVDAKTNVY  DEEAVEREGQ
RKASSQLAWV  LQAQECHEIM  EHFYGNVNSA  LANFQYELRV  TGLDVTPTYG  LREGFSESNE
QRNIEMPSI  YDENGELNRR  VNRAQVREAF  VEQISRAGGV  MEIPFQLQLR  NGAQLEESP
NPDMYQLPLL  SPHLRSDEDL  ADGSTRSHEY  TTRYMAIFDT  CYKLAEQAK  IDALQEEAQ
HGTPLRAAEK  RLSSESQKFD  QAQKKVQASF  DGIANDIVAS  RIETKNNVFK  DGFMSARQSH
SATAVWGTGP  RLSVDEVAMN  SSMARELGVL  DNGYAMVWRD  PVIRDGGVRY  LRVVINDDLH
GVAVNPVSVK  SFDGDFDGS  VGLVGNLPKK  AHAEALSRLT  VEANMLDLGD  KRKMEDGTMF
YGLTLHDSLD  VQVAQHHPA  MAENMKVIVS  ELNRYQREYE  AGEISREELL  EYNRAHMDLL
NEHYAQA

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> RXA01543 (1-2766, translated) 922 residues
MSLKQATIVR  NEYTIKQANG  KSGRGSPPGK  YISGYMARD  AVEAVAPIVR  NKLDDFIMRY
MARDSAVEQL  TDSNADYDQ  QPMNSRRRG  QGRRAATLQR  RAERSARRAA  LRAVNTDSD
TTNPSQVPH  RELAEFTQD  GORVHDLMLR  LDVSLSHDD  LHAASNVPQE  RAGVNTDSD
LYENRHTVMK  VVLSFTQDYL  TAHGLIPEDL  DIKRAQDYRG  QVDQMKLMA  VMHGVDRLAQ
RHYDLYRGG  RHYDLYRGG  AHLTMDVADY  GHRAADGTQK  QIKDKPGKAI  LRRGIDAWLD
QHQAHAHLS  AVGYEKRVNT  SYVKRWAFHQ  LTQESAAQFV  VACLPEDKRL  WRASNAKEM
DKPNRLVREL  VEARLGSTDS  PMPAALSQVY  QYAQKRRVKE  GLSKQDTQRL  IDNGREKIE
QAMNGVYSVL  SAISDEQRDV  STAMLTVMRQ  YEDLLDGLIA  RKSKDLDEG  GSSGSEVKG
EPEPSEIEF  GLRLRSYSAR  LNHHRQRE  FAVKKRSWED  ANSQGLADPT  SQVMSFYDT
EQYVHAMCOS  KYQHFLTFAP  PVGQWEKQWA  EVADYGRKVR  GLRALRADRS  LRMSDERAA
EALGRQLYDQ  PGGLLARTG  AEGKAGRAVL  DGRIERMMVT  YQKIDDLRL  EWAQLGARLE
VEGDVLMSDA  ADLRESGGEG  ADERQIQOOT  IELFVADVSD  SVRTYLDEEL  RDSRDVSAHD
PVHTLRGRQF  VVFRPEHDFE  QVGGPDRLRL  HYAWFSDQKV  SQPIVCSYGE  LVTQRRYAF
RAREWMISSQ  QEPEAVAEEL  DHAGADITRM  EATSSSEVST  GILRSANLAR  IREQARQRAE
RAAEQARRE  RELVAQRQFE  IDQETTQPAF  EVVQRHVQPE  SVQIKRGRTV  ALDKRVQPLI
RDAVDRAVLD  SQLRSTRDGG  LG

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> RXA01544 (1-600, translated) 200 residues
VKLDGAMVMI EQRVLKVRGA TKTQLAPYEH IQRNIAARGL RADDGGSCFG YGDASLSNDD
VATAEDIQD LFACGHTVIS AIVVFQKSYL SEHGIMSFDP NYFGQDIYAD THEPEIDLML
RLAVMNGLLG LEGTTFEDMR YVASIEVSRS YVYAHIMMAD AGVDDARGNA QVKITDTERV
LFRRGVESRF VEQEARNVVL

> RXA01545 (1-1251, translated) 417 residues
MKLAGFNVNS PAARQVAEQG EKVQLDAPVY AVFTPDVVEV EFIGTQHEPV LHVGEAIDSV
TALSGLPYDI QKITFDSENQ QRFSGFYKFS PQQHKELIDK GLYLEGFQFP REMMTSLPWE
LPMNADVTIV APESQDAPPI VLVGLSEIHG VDFSQESSGY ELTSMFEDYR SQREAGEADK
DFSEISRAE IEGKDI FADA NRTRTGVSAAH AQRLEQERAL SAAQLMAKLA GISFQTEPVL
VGAEESDRAE QFLAHLDDT AGMSEWEREV TEFYNEKIRA QEPVVEREAQ RSDSIEDEV
AAPTYSAAEI NDVTHDLDEL EFDVVIDLDA DDVNTAEVE APASVSAEAI SATDLDFDRE
SRAKTAQREA SRRVAQKIQT QESVREAYIR EQKHGYDASP AEGRKFEDEI AERGLDL

> RXA01546 (1-696, translated) 232 residues
MARANKKKQR QLQHAHDAQ AEIAEAVAVN TVEPINARTG GWFSWVDKVV KLTGSLGGWF
AFLVFAIAVW PVAIIAAGTV VTIIGTWGVS VLPSLVISSI GASAGVLIIT TDGFLFSWVI
PVLFLMIVLA LVVMKVLNLI FGALWREFTM LRQGLYAGRE KISRDDAKRA RAEKKLTQKQ
AKEAKQKRL DAIYSAQAE ETLAQQAQSE FEESDKNRH DALNDAVAAA RN

> RXA01547 (1-663, translated) 221 residues
MFDQVKKRFF RNIVMIITALI LAVVVIIVAT STSADRHAVL KRQTGEIMAL QQRDALNSK
LEGQLQEVVV DATGGMIDIEH KAADDVAVRE FLSMALTWDS VRDYLDVREQ VMRYDLDLEE
SQFMSVFMFG EMAGIARTDP TGEVHYAYDA DLSNRFSSLE SVVTRINGTE YSYVSTVTMK
SKRSGGAEAT TSTRLAYDV IDGKIRNLEA RTVPGGVKYS G

> RXA01548 (1-1008, translated) 336 residues
MAENNGSDDD LKPTISVDGVV NGEVRSDEKE QAFEKITGDD LRRRAEQIRK RRLAKAQEDA
RRKPLFLGGL RIATVTLVAGA VFIGTTLWIS TTSGGFDKDV SANNEQIVTL RNEVNDLKN
AETMPKKTET RSDQDAATSR AONVADLQNO LAGIITSVD DAATEQFKTI VDELKPKFTV
SAGTTGEFPA AGRWYQPEV VVGDNRRPTM APMGAESGW TVTPTLSMSD TEHVVMWNEA
RLTGGERYGA LLMWNTADYN INTGVFSSLA LAHTYEGHR IGATTSPSEF GAHGTNAEAS
AARAGSEGGG LEGEAFVDE LQRALEIAQL NKQENR

>RXA01549 (1-861, translated) 287 residues
MVDNKNSSSN SPTAASEYFL REWERPADVA GNAPIRAEQA SKWYAQMGGW QKNSTLGESV
IAMADGAAAK STARDEQDAL NDCPEEDRTS GGNTSAAEAM VTISHFYLDV RNSNGDTDIY
RYIHDEVLTG DPHYASCARG VATAIRWSGT DDTFPAQPTA AQEYEVVGTG SGRWEEIGNL
ATMSENDDLP GDVLLGAPNH VAMYVSNEV VDMLGPGNAE FNAAIHGHAL NDRSPGLDTL
SLDGWGVNFK VFRNTQAETN SVFSGVQIPA GKEIGEMTNP TRTTPAG

> RXA01552 (1-978, translated) 326 residues
MYLGMKEDSL APPQNRRESH KTVFSLKQKN IPIKDAKSD QVNLTWHYD GEWFEGGAVT
DSEKQDKVET FRNLGSDVA LFLVDGQKLH DYANEERYL SYLFDGFIEN LNQIKDAILE
GGKQKQQFVT IWVIALSKAD LWPDLQVKDF ENLNNKKAGN EITALLSKLL EPTNDDEAFS
FGKDFLLLS AKPTPGHIDI SQRKGVVDLL PLACVLPMQR HLWWQELVLR PINLADIILG
NEIAQMGFKI VSKVLKNKVS GTNNKAMAAL VFELVRDMV DQPTELLQKA REEAVGRREF
LKAITAEFRF KLNQAEADQV LVRDFA

> RXA01554 (1-2142, translated) 714 residues
LKKHVTSAVT AVVTAFTAA LGLSIAVSPA VAQVANPAPD LSAPYTWVEE FDSADALKGW
NIFRPQPDYGS DKVLYTEDAL SIEDGKLITI TORHCVDEDF AISDPVNRGK LNDSTAQVEP
CAPGQFEKFT SARIVTPKIA RGEFDLSVTA TLNTGGVEGV RSAIWMQNGE QACSSATNNG
LYGELDVLVEH FSYDLRSFWS PSNTHLGCDP ESNVGNTRAP RELKLDSDI QVHTWTWST
TRDGVVEYFD DEAINRQSWR NDVTLGHAEI ODFGISAQTF DEIVDREWTL TLNQKVESAD
WAKPRSEEDF FVFRSMVIDR IEVTGSPAVS EDTEMPDITQ LLTQDTLEYL GRMPVLERYE
PASADFDAGR PSWNYPNLK ESWQNPELEG RPEAVEFVDG RMDIVTRRH LATTDDIATP
ENAEQEEPCAG GEVTRYSSAR VHLPEIPAGN FRLTVRARAQ SEELVDGVVR AIWMQNNTNF
CADNDGRFYG ELDTIEFYSS RVNTQYSAVH LGCAGNRPKM KLRQMEEMES MFGDWHDWGV
EYFDGQIVFT IDGKAVTSSG KDVFGNSVTP AAAPLEPAHF KLSEEEYREV IGQFWHLILN

TMVEQSGKDS WITAVDNNEA FPEHRFQIDH VAVDIESDSV DNVWPDAAANE IPDNVGIEDS
 DSGSLELVGS TGSSTAETVS WISLFTALSS LVFTLALNQE ALQNLINQFM RQFK

> RXA01557 (1-816, translated) 272 residues
 VRSSNPVFSS LKETQRPPQG NPYGGYDNFG GYQQNVAPQ KAERPMTVDD VITKTGITLA
 VVIIVFALVTF GVWLVSPLGL MILTLVGAIG GFITVLVSTF GKGYGSAAVT LIYAVFEGFL
 VGGISLLLSG FTVGNANAGG LIGQAVLGTI GVFIGMLFVY KTGAIKVTPK FNRILTMGMV
 GVLVLVLGNV VWALFTGGAS PLRDGGIIAI IFSLFCIGLA AFSFLSDFDA ADRLVREGAP
 SKMAWGVALG LAVTLVWLYT EILRLLSYFQ NR

> RXA01560 (1-330, translated) 110 residues
 VGVSYIIAGD EQLDMAEAVR KIGETFKTEE IILGGGGTLN WSMRLRDGLCD EVSIVMMPFIA
 DGEKHTSHSL EADEKYSAPL PIGFSLASVE FLEDGGSVMMR YGVNGPVDAN

> RXA01574 (1-1035, translated) 345 residues
 MSNKRIGVVI VSYGHEQDVA NLVDTFADQL KTGDVRVVVD NRKPWLKDA VGERLEKHGA
 EIINHNDNGF AAGCNVGAH VDDVDLLFF LNPDTVIDDP TLFNSLRVD EQWAAFMFYL
 LLPDSTLNS GNAHLISGLS WVTGLDEKPV EGSSEVTDIS IASGACLAVR VDWWKRLGGM
 EELVFMYHID TDFSARLLA GGRIGLLHSA YVTHHYDYAK GDYKVIYIER NRHVLILLSVL
 PLPLLFVLIP QILGVNLGLW AIAAEKRVG LKVKSLRLLI RDLPAIFKLR RSTQELAEIT
 PSQYLAKMEW RLDNPNLGN GSNKIVATGY KTYKLCMSI LKLLA

> RXA01575 (1-1020, translated) 340 residues
 MKSIDLEQLA GTQSRTYQSR KITDEMVARP VHVIAIALWEV PWESAKSGKI EGWVIAVDSP
 RGRFVRSGQT KNGDAVNRTV SMLKSALKGV RGKAWIVTGR RQAALRAALV RENLYVTGSF
 AEQNAGVACA SAISRRAEQS ALYKAKKIGE FAERAPRVKE RQEAHWPRRL SRTQGTAGVL
 RLATDASTDG VFRGAMCFVA SNGDYLLETQ DTTASSDELE LESITHALIY LKTIGATQAI
 IESDSKAAL EIDFILNNRP RRGWRGITA CARNRFRDAW EALIDDCVVE LSRVLGHAGD
 PLNQAAQDIA YMGMRVIFE QKSAHPILLK GIDKALRKAE

> RXA01577 (1-375, translated) 125 residues
 MTQTTTQIII QILLLLATAA LALYFLNRNR KARAKAWVKI GFVVVFIAAV WAVLRPDDLT
 QLANFVGVD R GTDMLYALV VAFMFTTLSS YVRFREQELR YSKLARAVAL QNVVLPEDSQ
 GSDPA

> RXA01579 (1-384, translated) 128 residues
 LTEVFNTDQR VLNALFNVE EDDSGDITDE QHNHQNPNVRG TEFAGLVESH EQRSNGHRQW
 QHTKPFVHLR FFSGGFLHAE RQCEGSDSAE SSHDPEDGTE TKCFSPSPATS KRVHAADTTV
 DRGNNSSEK

> RXA01585 (1-627, translated) 209 residues
 VVETLSITSG AAGLQALVAR AVGLNELASA RFRQLTPEVV DVEVFTFPNV TASRRVFGVA
 GRDGAAGVAK DLLQALSEGR EDVGTSRDAS WFGSLPPATG FTLVDELPTH VVRTLADGQ
 ALARQFSGPL GPPASLMDQE VISAEENGKK AGIFPMRTVET CTSGLGIPGF EAANDVPRLH
 RVSVNGRWTR VDAPIYGSVYH SSGGLSLSVF

> RXA01586 (1-369, translated) 123 residues
 NNAAFIIEIA EARLAFADQ FRERGYEIPA VFVRHLEVYD LRAILPDTTQ AVVETQVTKI
 GNTSFSTRQE VKDRNGRVCC VVECVQAVN VQTAAPRSIS KVERKVLTA V ATDEVQSQEA
 LEK

> RXA01587 (1-1983, translated) 661 residues
 MTDFFGLIYN WSVTVGNLIG IPVSIGLFMM GALLFRMRDK GSAFKKVVIR VVYGVVGLPL
 LGVSYTGALD SFLDSGSSTS AGSNATKIVL STYVDFQSWA ENTRMRVPDK VTLAWSLEDQ
 APTGQSRMRV NMSALEINAQ SNESFTTFKN PGSMDLGYSM DWMEKMAPDA NSGTGDTSSS
 SATTFVQGTI ALLSRYIDND SISSGSFETS IRSAMESLTS KEGSGEAVAG GDVMAWV7GY
 NTASGLNEIT AAELADANNP LLEVSIDSAGL QGRPIDRNAV SFGSGDATAS CNNSVVTGSR
 AVVGDYRSDC NMSPLTMYNF LNTSFHPADA SVFSTSTSAS SYTRASHASV SLIGSGAMNF
 VVWFSAMSLS GSFVIGIGY AGAMLFNTIR RTLISLIGAVP FAAMGFIAGV AKVIVVTIAM
 LVEVIGTII L YQLITRFLMA VPALFEQPLA DSLSSNESAE LVAGAGMGLV GMALATSGNW
 ATAGMVIITVA SSMGVIFTI IAMKVRGSLV SGVDETTSV INRELTQVS SAGATSGDGM

MRRAAATGLG IGATHMVLNR DGDGGGSDSG SGGSGGSDS GLGEKAAGLA KVVTTVAGAG
 LVGKYATDAL DNYADGVING DGDGAFAAGG DATVDGDYVA DGDIAASADA NADFDVGDVAD
 G

> RXA01590 (1-1284, translated) 428 residues
 GKLEKYATYI GADPAQGFKD VQGPTEPEARL SHYEGSQKAT AIKVLFTGVA GKKEQEMVAL
 CRNLGLTKEA MAASAPQQS ILQAKHDPID ALYRAETIMG PVGDLVQGRK MRRENEQGR
 YEWEEVVRDEN HQFIQATKDE WVQQYMEMYA DDKGMGVSVG VDOVEKTAE FSDQEGYMRV
 LSHDELPTIE KPLALDQLAY GDKKNRFDLL CEMAKQQVNI YDGDAYDFAP RVVRANMKAM
 EDAAARFIGIP VEIQSISAQQ SLASFERVQP RSGFERIERR PAEVGTGLAA PAPLPDAGVQ
 GNYVQQQVPA TFPVMPVTFP AQQPVSPAQT DFRGVGQPLD QGGKIGNYGH QGPAMGAQQP
 VVPQQQNI PP VHNVPVQNSV PPTPVVPKPG TGNPFTHGGA NNQFMGRFDT SRYNQEQEPQ
 RQDGGFEL

> RXA01592 (1-1293, translated) 431 residues
 NFDRSRDNR SSARTPRGDR GDRGGYRNSR GNDRDGNRYQ NRDGESRDRG GYLGDRDRNR
 SGSEYQRDDR RDRRRDNRSD DRRGGYRSDR NFDNRNSMR DRRGGDRSY SRNDRSRGY
 RSNDRYDRND RDRDRDTRG GDRGDRRYDR RDRDRDRD DRRGGQGGQR PGDRRRHANR
 AGAGRDQQRD SLHFQGRAGF EERLNLRLNE PDLPGDIDIK DLDPLVLQDL KVLKSDNADA
 VAKHMIAMAT WLADDPQLAL RHARAADKRA GRVSVVRETN GIAAYHAGEW KEALSELRAA
 RRMSGGPGLI AVMDGCEGL GRPEKAIELA REEDLSLQDL DNLIELAIW AGARHDLGQH
 DSAIVELQKV NPSLKTGTFT HSRLSYAYAD ALVLARGDE AREWFQHAAT LDEDGYLDAE
 ERIEQLDNGN N

> RXA01595 (1-960, translated) 320 residues
 MTAPTNAAGL RRVLVPHPTG RSSNIESAIL AAKLLDDAGI DVRVLINDAD DPAAHESVLG
 RFTTHVHAAD AADGAELVLV LGDGTFLRA ADMAHAVDLP VLGINLGHV FLAEWESDSL
 EBALKRVDIR DYRIEDRMTL TVVVLDCGGE EIGRWALNE VSTENINRRG VLDATLEVDA
 RPVASFGCDG VLISTPTGTST AYAFSAGGPV LWPELDAILV VPNNAHALFT KPLVVSFKST
 VAVESNDTS AAMAVMDGFR PIPMPGSRV EVTRGERPVR WVRLDSSPT DRLVSKLRLP
 VTGWRGPQKQ AENKDPKPSAG

> RXA01597 (1-1182, translated) 394 residues
 MSLFNKRKADL PGLQGATRIC TPQKGKLRLL SEGDLAIIDA PDLRSTFAQR LLAAPAAVL
 NVSRFTTGSV PNFPGQMLID GGIQLVEFGF QELLDGTGKG KKGRLTEDQG LFYGERLISN
 GSVLSPGAEE NAFADAQSSL LDRMEAYFGN TIQFIHSEAP LLDGLGIPD TGNAGIEGRKV
 LIASPGDNHR SRLKELRSFI REYDPVLIGV DGAADTLVEL GYKPALIVGN PTGIGADALR
 SGANVILPAD PDGHAVGLER IQDLGIGAMT FPSSVNSSTD LALLLADPHN PQMIVNVGGP
 VTLDGVFENR EDSDEPAALLT RAKLGTKLVD GSVIASLYTV RSSSNLGMWM ALLAILVLVA
 VVIVIAGTAG SGSFTDNLID TWNSFALTQ GWFK

> RXA01598 (1-963, translated) 321 residues
 MAKRRGRGAA TFAALGFGAA AGIAFGTYVL APNLPENIDF NAPTSAELVE AETLAEVNAV
 QADQDQSID HIVEDVVGAT LTDRPVLVMR TADAESDVA DVSWLLQQAG AINAGSITLE
 ENFFSQSGAD QLKSIIVANTL PAGAQLSETQ LDPGTAGEA LGAALLNFE TGEPIASTG
 RGLLLNVLRD NGYISYEDGT ILPGQVIVMI TGDSDGSGDG AFAAETQSLF ARALDAQSGG
 VVUAGRHTA ADTGVIIGRLR ANPDAAENVS TIDSVNRWTG KMATVLSVRE ELAGRSAGAF
 SAASADAASP SLDGTAAAPA Q

> RXA01600 (1-669, translated) 223 residues
 MVSKMHIPGT HEFTVTDTEL LLESPIIGVR RDSLIMFGGS TARREVVEHF GAVAVVAFDG
 ENIAMVQKYR RSVGSDSLWEL PAGLLDIADE DELTGAQREL MEEAGLEAZE WSVLTDLITS
 PGFCDEAVRV FLARGLTKVE RPKVMGDEEA DMINQWVPLH EAVGMVFSQG LVNSIAIAGV
 MAADAVIAGR ASARAVTAPF TYRPTALAGR KKAHGVIPDM KKL

> RXA01602 (1-1530, translated) 510 residues
 MAKTHIRLQD LLSLYSTTPL ITKLNITVSS GQCAVIVGEN GRGKTTLLRA LAREFFPSAG
 EILTHGTVAI AHQHMAGDGL SVGEICDEAI RDSKNALDEL ERAGALLETN THALADGYQ
 ALDAAEVLDA WNAEHRLEKA LRSFGAITDR SRALSELSTG QRYVRRLACL IGGDADILL
 DEPTNHLDRG ALNLYTEAIT SHKGVVIVVS HDQALIKDVA DFIIIDISLP GKHPRIYHEG
 FDSYRRQRSA LLETWRQDYA AAQTVQQQLQ EDLEHARQVR NSSWKPKPKGT GKHTRASRAP

GVVQALKRAQ DALDSKALDV PPAPAPLLLP TLKVRPDKPM VDFSDFLVPH RLRLPGSHSV
VSGDKITVITG DNGAGKSTLI EVLSGLVTPA SGSVANHART GVLGQESLVG EVPSIARDHA
VKWGLLSVEE SRFALQEFSS QGRRRLDLAM SLAGNPPELL LDEPSNHLMS HLVSALTEWL
DTTAAAVIMV THDRQLLRDT AHWRRHIELKS

> RXA01605 (1-1515, translated) 505 residues
VTSDSPAPAT VNAVFNNSNG FIASMLGNQV VNTVVETMDT EFGVRIVDNM LVGFSTLGDG
MNQAAEGATT LSDGVGSAND GAVQLADGAV TLRDGIASAN EGAQSLADGA SLDLTGLGSA
ATGSGTLADG LSSLSAGTAQ LGQGATQVSD GVGLVDQVA PLTAYVPDIN SOLITLRDGA
ATIASELSDP SSTYRSGVDS AVSASQQLAA GLQTLKDGSS QLSIGARTLA DGTSQLAAGS
EQLVVGQAAL RDGTVQLDEG SSEALKLKTD GASQVPTFAD GADTTIATPD ETQAGDTPP
LFGIGLAPFF MAVGLFMGAT VAWMILHPIS RRALDSRMGG FRGTLASLYL STVLGLGQAT
IMWAVLYFLL DLNPAHPAGL WMAMVAISWV FISITHMFNN VAGPSAGRVL SIVMMSFQLV
SSGGLYPPET QPAFFHWFHT YDPITYAVNL VRQMIFNETP SNDRPFIQAI WVLLFIWALM
LAISTLANRT NVLRLMKDYH PELKV

> RXA01610 (1-729, translated) 243 residues
VSGFLTTPAT PHIRTATASI ATAVAVALS FFAALIPGSA LYSVLTAGGV ALGAASGVAA
LRHRGGLRIF QWLSALGGIV ILLIGIVVAV AKFGASAKLA TLGLVTSYYL MCPVALACIY
GGLGLPAKW IAPAFMATAG AGAAGWFSLG AGTGFERFLI AVAAVFSLMG PVSPVWGVV
KRFRQVAWL VALAALVLGA LMLFMVMVAV APGLLWLQPT TVAWGFMIAG VLATVAGLWP
RRF

> RXA01611 (1-357, translated) 119 residues
MRKFRNTAIA LVSAIAITLG GVTAAQED ETPPAEETET TSPSGSSGSS WNDYNEEYEG
DQEGYGDGF GSSRDDSGEE VPRWLETWKG VFDALITISV LGLVVFPPVN FLKYNGLIK

> RXA01612 (1-345, translated) 115 residues
MRSFRTAAVA GLTAVALS VG SATVATAES DQNLSSGFA LSSGGAAAVG EDWDADQPVAT
GEDIFGEEH RDNENTPAWA KMYDLTVLG GIASLLGVIV FPAYNYLVYT GVIKG

> RXA01618 (1-384, translated) 128 residues
MIIIGAVFAI LAVLLHVFIF YMESFAWTSE KARGVFGTTE IDAENTKEMA YNQGFYNNFL
AVIAGVGFAG FLFAGSTGIGA ALALAGTGSM LAAAVALAIS SPDKRGAAFK QGTFFPLAVV
FLVIGLLV

> RXA01619 (1-975, translated) 325 residues
MRAITHNTFG DPADVQLQITE KEIPTPGPGQ VRIQVTLATI HNHDLWTVKG SYGFVPDLPA
AAGTEAVGIV DALGEGVEGL QVGQRVASGT SFGIWAERYL VDASGLIPVP EQLSDESAQ
LVAMPFSAIS LLDFLDMKPG EWLIQNSANG AVGRMLAQLA ESRGIHVVL VRRDAGVQEL
AAQNISGVVS TETPGWEKQV EDITGGASIA VALDSVGGSS AADLVKLLGE GGTLVSFAGM
GNPIMEIPSG PVIFKHITVK GFWGSKVSRE MPAEKKTQFL GELIARILDG TLTLVPDSTF
DAADIVSAVR ASSEPGRAGK VLIRF

> RXA01622 (1-603, translated) 201 residues
MSDFYADRLF NAMERNEVAP GMLVVAAPDM ASDEFERSIV LIIEHSPATT FGVNISRSRD
VAVANVLPEW VDLTSKPPAL YIGGPLSQQA VVGLGVTKPG VDIENTSFEN KLANRLVHVD
LRSAPEDVAD DLEGMRFAG YAEWAPQLN EEIEQGDWV TPALPSDIIA PGRVDIWDGV
MRRQAMPLPL YSTFSDPSD N

> RXA01623 (1-711, translated) 237 residues
MSSENLEKIR GGIGETLTVG LGLPLGLAF GLLMVQTGFA WWWTFISFV IYAGSMEFLA
IGMVTAGIGP FSAAVAGFV NFRHIFYGLT FPRHRIKSGA GRAYSTYALT DESYALVSAR
PPGDISGTRV LTVQILCQAL WVPIGIGAL VGQVLPDDLK GMDFALTALF VVLAWAEAFKN
NKDYSPLPFA VVLALVSGFV APEQMLVIAL TTYFLILLR VRFPNLDDKL EIRTSHE

> RXA01624 (1-345, translated) 115 residues
MSEFGLPEGV TLLNVAALI PIATITLLR IFPPAAMKRV NSNQLMGVLG RTMPVGVMMV
LVIYTLFGQV SAPGVGASL TAVAFALLH WLKGSAGLSI VGGTLAYMFL VNVVF

> RXA01627 (1-495, translated) 165 residues

RTYSPLSKDY NSDEPSLLGP AEDPNMYQEF EVSYEQLGIK PEGRTLIGDS FSADFLTSNE
IGIVDEVPSG TIAFTNWKDV TEGRHWSYVR SEDPFGGVEI SPVQSFIAEG EAGGNAPGTG
SSNGSSSHGL WGALAEFFAG AALAGAAIA FVPGINDYVT NAFKR

> RXA01628 (1-1014, translated) 338 residues
LVLVGCNTA ESTTDTTAGS TETSSQISPT TPVSTTEAAP PEDPSANAE EYAQILANPS
IYPLTEISQF VPTGTIYATL VEATSDSIPE LLLRADSHFE APILVETIDE NTQSATOAGG
VLIDGVASAG GSRVKVRASN SCAGIYQLNW YSIQPVGESS LYGIQCNLSL QIADPEDFMV
RELLPDHHEI TWVDSNDPSG LSTVQTGGAN IQQAAPTVPQ QPASNLHYFS GVVTMQTAGE
LMRGERTPNG EPAIDLYLV LVDSPLEITA RNAATDPQTR TISEVSLGRY IPADGDNWDWI
GYLDTHVEIT ATTQVWFPT DTGLPLGMLR LADYKSI

> RXA01630 (1-1077, translated) 359 residues
MSDQKIVVGL LGITHPHASA RVRALREIDG VEVVAAADTD SRLQYFTDKY DVEPREIDDV
LNDDRINAIM VHSKSKDMVP HAKRALAAGK SVVVEKPGGG TVADLEELLA LKEAADPQRI
VQVGYNVRLS ESQRLKELL DAGLIGEVVS VQARGAAKVG EHTEHLNQAP ADMGGVLWIL
GCHMLDALVE VFGAPESVNA RVHKTAKLSD DTSREDSASA LLYYPDFSVS FSEFHDHDLLE
WFESSRLTYV GTKMGIEAGI LPQTLRVLYN ESRQGWFGW TWNTQSYFTT PFARTESNKF
SELPELENIS NRFTEMQGW NSIIRTGSRNV APVEDALTV RIVSACYESD NNQGISVNI

> RXA01634 (1-552, translated) 184 residues
MAVGQETDLL NAMETLAGVP SDLVVTIELP DTTSYDNFEF FEVHNHTGSAP VTIGEGETTF
AYSFDDSDAT SRDKALDLGG EVTVDAGETI VVWIEYSSST VDTAAFEQD FRDFYGMDS
ARIFRATGQA GLANGGDRGI RVLYNGEVSG WSHYPSDSAA VQKGIDFALP KVGEQASIAS
AHQN

> RXA01635 (1-741, translated) 247 residues
LIPGGLDTPE EPEAPEDSLF EGRTPPRDAS TRILITELMV NSTNMGSSDG FEYVEITNTT
AEPIDFSDYT LMYLYPQDEF TNTNEAVWAA EPGDVIIQPG KSLVFWIKNG DDEATAADH
NAEYGTNLVA KDLVLEISS GMANGTARGM QIQTNTGHIV NRGFYNMAGA SDVKANESLH
FAVDESLLK QTLVGSGAPT PGTVYTSQIP NPLSAVIADS SVPLITDNTA TSINPAEPFT
FAFKYHR

> RXA01636 (1-573, translated) 191 residues
VRTATLHVTS SAGEAATTIN LTEDDGSFNW ALPAADLTGK SWFEYTVTAT DGFNSVTTEP
VRVTVDGANT DPLRLNLEEN QWVSGTDDVI GASDVFGDKL ELLIDDAVAP TNSLSAAPT
FAMEVTQTDV FFRNGILAGG EELRIFDQGT YANTETISTP VPLYHINEDG TLTVSVYAGT
KAAPEIDLNE N

> RXA01638 (1-390, translated) 130 residues
VLVTEDLLIE APFGFEMRSD EQSRYLEGPD PNLRIHVGDV FLHGADAALV AEELRLRLITE
DPSLEEIPAG EMGKEKTIIDY RETPGDGSVH LWVTWFDTOR QLVNGCHSKA AETLVHKAQC
RNVIEHLTLK

> RXA01639 (1-438, translated) 146 residues
MSTQITITIV LETATIFDGP ETIYRYDLAA EGLLDGWAHS AVLDDQVKQIA GENWPTVEIV
VDGTNUVVNA LTSMFASKVG TCGGVGVEAP PVAEEPPKIK RPTSGRQVRQ FYGIKPLHL
LVLSILVGSIA GINGFRVSLG QWTHGR

> RXA01641 (1-1371, translated) 457 residues
LAIDNALRVS IRIDLTVGDA PAAVADVLP AGSSLADILD EILELTDAPR ISRPFWAHTA
AGSPDCGIP LAETQVEQGS VVVLSPERDL EAPVLRDVAE ALVEFSSMTR AGHLVELMTF
AGLIGAAVLM TSPAASGIIV PGRMGIFVAI CALLLLWLPP AHTPILRNVL PITLLGAGG
AVSVLVGATS GTSFGALTWT IFAGACTILA SLLLVHVVYR PAILLVATLS TLGLGLLVLA
ATTLLWKLKA TEDFSGPAAI TVTASTITMC FAPKIAASLA GLRVPSLPTA GEDLSVSDLT
MTDPEKRIKT KTKLFDQIL GLGLVLSGPLA LLSVTPGTWT TTVEFSLCIAV ASLLHANRHQ
APIPTWTLMG LSAIGFISMA LSASRSGSLI ALIGSVVITA VLVSVVALWIS TVPTLEPTTI
VWLERLESLE LAASLPALH LLDVFGMLRG LDIGFGG

> RXA01642 (1-1242, translated) 414 residues
MRRLIAVSLA ALFMLASTPA TRAQEVEALA CPEVAIADPS SAVLDEHLSQ SLSQAHLAT

GAGVMVAVID TGVSLHPRLP HLIPGGDFVG AHQSPDVPGE LIODCDGHGTI VAGIIASQGN
 PGTGNWYDGS SDPYIGVAPD SGIISIKQTS SYVRTREDSN VGTLSLTAES IHRALDSGAH
 VNISVSVSCL POSPDEAASF QPLTDALNCP ELQGVIVVAA AGNLGQDCPV GSTVYPAHSD
 TVLSVYSARFD SHTLAEYSMP GNQOILSAPS HIQAGLSPRG DGFASHMITT AGESPFECTS
 FAAPVVSATA ALLRQHFFFA TPYEIRARIF NSIDPARGAI DPLYALATQEI YPTTPLVHEI
 ALSVPTPPDD SPRERGILVT AIIVGLLAVL AVLMLGLRRH HHSAFQKASS SVIT

> RXA01643 (1-426, translated) 142 residues
 MGMTREMVSD RIDRLQEAHA RSKQKKFQFL VRPGTLILGW LVTTIIGLITI PLPGQGWLTT
 FIGVGILSLE LKWKANLLAW GVHQYDRFFT WYGKKSFRFR MAMLALMILL IWVVFIVTFW
 LMWHAGTIPW ADEFFTWLGL SR

> RXA01645 (1-606, translated) 202 residues
 VVRKLWPRDL LRSSFYWKII GWDRKYSIAD RLEERKGRPA RERVVDQVEV TIDKLEPEFLK
 WFFESSDIEP LWLCPILKRE VPGSSVGAGE ILSAEAIIDS GAEEHWPPLY PLKQDVLVNVN
 IGFVSSVPVD LMGSDAPEGA FNREIERVMA ELGGHKSLSY EAFYTREDFE KLYGGTIPAL
 LKKQWDPHRS FPGLYEKTVK GA

> RXA01646 (1-819, translated) 273 residues
 MSGLVDPDST FLKTIGKLSN SLSIGRGVDQ KEVIPKGWNA HWEAITKLKR SFDAPPAGER
 VRLAKTNSNL FRGRSDAGHG LDVAALGGVI AIDPVNATAD VQGMCTYEDL VDATLSYGLM
 PLVVVQLKTI TLGGAVTGMG VESTSFRNGL PHESVLEMDI FTGTGEIVTC SPTEENVDLIR
 GFPNSYGSGLG YAVRLKIELE PVQDYVQLRH VRFNDLESLT KAIEEVASSL EFDNQPVVDYL
 DGVVFSPTFA YLVLGTQTSQ PGPTSDYTRD LSY

> RXA01647 (1-888, translated) 296 residues
 MPRGVFVGVP DAPGLFSSTE EPEQDWFCVQ DVGTDGLHIT VPRGGLGPTL IAEGNWLGA
 SKSETGEVTV NLITADGRRE LPWAGSEHGR IMRRHLGISE DTPRVVLITE LLNAIPEHDA
 VRFFAPLPEL VDASTRNWLRL LDGALAEITP LQRGLLIDAG SGVFPDPTAL LVGHEETANT
 LTLPEQTVSW QDLQGGFACA DGEQIGFLE TLESQVVALSG DSRKSFSTN AGGAVGVDSG
 FGYYVVSDFG LMHPVSTGES MVALGITDVQ VVFWSLRLLL FQSGELAKET ALAPTY

> RXA01656 (1-897, translated) 299 residues
 MTETQETQQA TRVRKRGGLAD MLKGGVIMDV VTPEQARIAE DAGASAVMAL ERVPADIRSQ
 GGVARMSDDPD LIEGIVNAVS IPVMAKARIG HFVEAQVLEA LGVDFIDISE VLSPADYTHH
 INKWKFDVPP VCGATNLGEA LRRITEGAAM IRSKGEAGTG DVSEAVRHLR TIRGDINRLR
 SLDEDELEVA AKEFQAPYDL VREAVASTGKL PVVTFVAGGV ATPADAALVR QMGAEGVFVG
 SGIFKSGNPA ARAAAIVKAA TLFDDPSVIA DVSRGLGEAM VGINVSDEPA PHRLAERG

> RXA01658 (1-1485, translated) 495 residues
 DPQILSPFTT QQQQLRNIFYG FPDQLAMDRF EVDGKLDRDF VAARELDPNA LQQNQQDWIN
 RHTVYTHNGN FTAAQANQVD EVARDVGSTR GGYPVYTVSD LQSNARAAS EDAEELGIKV
 DEPRVYGYPL IASATDGADY AIVGDTGDGP VEYDITDTSY TYEGAGGVDI GNMVNRAVMA
 LRYQEMNNLL SDRVSESKEI LFERDPRSVR EKVAWPLTTD SKTYPTVIDG RIKWIVDGYT
 TLDLSPYSTR TSLTEATQDA VMPDGTPOPL ITDRVGYIRN SVKAVVDAYD GTVLEYEFTD
 EDPVLKAWRG VFPTTVKDG S EISDELRAHL RYPEDLFKQV RDMALKYVND DSGTFTFNDA
 FWSVPGDPTA AEGRELKQP PYYVVAADPE TGESSFQKIT PFRGLQREYL SAHMSASSDP
 VTYGELITVR LPTDSVTQGP KQADQAMMS DQVAQDQTLW RGSNDLHNGN LLTLPVGGGE
 ILYVEPIYSQ RKDQA

> RXA01659 (1-486, translated) 162 residues
 PEAVTAVNME SDWLAETIK GSTPSDWEEI LRPLALLTDA SFTLPPRSTR AQTLDLKHLH
 PSRLKPEQPE KPAPTFNASE EDLSQPLVIR PEEPLQMPVR GVQSGRGVVE PRSLGADDVE
 SAEGDDPERP SDLYGTRVLR DLNGQSSIFQ DSTDADEPPK KW

> RXA01663 (1-435, translated) 145 residues
 MEISVLIIAA LILVAGIVLW RADSSKQAAK KAESPVGSGA PAPVLVEEPE DPEFEPELDP
 EPEAQPEPEL EVAPRFAPPE VQDLEPOQAE DIYFDDSPFL DADVENALAE LTVEDYEPPE
 PVQSEQPQAP ATAEEVADEE QRGVD

> RXA01665 (1-720, translated) 240 residues

VKIDELIALA AEQPTRISRR SGVSRSTLKR VGDGTSEPTL STLREVALAL GLDIKVAHH
 ACDPFAAAAA RTLIDASVPE NPHNQEILAW LHRFERWNIN DPLTLVSEAG TLQGITHRQD
 AQFVKLNPRG IAELELFQQ HKTQWALSGA AATVIMQGI VLGNISVWHE PAHDLVDVAL
 GTIVDVAEDA DLILLPATVT ELVGSYTQDR INFVAVPQLV IDLHLSLHMF EADYLTSGWR

> RXA01669 (1-732, translated) 244 residues
 HNLSDAITAI PLWIAFILSR RAATQKYTYG FNRAEDLAGL FIVAMIALSA IVAAWQAIDR
 MNPFRPMENI EMVIAAGVIG FLNGEAVAMY RIRVGRKRGS AALVADGVHA RTDGGTSLAV
 VAGGVGVFLG PFLADPIIPL IISAMIAITL VGTIRSVGRR LMDGIEPELV EKATHAIWHV
 KEIESIDRLR LRWWGHRHLG DATVSTSTSS LSEATAIALE AELSVMQHL P NVDEMTVTIT
 PSKP

> RXA01671 (1-615, translated) 205 residues
 MNHVNFVASH LEDAALKQAE ATATMPFIYP HVALMPDAHF GLGSSVGTVF GTKGAIIPAA
 VGVVDIGCGMI GVCTNYTASD LEGRDLVTLR DYIERVIPLS PGNYNSTPLK ETAKVKVAEL
 EELAERDGDV LSHSPTWKRK LGSLLGGNHF IELCLDELDR VWMFLHSGSR GVGNKIAHKK
 IKNAQAQCKN EELPDKLAY LDRGD

> RXA01672 (1-309, translated) 103 residues
 SPLATFRVAL AMSIIGLVAV IICVTVLYFG LNVAGVWQNF NDVIGGVGAE QTITFGLVLS
 ISALLGAIGA ITVAVLAPLC AIIYNSIVDL FGGLQIQLQE EVD

> RXA01673 (1-1035, translated) 345 residues
 MSTNLLESTP PFTQLRTGVL QKYTFGLLLC SIAVLIAMIV NHFFSGVSPL IVAIILGIIL
 TNLILQLPAST SPGITLASKK LRLRGIVFLG LQLVFSDIIS LGFFMLAVIV CIVAGGIFGT
 ILMGHLLRMK PTQVLLIACG FSIQGAARA VGEVTDSEEE EEEVTVAVLV VIFGTLMIPT
 IPFATKVLGL SPEIGGMWAG GSIHEIAQVV AAGGVIGGGA LGVAVVVKLA RVLLLAPIAA
 ILSFQRRLQG YTSFDGKRFP VVPLFLIFGL AMVVLIRSTVA LPDEIVAAAG FLQTALLSAA
 MFLGCGGVKI QNLHVGKVP FIFAFGSTTL VTSIALAGTL LTHLG

> RXA01675 (1-411, translated) 137 residues
 MNEIPEWLTL VSEVAGKRLG RFGPLVFPEE LVTAVEGIE LIELEPSWTS DLPLPEFGFL
 AADMVDFYDD YEFSEWIPGA WPLALDGGGG FFCLDLRAAN ADGEIPVWVW HASNLGWGDD
 EAVRVAAASLA DLLSPSK

> RXA01676 (1-756, translated) 252 residues
 MILHGVVFYA GLLVLLVPLG LGAGILGELF ITQRQTTIIV SSIVLIILGF VQIFGGGFDF
 GKALPGLDRG QSKATVTSGL GKSFLLGMTS SIAGFCSGPI LGAVLTAAAT SGNSTISALI
 LSAYGAGMVL PLMAIAALWA KLGQRGQOML RGREFTFLGR QWHIVSVISG ALIIAVGILF
 WSTNGLVSMF LVEPMDTIW LQEATFSLGS PLFDIALIIV AAGLFLYFWN KRQKRKEEAQ
 RPKEGSGVIN PR

> RXA01677 (1-744, translated) 248 residues
 VNQSKKWLIV PTLVVIIAVL LIADVLLMYR GNASDTAEGV SAAATSDSAA ASTAASGSAS
 GAADSDLTSTV EARDPSDEVA VGDVDAPVGL VVFSYDQCPF CAKWSDETLP QMMKHVEDGN
 LRIEWRVNI FGEPSERGAR AAYAAGLQDA YLEYHNALFA NGEKPSIEDL SEEGLIKLAG
 DLGLDESKEFT ADFQSPETAV AIAHQHQLGI DLGAYSTPAF LLGGQPIGMA QPASVFEEAF
 EQALAAKE

> RXA01681 (1-633, translated) 211 residues
 VEVLIIAIV VGGGVFVASK MGSNNKKQE EAKFADAQAD ARRWERLGS QVLTIAGTDA
 ASTQAIADIS ERYTAASSQI SSATTPRQAE LARESALGL HYMNAREIM GMTAGPELPP
 LEGQNRAGRV TEKRTIEQEG RQITASPVAT DETPNYYPGG NVAGRPVPAG WYSEFWWASA
 LRSGLWTAGS VMFMSAMENG MAGVGSAAAD L

> RXA01685 (1-579, translated) 193 residues
 MSFAIGITVH AGLGTTTISL LPVVWTAASG LSLGWTTIYF NGFMILCQII VLRSQFKPMQ
 LVQILWAFLE GFLCDLSLQL TTWAQTDNYF VAWIWIIVST ILMISGVFIQ VLPNITFIAG
 EGIVSALVKK FNFVEFGTMK QIVDWTFSV AAILSWITMG GLTGVRGRTV FAAFFIGFVV
 RQWRKLYLRS IGH

> RXA01686 (1-441, translated) 147 residues
 MTSLRDILLVS TNADAAIADM SAFIEETVGK QSGISGIALK GAMGAATKID SDIVAKGSRR
 LLPEIADSLD GLWQEYQNGG TAADFAGHLE ANSSTALDAI LSVADKNAES INVPGLGKIV
 KGVGRKAAKV IEQELPAIGQ LIEKNAQ

> RXA01693 (1-1422, translated) 474 residues
 MNTAPFKLEA DFASALPTMA APWQGEAPN PELVILNDDL AYSGLDPTW LRTPEGVQFL
 LGLNPEPLTK AVAQAYSGHQ FGQFVASLGD GRALLLGEAR SADGVHLHDH LKSGSRTQFS
 RGADGRAVLG PVLREYIIE AMHALGVFTT RSLAVISTGR KIQRGSVAPG AVLVRVATSL
 IRVGSFYQSN ISGGIELSQH LANYTITRHF PSLVAELSAP TPATYVSLEK AILQRQADTV
 GKWTRLGVFH GALNTDNTLI SGETVDYGPC AFMERYRGDA KFSIIDTYGR YKFENQPMIL
 GWNMARLVET LPLLLGATPD EGMTAAQEAL VFDDDLCEQA IRKEFPATAG LDESDTGTVE
 QFREALLVHN PDITTLRLAL TDNTAPPSGF EAFVHDWKTQ DPDIEMARAV NPLFIIPRNHL
 VEAAALDAVE GNLEKFEHLL AAVTNPFDP T AGPDELRLPS EEGFEEDYMT FCGT

> RXA01694 (1-900, translated) 300 residues
 MQKITPNWIC QGTADAAEF YVNAFSEFPG GAEVLTTVKY PEAGLLDFQE PFAGKTLTVE
 LAISGFKIIL INAGEEFTPN PSISFMVND AVRDENAKEH LDMVWEKLEH GGSTLMPVDT
 YPFEYYGWV QDKYGVSWQL MLRSPEEKPG PAVIPTLLFG GAAQNQAGPA QENYVEVFPN
 SQLGDRAPYS QQTGPATPEA LMFSQFQLDG QWIFAMDSGV EQDFTFSEGV SLMYEAHQGE
 ELDAIRNALS AWPPEAACGW LKDKFGVSWQ IVPDNMEELM AKPGAYEKLL AMKKINIAEF

> RXA01696 (1-597, translated) 199 residues
 HSDPVLVMEA YRLAEQSDY PLHLGVTEAG PKFMGTIKSS VAFGALLSQG IGDITRVSLS
 ADPVEEIKVG DQITQSLNLR PRKLEIVSCP SCGRAQVDVY SLAEVEATEAL GDMVEVPLRVA
 VMGCVVNGPG EARADLGVA SGNGKGQIFV KGEVIKTVPE SQIVETLIEE AMRIAEEMDP
 EVLAASASG MKAEVKVTK

> RXA01697 (1-726, translated) 242 residues
 MFQGLKELTA AKGRTLLITV TVGLIAVLVT FLSALTAGLQ HQSVSALKYL AGDNELILAD
 SGSTTLGAST LSDQAVAQLE DEGAQMLQWV RDRVADTPTM LLNSPDLAPG EVSLPAELAD
 SELATAHDVV DSSNDLYLDH LPVVLNMTSD LASLAQVRGV TGPAGAFASD VALPSDTVAL
 SGERWNASA SYQGEQMSLN LMIVMLYVIS ALVLGAFFTV WTIQRLRGIA ISSALGAARR
 VL

> RXA01701 (1-333, translated) 111 residues
 MLSHEEIVAI AEDLLSKRYG GVQTLSDVEQ LNSGTSAVL RARVANSPL QQRSSVVLKYV
 PSTGDVFDSD ALVREIVSYQ FTTLSLEDVR PGPVILAYDI DKRILVISDS G

> RXA01703 (1-471, translated) 157 residues
 LKYFAHIHAV VQAVSRKMTN FHGVIDWDGT DGDGGLFKGI LVRYLADVAI RLPDDSFNTN
 ETKKIAARLV LESAESVNH RLEVDGLPVF ATDWTDDARL PQNFGLSSSS LSDLVSVVRV
 DERDLSVQLS GWMLMEAAAK VAELENNNGN SYTGRSR

> RXA01709 (1-330, translated) 110 residues
 MRSQVDMILN ETGGEKMLAQ ADLVITTEGR IDAQTLSGKA PTGIKARRA KGIPVLAVCG
 QSLGLPAISN ELFDIYSFT FDESIDINECI RNPLPILEGI GFNIAKHLS

> RXA01711 (1-1158, translated) 386 residues
 MLLMAHREFF LAINGAVTDD FTTVYSALRR FVEGIPVYNE VYHEVDPHYL YNPATLALLA
 PLGYITHETL ARWMPFIAVNL LAIVLAFGL TRLSGVALRS MWVPIAIALA MLTETVQNTL
 IFSNINIGILL LMLAIFLWCV VHKKSWLGGI VIGLAILIKP MFLPLLFLPL VKKQWGSLLI
 GILTPVIFNA VAWFLVPGAS EYVTRTPMYL GETRDFANSS LPGLAIYFGM PTWMEITWFL
 IFGMAVGLAV LALLFRNTE PYFWAATTG VLLTGVFELS SLGQMYTSG IPFMIFTLG
 SRSVFHNWVA WWAAYFLLSP DFTTSQRLPD VARWMEFFSA TVGWGLLIVV TFVSALIWFI
 GDIRAKGTPS SPITTDPTH D HILRTA

> RXA01714 (1-615, translated) 205 residues
 VIDSEATSQH KTSATPAEST PAEFSEAVES MHRARLRPL TLGTIRPPQR LAPFSHAIGL
 EVNGQEESDD VSTNSEGDSF GRLILLHDGP AEETWEGAMR LVAYIQADM HAVASDFLLP
 EVAWQWLNEG LEQAGAGFTN LGGTVTSTTS VRFGEIGGPP SAYQVEMRAS WTATGTDLTA

HVEAFAAVLA SVAGLPPEGV TELRR

> RXA01715 (1-696, translated) 232 residues
 VSELDIKQLN KLQRYSQWAV FRAIPGALDD DRTEVTDQAA KFFADLEAEG KVTVRGIYNA
 SGLRADADYM IWWHAEEFED IQKAFADFRR TTILGQVSEV FWIGNALHRP SFENKAHLPS
 FMGEEAKDVF ITVYFVRSY DWYIMEPLKR SRILREHGQA AVEFPQVRAN TVPAFALGDY
 EWWLAFEADE LHRIVDLMHK MRYTEARLHV REELPFISGQ RVDIADLIKV LP

> RXA01729 (1-519, translated) 173 residues
 VKLRTIPALL AVALLAGCSG ESADSQAVSA EETMEVTTTS TPVFEAKEVS PITVPSGDIR
 VEDPGLNVEF IFRGTRYGTN GGSIIHIAVK NLNDVALPAD AIDPPTLDIE DYNGKNTNIE
 TSLSGDDNIPL DLPLGAGATT NLQYAFNTSN GSLSNAKFQI GNVIYSGNLN SLA

> RXA01731 (1-699, translated) 233 residues
 MNASSISSRF KDLFVTPSIV FDFDGTLAGI HGPVLAYALC VAPEGSKDFL ERVRRELRRY
 DDGQSIYRDG YDIVAKLASE LGIDDGTMVS AYGESRKLIG SDLAPVEHVR GIKDILSSLK
 GHARLVLTAN APENGVHDLR QWGVADLFD QLHFVVGKPA GLISIISDLQ LDGPFVLAVGD
 IYEFDLSPAA QLGADLTALVG ATATISEAKV SMRGDSIADL FLLAWVCSRVR SSS

> RXA01734 (1-534, translated) 178 residues
 MTDPIEQAFE RIRAEAMRRN GSVPDNLKND AFRPPAPKGP GVEKRKKGRA SGLDGRQKRY
 VRGASLSGVS LNKETIQRGW GKDIAGGWVT SNWEELVGAK IAQHTRVEMI KKKLFIITCD
 STAWATNLRM MQRQILQVIA EKVGPNIITE LRIFGPQAPS WRKGPLHVKG RGRPDYTG

> RXA01738 (1-714, translated) 238 residues
 MRILPIGPHD ETAVNGSIV LSEHDGDIV VGPDLGTVRV TLEEIESLGT PTAPRDLGSR
 EVDACVSLLR NRELVRFDPH DGESELYREH SVAYGASGKP LFPRLDPAVI GIVELRGEDR
 LLLGMNAQKR QRYSLIAGYV SHGESLEDAF TRAVFEEAAR RVSEISYVSS QWPVISGSLM
 LGMGKFTDEE LPQGETDDEL AETIWASPLD IIDRKIPIAP PGSIAYDMIN AWARDKQN

> RXA01741 (1-798, translated) 266 residues
 MTHIALANSA QVLIRPDSAI QFGIDATRAG VINIDPSLSS RVVPVLRNLR TARPIVIDVIA
 DLTTAGLAPT AASSLLEDLL EFGVVRESAA AQVLLFGDGS LVDVTSFLE TSGFVPRPQI
 IDESPREFFE LPSSHILVLN KLAHSQRLSP LLHKYAPTYL CAAIVNDRGI IGFGRRSRSG
 PCLMCVDLHR KCDPHWLSI INQOPNGPTF PDPVTMATA ARLVAVWTAD TWLPGVVVEEV
 NPHDRNTSVR TLPVHPKCPM CWSLGS

> RXA01742 (1-504, translated) 168 residues
 MQEKPEMPAI EVIRSAKRTR TVQARIVDGQ IQVRIPARMS KAEEEKAVGE IVAKLKRRTQ
 SAVSSDADLI ERAHKLNKTV LEGRARVESI RWNVNQKGRW GSCTVATAEI RISDRCLKHV
 DVLVDAVLVH ELTHFTIAGH SAEFEWADK TPLAERAKGY LEAYQRWG

> RXA01748 (1-780, translated) 260 residues
 MADAKKQADK AAKQVRAAK KAQRKETRSQ MWQVFNMQRK QDKALIPLLL LAILGIPLVL
 FLIGLIWGGQ WWMLPIGIAA GVVAAMFIET RRVERDVYKR AEGQQGAAGV AVENLRSGVG
 MTWRKTAVVA VTTQMDAVHR VIGLCGVVLV GEGSPHLKP MLAQKKRLN RVAPGVVPEY
 IITGMGEGQT PIKILQRELK KLPRNYKKND VAALAARIEA MDNVGNAPGG SLPGKPLPKG
 ASMSGMNRRA RQAERKGEA

> RXA01749 (1-1617, translated) 539 residues
 VSFLVNEQLL ALVVMITVGL LLGRIRKIFGF RLGVAAVLV GLALSTIEPD ISVPSLIYVV
 GLSLFVYTIQ LEAGPGFFTS MKTTGLRNNNA LTLGAIATP ALAWALITVL NIDAAAGAGM
 LTGALTNTLPA MAAVVDALPS LIDDTGQLHL IAEPLVVAYS LAYPLGVLIIV LLSIAIFSSV
 FKVDHNKEAE EAGVAVQELK GRRIRVTVAD LPALENIPEL LNLHVIVSRV ERDGEQFIPL
 YGEHARIGDV LTVVGADEEL NRAEKAIGEL IDGDPYSNVE LDYRRIFVSN TAVVGTPLSK
 LQPLFKMDLI TIRIRGDTDL VASSDMTLQL GDRVRVAPA EKLREATQLL GDSYKSLDSF
 NLLPLAAGML IGVLVGMVEF PLPGSSSLKL GNAGGPLVVA LLLGMNTRTG KFWVQIPYGA
 NLALRQLGIT LFLAAIGTSA GAGFRSAISD PQSLTIIGFG ALLTLPIST VLFVGHKMLK
 IPFGETAGIL AGTQTHPAVL SYVSDASRNE LPAFGYTSVY PLAMIAKILA AQTLLFLLI

> RXA01750 (1-1641, translated) 547 residues

MCINDPKGEL LKKNYVRMSK RGFQVVFQNL INNLKTDIYN PLGLAAEAAR EGNMGKCATY
 VENIAEVFFP VDGADDPVWP NAANNAFKRA AYGLIDFYLE EEREMRKQAA AENWDAKVLVD
 TRIDQMQLVF TLYNCYQLFV QLSAKKLKNP VERLNERARA GEFGNLETDE NAAMMFQDAV
 TEAEENEMFL WEGEKEKMDL TLFFSATDGL PKSSVRTLVG NADKALKKAM GAEMMASVY
 GIAITAMSF TDPSTLTLS GTLSQNVDLA GLSFPRRMGV RFAAPYVKRY NLVGSQVWMD
 AYSDAKFTKP LCKNFVHDDT LSVGEWARFY IKDSFSPNTA YLRRLRLNGT SGTLLIKTLFY
 KFTKGYQTNL KGRAFITDPV TDEKLIKNGL LIELVKNDAG DFVPGHVQFK TKKLNLDQLT
 QEQINMPGHD MIKQVDAMVD AVSALNVRY S EKP KAVFFVT PPHLMKYAKL ILILIKQLVD
 LNFDSSSYMR ENQKPDYKTR FMDDELGNLQ SEGHIAGFE TMLSIGLGQE QQFSATSCVA
 KNYALAA

> RXA01752 (1-552, translated) 184 residues
 MMEQDLSYRE ILPLNASEEK KKAALIDAIE GLRVDPPLLS ASIAFTRGQK VAFIAVVVGF
 ILMILFARQA ALIGLSATCT FMYLITLLDR FIMFSRGIRA ESIIQVSDDE ALAFPEDYKX
 TTYTLVLPAYG EPEVIAQLLA SMHAFDYPKH LLQVLLMLEE DDLFTIAAAE AAGVDQVATI
 IKVP

> RXA01753 (1-1539, translated) 513 residues
 MSNPSPLEPLE PIELSDGTEI EVSDVDPEPQ AGNAQMEVPS LRTYVFRGII AIACLIIGFY
 ESFVLMWQNL RIGVANYSL LVLMAIVFI GLDRKRARAL NIHDREVDYI IGGIVVLI AI
 TIKSQLLPRF VDWETLLRLD MFALLFFAFG ISGLVFGMRS TFSFAPGWIL LFGYNVAHL
 IISVIFGGGF WGPVMANIIG LSLAVLVSSN RDLVQATYLA LMTVLFGVII AIIWALTDG
 SKFLTLPVAV LATITVVLVS SRWRLGQWKI RRRQPTVEKA GPALIAVVVA TALLAWIPTP
 YVERVNNLPG LQMLAKPAPG VIAPIGWHID DVQYVNWASR YFGPGSSLLR QMTDADHYNE
 ANDPDGLDRV VVVDTLQSAE RFQQRAGFE TLYSTLRGK SDTVQVLDLGY GVDGRAYTVL
 DETDFELTYTK LVFEWQTTNN TVEKISVIAV DDHRAEAKFP ELAPSVTRMF IQVATILFRG
 NDVTIDTNTQ LKDLDLVSQV GRQIVAEQQV GRS

> RXA01754 (1-1941, translated) 647 residues
 VKIKSVFLST ALSASLLGI TTPVLGATIN PSLPLSALS SDDIAVPNFA KELPLAFDVP
 AGTVPQSLSG TLQIPAEFSG GVVEFYDGRD LFLHTLRLEVN DSRAHIEVPL QSVVPVEDGRA
 TFWLRAMLDP VNNQWCYEEQ EVRFLDGNVT FEGATINPVA VADYFPSVL R ALTIYVPENP
 SEAVQEATLE VATSLDSVYR RSGLDVNVET LPTGTDAPT RPQDFERQIV LVDEATESNT
 QKTELNVNPG DNAFLRLNGN ADELYDQARL LTDATLPLAV DTEVTAGSFG DVPNLSDDVA
 TLQELGTLQL TSESVARTSV TLGIERSRLR TYSQSMDLHI TGYTTPLPQV NAGQITFSIG
 DTVLDSLTTD DTGIIIDREFN VPGDLVNRVT AIVVEFTSTG DVNCGTQPV GLNIDSBLV
 TSQHSVDVPL NGFRSLPQSF QPRVDVAFAD PSVQELSRVA SVVLGQMS SQRIRPHLVN
 WDEAVASER TIFIDAAGAK TDQVPSYLAQ QGQTLLEITS NDQNDAGEQL TRSLQTNAAAL
 VSGSLQAVWD ADKKRTVIVA SSQDNPPDL ALISWMGEDR ERWSDNLGDL IRLVDRREP
 QLTTVPEAPDQ PGRSATAFIA IGVSLVLVIAL IVAAVSVSR RSQKGYK

> RXA01760 (1-282, translated) 94 residues
 MAAPLEITLK INDEGRPSAA GYQYQYKQPF LSSIAGATSK ELLIREEDVQ VLHGCDTVAN
 AEDYLVSELF TADVVGLAP LLQADPEIRI YQVA

> RXA01761 (1-1518, translated) 506 residues
 ADANADFVGD VVDGAGRASF SNAAYSSDGT TLDGEGASDV AQGNPLHADG TPMSAAEAEM
 KWAGLSSSGT MMEKSGVKSS GITTAADVMD DQSLASSVTE SGLSKIPDPT GADVSGAAGT
 VGTGTADYSA TDSSAGLNMS EAAQLQSGTGM GALAGGSVSS SDQAMNDAL QIAASQGLAP
 AGSIAGMEQL SAQATEAPAG KAGKQLGDL S GALNTQLAS MGQQVGDVSN SATYAGGMMG
 VDVAGKVTEA AQHLSQVPGQ IQNAVNTNADA GSSGASFGQM AQGAAGIAGV AGVIGAGAAA
 S8AAQAGATV AGMAGNAAAG AGMINNAVSG AGMISTGAH VVNASHGPVA PGQAHYQESG
 HAQAFVQNNQ ANTAHTANTR APSSAQIMGA NVAGSLASQA VRGIGQPGQM GANVRDAMGQ
 SGRSGRGGA TQGGRGARQS GVSANKGIRA QRQKPKSVTG QAMNAAMRA AVSGRMANMD
 GNSVGGTEAD PQQSGSVTEK GDKGVK

> RXA01765 (1-942, translated) 314 residues
 MSNNVVYKEC AVDADNIVAV DMHVHLEVD GCHKSPADI MAASSKYFKT AERTPSADAI
 ADIYREHKMA AVVFTIDART QMGHLPSNIS DLVASCARNN DVLIPFGSVD PRTGEDALVE
 ARRRQVELVG RGFKEHPSVQ GFDP8APEFY PLWELLESFG LPCVFHTGQD GSGAGLPPGR
 GKLFRLSNPM LDDVADDFP NLTIMAHPS VPMQDEANSI ATHKANFTFN LMSGSPKYFP

ESLVRQSNV LSKKVLFGTD FPLITPEKWL AAFANLPLKD EVRPGILKDN AVKVLGLAAS
TERGSQAQKV VQHA

> RXA01767 (1-336, translated) 112 residues
MIDHKLWFNT VTNNASVREA AGKCDIPIRT LNEQLNRRIL PEKTVIALAR AYDLSVPDVAL
VRTGHLTEEE AGSREEDASP DSADDTPTWA LNSHLDYGIL GAFGDIAEEV NS

> RXA01768 (1-378, translated) 126 residues
MSESTSSANS TTILNDTFNP KPGVPYARVD NLEFATRDEF RAWATAEMEA GNVISATIAN
APREDRIKSF VMDLVRDGID DAAEEIVSRI DSGDFTMKEA LTAIAASIND LDADDVSDI
VENHFN

> RXA01769 (1-429, translated) 143 residues
LGRAPHSLFF PIGFYITPMT SITTTDITPLY TALPHTRISD AELLTPTTTV HEILVYGPAE
CPGCTATLDF FARKNMPATK VTVAAGDVAH TYITQDLGYL QAPIVTVRIS SSASNHDNEH
NTQILHWSGV NRYLMQALSR THF

> RXA01770 (1-3765, translated) 1255 residues
MPIIIDNLNS DDDSTIGTAT EYNPDTDADL LDAINADADL DGDATISTNA TEEGVDAEAAE
KPKKKRKAPA LKPKGLTAKF FHRDLTGVG G RTGRLNKNVH PTNPDL SYQP VSDVYTPQSA
DHKGKTRTMY LTHPTPAVVL SESISNAFHV STLRNNNNVN NSDELAAPV YLYQLDIPQL
DQMINVADIC DYHFGHYNLW VDFTPQTIAL RSGKTVLDDG TTASDNTTHV YRVTVVHVIA
GQDHGSLTLD DQGNQVLDRO DNPSTPSIK RIGAVTDLFD HNPFGFASVN SFADFDFSD
PATTLVDMNL NDSYLSNHI NIASSPTPIA LDMVVLNEWS EKSQQLCERV VQAQKLINSN
KITAHVSDVI KQNAHNILWF TEQMNPGTTN LSEVPISKKS MLFMSRQLRI LEHYDVPLTA
YSALWTVSA IKNESMVQYL VRQNMQLTSL SNLDALNSIV SOLFVPDQDV VAASGYQIQP
HFSTQREAI TTDNPLAIQ ACAGTGKSTV ILERIEYLCA AGTNPEEATV LSTNNAADN
ITAKNDKVTIS MTISKMVHEI YAHNFPDHEI STIDTIINTL DIEYGDQMTV SDYMIQLRDL
LYKVMTPQGGN ANLTALSI FM ESHIEAFISV LDQIKQTSLE LEIICLYLL DKLEPHASP
KYLIIIDEVQD NSVFEFVFAL RFAAKHNTSL YLVGDSSQTL YEFRSANPKA LNSLEASGVF
GYTRLTNTYR NSQEILDFAH IHLSDIEANQ FAGIQLYANS FDAPTADSEK EKVPLDMHNV
SKQSEFTDSI PYFMSNKAR FDAAILNNEQ TIVLAHSGRE IRAAQALAE MYPSITVRNL
QSDKGFNNTV FSTFIKDFWF EVTAVDPAHA AFTFTSQVTA HLKDLVRGKR EQMEDRVIRS
MAAWWRNRE DQGWVQQTQ SGAITNEEFF YRLRQCILDY EIRNNRQKS MLNARNNANK
EAVAQEKPLL MVSTIHSAGK LEFDNVIVLQ KPSSDAEMTE EGKRATYVAL TRAKKRELI
AGSTRAYPRI VTDYEQIVDL LEKRDEERKI KEEEAALAT LEAEQETRAL AAAEAQALQ
LLEHNPLNVA LSDSEVTALT EQEIINNVEP ALQIEEEEE ARALAAAEPA IQYLSQFAF
DEFPPDDNVA NTVVHVAPQP ILHQAVPADV TVQSSAPVT PVVADLEVTV VADAVPEPTI
VAAQPEVDDN LVYSTSTPNS HSDVIAVNDS TSENAANPNV LSDIEALRAI FNNQD

> RXA01771 (1-702, translated) 234 residues
MHQAQQLIND PSQGLWRTSA LRSVPARVGH AVLRQRAEIS SRMQGREFSR PGDQFRQVDL
RRRLIQVHQP SIPTADAMAV TITMALTAAT IDPVKFVADS QNPDEIYLA AQIALREMI
AMPLEDPIGV RIDLEPVLVA AQAAAKNVGV EVSSILLKDL NLPQEYSQAL QESIYAKIQA
ETDLERARNE VKTTRARLAS AKVLEQNPL AKIRMIALP FGSTIEVREG DSKA

> RXA01773 (1-411, translated) 137 residues
MITHIQAGHL LGGCRAAGLL PIPAHIDHIV RLTAADFYDT QSAFQLLSNT VLDVLDTTTQ
DLKALWPAVE HIATTIPSE NVLIHCQMGMI NRSALMTRV LMLRNDCTAD EAIALLRDRR
SPFVLNFNEH VEQLRAL

> RXA01774 (1-783, translated) 261 residues
MSPNFQARGT TAPTVALSMR QIAHIREEEK KSPLAASVFI TPTTKQMVRV DLESFLQQLY
HTDLPEPSIK DSGLLISAIGS SAGNTNNPAL ALETQMAHYL VLAHHTDVA THWVHTKNI
TESAAAGDAA VEHSAKYDAV YDAAQLMGIT VEEGNVGSIA IAFSTARADG KSDWCVSGIS
RYIEVTEALD AARAVTKNTD ALNKTALPDV QPAFVVHSAQ FMNKSADHDG VNTAEKDQPT
CLKTVHLQPH RYPRTGFKAI Q

> RXA01775 (1-564, translated) 188 residues
MSYSLIISKA PTHSMFPNEA ELLELVDLH SDNTVKKPVI VPLPDDFSYK VDSAVRLHDL
GVDQKLTDWI TAQVAAAYPN QIVSEIAAAP DPQAKTLFSA NAYNTRSGT FWEHFIPTQL

QYKRCYQIVI ENVTGVYHPL PVDNYRYVPP VTPSLPQPVY HEAIALNESD VADHGTRAAK
HAMINRNV

> RXA01776 (1-1452, translated) 484 residues

MTHTDTPAPA HGVTPSEFAV TSHELTTSPT PSPTQVAIAA QEKIRQRKLE ELKAKKRTDT
TAQPLLPAFV LHTRPLPSN PPRSPPPAPT TGHWELLIVR SQKKMTAAN PFLKFLHLGK
AFNVKDLGLT CDRTTDDVLS RLGLKLNPPSS LILELATALD LHPFLSVALS SHSAVNARRN
QLELTLNHHO TQGTALGHVS TMVQLPEVIN RAAVEPYIKV KSGNDPLDQ SLNHRAPTVS
DVQKALVQEN TGTATDSNNY LLPFDPDGSA PKTALNAPN KDLQARHEL AYIPEIPAIA
SWLDHLDPIM RVHRSLSLSI FEVQLLRAAV ENLPHNVTDL HNHLDPEDLL PEELTTLWLDH
LFDADLTALA SCPQLAPPIV RSHNHAKAIA AITVTSVMDA LIAKTLDAHD DPLPSLPEFV
ELLRDAVAQL AAHFQQRGE VLPQPNGLRY ATDFGLLSYI ADGLHEYALA IDFGLIYPNE
LITE

> RXA01777 (1-459, translated) 153 residues

MSRIITAPVH KPVIAREVK GVSHVHDTVQ GKWQATLHTL KPGPSWPKPS QFTAPKSTSI
WFIAVATHPR NFRARKGTLL GRGGLYELKD TDLNFLTERTQ DLLATSTSRD PEDCLRLFNS
RHDAAPFLHA NARHINKLFH PALGHARYDL IDV

> RXA01778 (1-1137, translated) 379 residues

MLYQATTTRGL IISDAIIAKI SQVNQLLLLR PTLQDKDMH HATLSSSDTPS IRSRRRSYRE
NKAAVATST IKNRETFFST SDIDFAILLI QDVQESLVSF DPTLAQDMKP RTRNAVIALN
ELREPLDTFY RAHEYGDIIS OGAYEFDHAA IDAQHSLSEL VAGLHNYDNL MFPQETAPLM
SESNGIQLAQ YKSTKLDIES QLTVEPNPFG ISIMWHAHFD TWGSLVRYDD MNRYPEHFSI
SFKDMLPEQ IYTHFTPRE AMQLRKGLFN AIAAYKSQWV GDENTDLTKA ELEFGGTSMT
FRAGLSQLSV TGGPDHRQVF CLSSSGREDH NTPPNMRDGH VIDIAVTQLS TLRNLIRVLC
TTPDHPSPAL LPIYQQQYTI

> RXA01779 (1-1419, translated) 473 residues

MRYTPRTHRA LGLAALTATA LLLSSCSSTA DLLGADSVAQ AVTDGGSALD PTAHHVLTIT
NATAMTIAEL PENTDPDAAN NTEPTMAQSA LKRIYGLEIA ADGTLIAVAA PLTSRNSGSE
QPTVAAMADD ENNAELTAAH ILEIDPATGT ATPRQDIALT EDFQTMASFF SQIRNGWGTT
QLIGQHPPDP KQPIRSADTW TWTGSTQITG FNTNTPTGTG DAAYTMPATE PAVGLCALES
GSDAPLDEHR ELSTSALRTA SVLSSSSGSAT LKLHDFMVMS ATGIVQARAY VDGVEVINQHE
IGDLREQLGI TIEESEAAQA ESDAQAAATDH PLAALGSLNP TSSALVPLGA ELDCLSDAQQA
ATWHLNRTSI GTGKPSVLAV INAEMADDTF LQLLSSGATT AETQLAQPLD ETAFVLIDPS
SGAVTDLFFI QSLNTDLPAP TTQINSIAVD ERDPNIIYAT FSGDDHLVQM MLG

> RXA01780 (1-375, translated) 125 residues

MTFLHPKAAF YPLTMDHLTD LGLDPEQLIN ELPTITYDVQ PHNVFVLQFS TADVRVYQEG
NTLFFRSACL INPELRQRQR TQLNDDLNNP ASLRVCDEIS GRSTVFLKDK SVVTHDHGTN
CCDSA

> RXA01781 (1-261, translated) 87 residues

VLSLIITGPI AVIPHNPDAA SAKAVATKHK HTLSGATSDH PYAGMILKDM IEQGFTLTPL
EFPLCAVDDP TDSRTMHVI NVREHSM

> RXA01782 (1-396, translated) 132 residues

MTTFALIASP NNVDPTAESL LAIEIHTDDE SSYPLGLIDS DHLVPAVIYG DMVIYTKTLL
AQTPDDVST ASAFEDKLTA LDAQGRTRDL VYSATYSQLV IAGHNRTVLT DDSEFYDEFY
QVIEAAPGVI LK

> RXA01783 (1-237, translated) 79 residues

MINLFMAALP AFEPLSITSI LVLGAVALIC GLPVFLALEK SAELDDLFAA LIIAVLLGFA
AYTFVLPKLV ELGCTICQL

> RXA01785 (1-576, translated) 192 residues

VDQFVEFGGG QANINPDGSA TVDWECSFSI NFDYGLVPFT ITNPHLEVSV AGTGVLTGDL
TSYAVEMSNP NEKFTLTDLY EDVITITFFG VNLDPGEVVT SNPDYDGVIV DVPLDATSQV
TSGAGWGAWP QGFGLDFHEDT NLPYWYSSD GAGDPKKAPM SFNVDTNGP GLVNSQLLHR
QVISMPETKA VS

> RXA01787 (1-354, translated) 118 residues
TEKIDKAQPP VDQLGSLHG LETSVADLGV GDRVFLPRFS TFDKKLGRYR IHTVLGFAEN
DPFNPMTSSE RFKKGKPYVDM FDNQDNANFP NSYITTTDTR IVVDPVPETN PDDEKAGR

> RXA01788 (1-441, translated) 147 residues
MSRSYPIYII SFAPADDLHG VGGFEWVPAS TPENKAAAF TFRQFDDSR NNGGSHIVRL
LNISDPNITA DMTQDDITAY LDSNIDRWES TEHALKQFVP LNAGADRVP GTGADEHITHA
CRIITVQRSC TRIHLRCGCI PTPQHRP

> RXA01789 (1-642, translated) 214 residues
MPHNPIELHT NDVLDAALDID AICDDVFLYT DFHTPGQLD RFEQLAFTKI YDMLETAEEK
FPDVAINDCT STGNHAAEQY FLANPGNIIV LTSFALNQTD LRLDIISPCI KYTAHARALM
RAVTRTLCCT NNVERATIF PVSVALNSI EALCSEYHAF RTKQVLNTAA LINPONTLIP
MLLSKAYEAY AWHKGVESAQ RGSNLAREYY AGLI

> RXA01790 (1-60, translated) 20 residues
VLIAEDIRDM DDYGEDHPDL

> RXA01791 (1-363, translated) 121 residues
MTSPPTTLKPW SIRGPIDGEX TMLAAYPFQY VANTRPAIML YALDENGVEP QYADLTINLA
DVELKQLNHV IINPDLHADV TELCISAGLL RFGVLGQHQP GSTTAKVYRL TERADGWLQL
F

> RXA01792 (1-273, translated) 91 residues
MPQYITITID EQKAVLHSLT NPHIATAEHG AITAIEIHDH HDVVVYHVQP DGTILTYERLV
EGFHYGWTRF DSEGEFIDSD NNRVVDGLRD E

> RXA01793 (1-234, translated) 78 residues
MAQYRVSFIA LAESTIEVEA DSPEEALDLA NAEFDYPVTL AGDPYELHDW EARAEIEWLD
TSSTPQQLRG EHVVKIED

> RXA01794 (1-234, translated) 78 residues
MATHRVHFVA TASAYIDVEA DSPEDAIEKA YDLAGDLPLG IADNEFDLGE WEVQADVQWP
DNSVPREQLR EEGVDLLD

> RXA01796 (1-483, translated) 161 residues
FYCPSDQDAY VDLTLFDQMR QFGAENAPLA QMYIVAHEYG HHVQNLEGLT GLSNYNDPGA
DSNAVKIELQ ADCYAGIWAN HSSEGPDPPL QPITESELDs ALLAAASAVGD DNIQQRSGGD
VNPESWTHGS SQQRKDAFLA GYNTGQMSAC DFLGRGVYND A

> RXA01799 (1-1194, translated) 398 residues
MEIPLPSTSLI DVITDGAALGQ TCIDQAFAAQ LGRVTGVEFN LSDDKTAAEV RINKASGSPF
DTTGEVIAWI NNQEFEWVST RGEDLGLPEL QGIQPLDDDL ITAARTLYSN APAFIAPLRD
GRRALVAINH TPKLVGIRRT LIEGLQALKP GTDLKRALTS FAFACELGIR FDDNRISFSD
GTSLLLRGGK VIEIAGGLSL RDVRADAAM SAEHQQLLFA ISSSHNVTFD PHTNVATVAN
EHQVHAIPLA VFDGTRWVWT WSLKELNGQA TEGLARFGFD NGLLLLTNAE ILAEATAFN
LIDVAKQVLN TWTHTIVQQP DGTGIVLLLD HPRQLPPLAS HAAVEATLYH QLPGLDIDARR
AVASVAHRQ LFFDGYALTV EGQQVGVTFD GEHLTKVG

> RXA01800 (1-720, translated) 240 residues
VKPLGKIAPV WTWYLGIVGV IIFDVVAAIT MLTLVPNKMP ERVNSGLVAL GGSYAPPMR
ETLIARVIAG AVLVLVISLG ISLLISAQSK NLASDHPDAS AIQIARRWAF LNNIQSCIGW
FSFFLAAILS ISSRLRNGPG ATTHLEMAVY IIAVSVLAWA LMISLRGGQV AIDRAIPRE
DDSELKGMGI YHDASDKRVF VELDDGHTTV INMARGGAWL LIAMVYLPAL AIVGWVLEN

> RXA01803 (1-960, translated) 320 residues
MRKKKDGQNL PDRKNPPKL DKKAYEKELK RLQAEVLVDLQ QWVETGARV VIVMEGRDAA
KGKSAIKRGT QYLNPRASRI EALPTPSNRE KGQWYFQRYI EKLPAGEIV IFDRSWYNRA
GVERVMGFCT SQEYRRLHQ APIFERLLVE DGIHLRKYWF SVSDEEQIER FEDRLSDPLR
RWKLSFMDLQ SITRWEDYSR AKDEMFIHTD IPSAPWYTVS SEDKKRSRIN VISHLLSTIP

YEKIDRPLPE IPHRPDSESD YVRPPRDEFR YVPDVAHLE EERIKKEEKA KKAKKPAKAA
GKNSDKQKSS GKGKKKSKK

> RXA01804 (1-321, translated) 107 residues
MHIVNIRFKP KAKYVDTRY TVDKFTESTR TEEGLYFDW FRNTDYPGEY LVIGVWTDG
ATEHKKSEHF LRAQETLPL LQQTPMIQQ EFSKKKGWER FSDFTVY

> RXA01805 (1-330, translated) 110 residues
VVVVILINVK FKPLPEYVDY FREQVAEFTE KTRAEGNIF FDWSINTDNP NEFILIEAFQ
DDAAEAHVS DHFKAACELF PTILSETPEI INTLIEKTE WDRMAEFAVN

> RXA01806 (1-480, translated) 160 residues
MSSLDNAPLL ELDVQEWVNH EGLSNEDLRG KVVVVVEFQM LCPGCVNHGV POAQKIHRMI
DESQVQVIGL HSVFEHHDVM TPEALKVFD EFGIKFPVAV OMPREGQRIQ STMKKYRLEG
TPSITLADR GRIRQVQFGQ VDDFVLGLLL GSLSETDET

> RXA01809 (1-636, translated) 212 residues
HIRHEQAMRD GHQDLSVFGV ADGAIMELEL KNRYQRPEN EPHDDVDTEM IKTEETEKE
NVEMQDIAV VDNVDEQVVV TPAHDADSV VVAEQVVASE PTPEPVKVE HVEMSVDLAG
ETITPIDQAI RSFQMLNGIE HSVVLRRLGL MTQVAHNKEL DEVIYAKALAE GESHAQQQHE
LEAENLRKK EVDLAAELLS AALMGECCGD HD

> RXA01812 (1-1230, translated) 410 residues
SFNDVDPAVT HPHLTIVYYP LTPASEEKN KITSVAASK RPTTLPYFRA DGSPTRGFAN
FSTGGIHGAE VDNDFRDHQQ DLHTVATREF FAILDATLAA LYAAHQAEPE SADYQIAQDA
LAWAKNVLSO QKLIKSPQL YNPETGVTYE WEFVAQAANW IRNKPVEVIL PTGESMTVKH
KSVLASASYP LONVAVYWR EPKTFQLFPV AKSGGSSLEK KYNNTSVGTA IHEDFSSYPY
LLLTNMAFT NADLGIDEKT GRPRDRIYET YEQKEIYGAQ RKDPSIDERT KQRLGILREG
TKLILNSATG AADAGHOTPI LMNNRVIAMR IIGQLFSWRI GQQAQSLAGAT IISTNTDGLY
SVLDMGTNRQ VLDEHATAIG VQIEPEELDI VSKDSNSRAE FLNGYINAA

> RXA01813 (1-630, translated) 210 residues
MVAIVVVAIV VVGFIYQGG GSKAAKLGDR DYEDTSLAME VGSDSITLTS ANTSADAKSV
QLFEDFSCSH CSELSLATDA DMKTQIEDGN LVVEIKPLNF LDRENIDGHS THALAAALAV
ADSNDATLYW NFRAFLEMDQ SEIYNQWSD DFADGVEALG ADSSVVDAIR TATTSSAHTT
WQPQTIVKNSL KKPACSYHA FFKTARMLKA

> RXA01815 (1-792, translated) 264 residues
MNRSTAGPE ARQQFRAGLI QPTSGWSAGF AQANLISMPQ DLAYDFLLFA QRNPKPCPIL
EVLNAGTEFG GIFGSNATEA DIRTAPQYR IYAHGELIDS PASAVDYWRD DLVSFIIGCS
FTFHEPMVQA GVPVRHLEAG RNVMYETSL ACRPAGSLSG NLVWSLRIMP ASQVADAVRI
TSRYPAVHGA PVHTGDPSLI GIDDINPDF GDAPLSEPSD VPFVWACGVY PQAMVMSSKP
PLAITHAPGH MLITDAPDGL FQVP

> RXA01816 (1-732, translated) 244 residues
VQLLHTPAAI SISFDDPNLI STAGLVPTMA LAEDRLTVPT DKGANPGAKI TTLIAGMVAG
ADSIDDDAL RHGGMHRLFD WIYAPSTLGS FLRAFTGHV RQLDAVASRF LVGLATQAPA
LVPVDASTSD YVFIDVDVTI IKVHGQKQG AGFGYSGIRG LNALLATVTT PESAPVVVAQ
RLRKSGCSGP RGAGRLIADA VATRRRLPGM EDEKILLRAD SAFYGHPSIS AAIKAGADV
SRGC

> RXA01817 (1-633, translated) 211 residues
MTPNVKKAIA QVPDDAWQTI KYTNAIFDDE TGRWISVAEV AEIPFTAFTS RKKTDHIPGL
LVVRIPELN NKVDQPGFL DLHRFHAVFT TADPGILDTV AADKTHRQHA IIEQVNAVVK
ASALAHMPSG VFTANSALV CAVMAFNLTR TAGVIAAGAM ARATTATIRR KLVAVPARIA
RSARRLLHL PRNWRWETQW SRLCDHGRLP P

> RXA01820 (1-1374, translated) 458 residues
MSASFDDPNL ISLAGLVPTM HLADAASLST LAQDRLSITG DKGANAGAKI ASLVAGMVAG
ADSIDDDMVL RHGGMRRLEF RIYAPSTLGS FLRAFTGHV RQLDAVASRF LVNLAQAPH
LVPPPPAGSG RGGVVFVDV DTIEVHGHT KQAGFGYSG IRLNALLAT VTQAQSAPII

VGQRLRKGGSC GSPRGAAHRLI ADAMTTTTRL PGMEDKKILV RADSAYYGHF SVSVALRSGA
 DVSVTVRMTF NVKKAIVAIP EDAWQTIQYT DAIFDEASQS WISLAQVAEV PFTAFTSRKK
 ADHVPGRLLVV RRIPELNKKD VYQPLGFDLH RFHAVFTTAD PGVLDOTVAAD KTHRQHAIE
 QVNADLKASA LAHLPSGTFT ANSAWLCAV MAFNLTRATG VIAAGGMAKA TTATIRRTLM
 AVPARVARRS RRLVLHLPEG WTWQPQWQKL FDHGHSP

> RXA01825 (1-270, translated) 90 residues
 MPKARVTKNE TAPVSSNPISA NRTPVKINSA GTPMWYKVM FAFMIVGLAW LIINYLVGPO
 IPFMADLGAW NYGIGFGLMI IGLMTMGWR

> RXA01831 (1-462, translated) 154 residues
 MDLSVLLGLR IALLVVLWFF VLMALRAMRA DLKVTGQAST SSSSVAAPQG LARAFNRSSP
 PRLLTVVEGP LAGSSIEVSE DMTMGSRSPEC TFFVGGDDYAS GMHARVFKRG SEWFVEDLDS
 RNGTFVGGTR IDGPEQIAVG TDIRIGRTAV RLVP

> RXA01834 (1-702, translated) 234 residues
 MLGGGGAILA IPLLIIYGFSF SATQATAASL IIGLGLALIG LISQYAAGHV RLKEGLSFLG
 LGLVGSFVGS HIASNIPDSL LLSGFALITL VVALTMISKL RSTREYITRR PSILALIALSA
 TGVGFITGFF GVGGGFAIVP ALIFALGFSM QOASATSLV AVNSAIAMG FRYSDLASID
 WSVISPIIT TVLGAFGSVK LAKKVKASSL QLGAFAGFLIF ISIIYMGQNF PDLF

> RXA01842 (1-918, translated) 306 residues
 MSKVYVSNEY GGFENQELIT RNTPOGPGE LGVKVHAAGV NPLDWKVRSG VAGTPRELPA
 PLGEEASGIV TAVGDGVEGF AVGDPEVLGLV APGVGGYAEQ TLLVAESTVL KPEEISFTDA
 AAPVAGASA YAGTHQVELE PGQSLLINGA GGGVGLMAAQ IGRVHKFQV GVDHEDKREL
 IESTGAIVFA TGDVAEQVR ALLPDGVDVV FDLVGGEARL VVAPLAKNPA HVISAADRAAT
 VGELGGQVLR RTPEMVQGIT GVVQYGLVDP KVDTTYPLEQ AGKALAHVEQ GHARGKIVLE
 LITSQD

> RXA01844 (1-180, translated) 60 residues
 VVSIQAQLEI IEDGTGAVLV SEQATTFDNG FIGYSYFTTG TDGATCITDL RLRASPLPQV

> RXA01845 (1-408, translated) 136 residues
 MISNSWAIEI TCALYLPVEA LAEVVDAYPO LALAIRMQQ DQLVRSRERE TAQTTSTVEQ
 RVAAALQHLQ AKLGGIRQDG SLLQVRLRR DDVAGTTVES ASRAMARMKK TGVIDSGREW
 IAITNHQALA DLVAGL

> RXA01846 (1-258, translated) 86 residues
 MSIPGNVSYV AQGGTGWDGA DQYTTGESWD LQSFLNSTD YLMIIGSSLL ALVGGAIVIV
 GFVNVMRXL FGGSQQIQW FTTILL

> RXA01847 (1-735, translated) 245 residues
 MLIVLPPSET KTHGGSGKPL DFHHLSPFSL TKARQILAD LQALEVDEAL KVLGISEKLR
 PEAESNRAL TSPTMPAIFR YSGVLYDAL AATLPEKALE RLAIQSALFG VIHATDPIPH
 YRLSGGKLP TKSGLPTMK ARWGTISEA LIDVNQLVID LRSQTYQQLG RVKDAVTVRV
 ESMEDGSRK VVSHFNKHYK GELARVLALS EKEAHTAEDV MSIAQAAGLV VEENPNHKET
 LTLVV

> RXA01856 (1-546, translated) 182 residues
 MNPFSLDTLI VQQTSSFLSN NFEIYNPDGE VVIRIKTEFS LGSRLVGDR RFTLEDAFTG
 PLMQVRDPMN FVRDTEYIDD PNGNPIAHVR KRFTTFNKRK DIELPGDRVI EMHGNFLGFE
 FEFMRGDRIP AKVTRKWSGA GNGYLGRSTY ALIFDEAEP EIRKVIIGM VADLIRREKE
 RN

> RXA01857 (1-651, translated) 217 residues
 MASRRFRMML TASITAASLG FSLTPAIADE AVTVATAPSV GFDSGVERDA PFTAVPHDVV
 LGVGATQSEL INFNWITAQGL TGQVAQISLD DTFASPTVD AVSENVISVN TEGDSRDRAE
 GEYVEYRDGA VNRAITVDSL ENTYSYRVG SEADGWSEVQ TFNTGTYGDN WNLFFGDTQ
 LYNTHSNRAE EVQNWANNLE RRPTRNRKPRN LLHPLRG

> RXA01858 (1-573, translated) 191 residues

MFMTPRALTE DNELTLALKS LGLMLVSPNE CSVVTEVMPT WRELWHQRLR WQRGALENLG
 AYGITPQTRR YWQQLGIGY GALALVAYFA VIIITFLARD QMIWYFWMML LGLLFMIERV
 LTVWRSTWFA RFVAALLIPE LIYASYNLV FLKGVVDILL AKQAHWGEHG DKTMQVADAA
 AEINDEEGER R

> RXA01870 (1-675, translated) 225 residues
 VGVAVVLLLL PTILNLVVPD KANDYKQLEI DLLGVDWVSP ITTEESAVAL CEETSDEITQ
 KYWDCNGDIT VVTMIVEGVK DPSNTLRRMV GSSLITSVDL SLEAVSDEGD RAHALYVPCQ
 QEGSLMTLPI VALSVQSGSD YEDLTAIAII NGTSLDYYST HIWSSMAADR GLPYQQDFPL
 MLEEEFPQDIT PGDRPFPELP NDFFDQYFPL FGPGSVIPNL EGESL

> RXA01871 (1-963, translated) 321 residues
 MSRMFSITLW VAILLSTPAL FLSLATFIFV DGISVLNVIV FAVLYLVVIV FLISRTPLWP
 RFKSGSGSKG GGFAWAASSL LWGAFVGFEG VMLFAGPVMD LTKDLGWDFV AMSFTGAYPE
 EIAKALGVAI ILLSFRQLNR PWHGFITGAL VGLGFVFNEN LLYGATGKML DPNADLDGVL
 MMWQYRTMLG PLIHTLLTGF AGYGIALAFF RARKTVAWRW GVAIGWTLIA FALHFSWNLM
 WENIVGSIYV IIVVSVVMYG LAIYILWSNW AEARNDSSYA FVPGIITNTK DLSLLDAPIP
 VGAEVPESRI PQQIEEPKAE N

> RXA01874 (1-348, translated) 116 residues
 VIAYVASACC LPFGAFAGAL LSKELSGHLQ ERVLLTHTVI NFLGFVGFAA LGSLSVLFAA
 IWTKIRIHNF TPWSVGIMAV SLPIIVTGAL LNNGYVAAQV WPRTWQHGCW PWNGGG

> RXA01875 (1-798, translated) 266 residues
 VDSLNLKQVA ASDIVAIVRN EEKAADLKAR GIALGVATFE DEAAALTALE GVDRLVFISG
 SEVQGRVAQH TNVINAAKAA GVTFIATYTS LNLGTSKLAL APEHIATGKL LAESGDIGHAL
 LRNGWYWENY ESSIGAAKAT GKVFGAEEGA RVSAARAKDY AEAANVITS DNAGKVVYEL
 AGAPALTYPE IAAGIGEVIG SEAEYVNLVS EYQNALEQA GVPAEFAALL AGMDPIIAG
 ALYSDSTDLQ DLIGRPSTSI VEALSS

> RXA01877 (1-1065, translated) 355 residues
 LRLATGGVLA TLLIGGVTA AATKKDIIVDV NGEQMSLVMT SGTVEGVLAQ AGVELGDQDI
 VSPSLDSSIS DEDTIVVRTA KQVALVVEGQ IQNVTTTAVS VEDLLQEVGG ITGADAVDAD
 LSETIPESGL KVSVTKPKII SINDGGKVTY VSLAAQNVQE ALELRDIELG AQDRINVLPLD
 QQLKNNAAIQ IDRVNTEIIT ETVSFDAPET VYDDPEAPAG DETVVEEGAP KTEKVTRTVT
 TVNGQEEEST VINEVEITAA KPATISRGTK TAAANSVWDQ LAQCESGGNW AINTNGNFGS
 GLQFHPQTLW AYGGGAFSGD ASGASREQQI SIAEKVQAAQ GWAQWAPACTA SLGIR

> RXA01879 (1-588, translated) 196 residues
 VKITAKAWAK TNLHLGVGPA HDDGFHELMT VFQITDLFDT VTLTTLDEEL VEEGSVVKQL
 SVTGARGVPE DASNLAWRAV DALVKRAEK TPLSAVSLHI SKGIPVAGGM AGGSADAAAT
 LRAVDWIGP FGEDTLLEVA AELGSDVFPFC LLGSTMRTGT RGEQLVDMLT RKKLHWVAA
 MAHGLSTLRY SKSMMS

> RXA01880 (1-408, translated) 136 residues
 LGGGDGDGAWP VHEPVFKKHD ELNPESHMDI SDLSAALLTG NTAEVQGWLH NDLTSAALS
 RPELRSVLQE GIRSGAHAGI VSGSGPTTFV LCESEKHAQD VKEALIDAGQ VYAAATATGP
 AASTADQKGA HLTVS

> RXA01896 (1-579, translated) 193 residues
 ARAALHAWSP TVGVDTDVER WIELDKWGFA RFERGETTHL QRRDRIRAY LNRELDATC
 DDIYSGYLKA YEQNWTAYPD AKGVLDRAVA TGAPVGILTN GAAPMQQDKL DRGLGLPEL
 VMLASFLDS AKRPFEMYAR ALTHLGARTA TIIGDDWTND VAAPRELGNW ALYLDRSRGT
 PRADHSLDE LEH

> RXA01899 (1-786, translated) 262 residues
 MSRTLWAVSD LHVTFQANQN TVDALMPQDP GDWLIVAGDV AEKIPDVVTR LSALVKRFD
 VIVWPGNHLE FNKRTDRVNG KARYALVGG LRAIGVITPE DYPYIFGGVT ICPLFTLYDY
 SFRPLGLTAK QALQAQIKIL DDELAIAFV TYTEDRLKAT GKPKVLNVNH
 PLVIEPHTRL FQKDIALWCG TTATRDWAVR FNALMAIHGH LHIAETRVD GVSHVEVSLG
 YPFKEHPHMH KRPWFPPVMQ IN

> RXA01902 (1-864, translated) 288 residues
 NYDAYNAMY P RPNOVDENYF FEYNALFLS LDSNDYLDID DDIAFLRDTV AAHGDDKDWI
 VLTYHHSTFS QAYHMDARI KYQERLTPV ISELNVDLVL GGHDIHYTRS HLMNGETPVD
 AGREAVVGET LNPKAGEVVY LATNSSSGSK FYDFYDFQLG QRYDTGLDFQ ETVDQKKIRT
 YTAWNQDQV QDYTNVELTP EGLTVTTKDA VSGELVDQFT LSKQDRDEES EUPVEDDKDG
 DNATGSSNLG LAAILAPVLA IFGFVGGFLV GGGSLAEFFA NLGVKMPF

> RXA01903 (1-279, translated) 93 residues
 AHLDDRGIYI IPAQYPWGYE EIINLPARAT STPAVAPRTE AAPATVSDAE VQSLLLEYLRAT
 NAFVSRHGDG TTKADIFNKH ADTVNKLAAL RAP

> RXA01904 (1-423, translated) 141 residues
 MSISPKNSGT PNENAAAAQV AANLANLTSQ ATGSMDETNE QVIKSNEHGS DAYLADIKAS
 REMWAKIALD PNQSEETRKE ARENMARIDE YAREHDKDNK GLLQKLAKNK AELIGTVAVA
 TLGVAAIAN NGKIPMIQLK K

> RXA01905 (1-531, translated) 177 residues
 MKASQTLTRN TRARKLGMGI LAATIMATGA LAGTAPQATA AVDTTAPYVS YVVDIPGKVG
 EPIKPYLTI SDQSAYVTFT KYMPSWLKYD ANKKMLYGTPT TEVDVVTPEV HVVDAGHGNKT
 VRYFTVAVAP ANTGTPTTTP STSKPSTPQV TTPTPKAPT LPKSTFDWTL WGSIFGF

> RXA01906 (1-465, translated) 155 residues
 MSEFPTPTTF HVEPETLSSA TDLTVDAHKI AELLSTTQY RVFYMPLRAG VTPIVSYLYV
 YDGENFLVIG RSTHVPWEYY VHYPIKPSRE FGSAIAPLVD DSDDPYDAE VVALVKYMT
 PTLTPGEGYM QGFYKGLTFT NHDIDRPLT QIISD

> RXA01907 (1-612, translated) 204 residues
 MSAPDELKRN YRYKFTDTWP ANAVTGTGYI ANPAFIIISA DAMTQNTHAD SNLITVKEHL
 NTLFPYSVQR KDRAFVSEIY TPINLLEDNP ELAQEILDVL DTLSNNAVFN DAHYSELELE
 RLNEVVIDTL AYDMKSDMMR ALVKARPEAD LEAMEELDIA NIQSWINLHS STVSEHNDGS
 VDDAPFNLSA LAEYILQQLA DHTV

> RXA01908 (1-483, translated) 161 residues
 MHSDFEFHPD NGYGYTIRQD TDAENPMTHH DTKDAALWVH NRPRRGDTVA DKPEGNEILD
 IFAKIFGQGH DNDNPFVEVW SDGSDASLAI RTKAYVAEHH BELIFDISAK TITGYSQGDW
 LDVVCVTTAA TCDELIPADS LIDIYRQWAF GDVWTVIPDS Q

> RXA01909 (1-879, translated) 293 residues
 MANFRSKDKD GNVINPNAST KGVLDLVNVY DSAKHVTEKG NTVHFVDVQV AQIPIDAGT
 RANANLAPQT MFHLHLDTKD QGRNTGVAYS DAQIQAMQTV AAQRNRHMT LLSKDGGETVG
 YSMLVKADVM FPKTKDGKSL PAVMNTKSLQ PSGVPSIDAM NIQQQQFMV AMNRQAAEAQ
 KAAQAQATQA QAPQVAPQPV MQNQQQQAPV PQQQQPAYAG APVYADAVAH ATNQAAAAA
 QAPQAPAGNP FNQPPAVAAA LAPQTQPPAV AALALPQTQQ PAAQQPMQDNE PPF

> RXA01910 (1-846, translated) 282 residues
 MAFPLLAAGV TVAPVAAGWA KDKFLNSQNG QQQAQQQMS FGQVNSNAQN SGENSGFMG
 QYGNLGAAGL GAATGAGLAY SDFEDGQSLS SKARNHVGKG LAGAGAGVFT KLANDAIQAE
 GSGMKASAYS ATASGLGSLY KNGGPGVIKS AMASGAAGFG ADKVRDKLAE SGHEGLADSL
 SGALQGGGLG YSTLGGVTGA GIGGATGGLA GLAQNYFGGG DRYSNAGASA SGFSANQVNS
 EISTEIPQFA NLGQPQRSEL EQLALPQESR SVDKSYDQGY EA

> RXA01911 (1-846, translated) 282 residues
 VFIIGAGLPL LYVPIFVTYI VMVYALLRY EQRMSTGYVE EADPVEMDSV IWEGIKCDIA
 SDIAARAEAK KAKKPVASDA VAVGNVIALS RQHMLVETQR RYHKLGLREL HNDPAQLEDY
 GSGLRDCECR ACVVAQKLGV TVHAHGVVQA SARKKDRVII GRADGIDVAG WNNHRQEARR
 KTSAAKQLER DAQRKRTQAE RDKEIERKRR AQEFVAEQSG KAAAQRRAE KKAQKQARVD
 ELVAQKQAAQ EQKTHCKRDK QRAKKAQGRK VGAVDVSAYD DV

> RXA01921 (1-939, translated) 313 residues
 HIDIQRLNEK QLFVGLKRLI GLLGHQILES DRLSGDDAHV DTNEDVLDLI AYNVSDVVG

RLLAEDPVYS GSFDLRAGLL STYPETVFDH DGTFRQPSQ MRKDRLTINT SSAQFAARIL
 APYRPLRDVP DAIGDMPVVS YLYPDAVAE ATGQKQVNLV DESKKFFYDN ITDPEARAAF
 DEVFAFYADI EGRNFNHNE AIDTQINQLR AYLNQVAFD AAGYALYDVR TRFEQIFPKD
 RSYINDATDM TPRAVSSFDD LVALCDDIRG VLDRGLEISS PNHHMVDAM RKQLHYIQAF
 TVPGTHQRRE NDA

> RXA01923 (1-429, translated) 143 residues
 MSALIKSGGP HHVVVLNGWF GHAAGWGAFD DYLDLGNVYV HFWDYRGYGN RKDDAGEFTL
 EELISADIVAY IDSIEAEKVS ILGHSMGGVF MQKVLADSAT PIASLVGISA VAAAGTPFDE
 DSRKLFITAG HNPDSERRAI DFT

> RXA01930 (1-951, translated) 317 residues
 VISTNEIENI HSTRRDIEIA LDESSTSEPK RFSEISHLYL ALAEGKISFP ESPSELRELY
 DHLMHGELGK ENELDGEIFR QGPVEIRDSR OKVIHSGFSP ESQIEGNA IILAHSEEE
 SNLVGIMMSH FMFESIHPFY DGNNGRTGRYL LGIQLSKILS PATALTMSSA INQFNKKYK
 AFHAVEHRLN RGDGTPFVVIS MLELLIAAQE GLIENIKQRI DFLASLEDAI KTLRGNTSFK
 NHQINLLYIL GQIQLFPKDE TLSLESAAKE LKVSKATATR YFRTLREML VHEVSKRPLR
 FALTDKGREI VGLEVKI

> RXA01931 (1-654, translated) 218 residues
 MSTSFESIPG VTISARKALS TAGFKDLESL AGTNYEEVAG LSGIGARTLE RLQAALVEKR
 MSFEGKVPPEA EQRTATWTTL DSAAPEATEP SESPEYFIQN LDIPRRITHG RLLLEIFNRA
 TGQKPYVAGS SIVGYGRVHY RYATGREGIT IRVGFSPRKA KISLYGLTSA PASRELLKKL
 GKHSVGVSCS YINKPEDVDL EVLEEMIRIS WEAEPGEC

> RXA01941 (1-435, translated) 145 residues
 MALTSLLHLQ ADKKHSDLSR EDIVPRAFTV PTSTDAHAH QDLEKLNRNSV LKEQNHLTTV
 LGTWSEFLTS NSDNDSDILS SAELGLQLEQ VRDKALEVEQ RIKASAQVDL TDLAHEIEIC
 NQHATLISA QVRLQSHTA ELRAG

> RXA01942 (1-600, translated) 200 residues
 MLRIGLTGGI GSGKSTVADL LSSEGLFIVD ADQVARDIVE PGQPALAELA EAFGQDILKP
 DGTLDLRAGL KAFVSEEQT ALLNAITHPR IAESARRFN EAEDQGAKEV VYDMPLKAEK
 GLDRKMDLVV VVDVDVEERV RRLVEKRGLT EDDVRRRIAS QVPDDVRLKA ADIVVDNNGT
 LEDLHAEASK LIAEILSRVN

> RXA01944 (1-384, translated) 128 residues
 IRNLRLILPD GRTLTAPAGIS DSNAWNMGD SAGKLDFDFA TFALPEDAFT GVAHAWDTTQ
 STDGHEHITI SREDDGEISR TIRVDNTEPE LTVSGVEEGQ ELRGTVETIDA QATDAGAGVK
 SVETLLDG

> RXA01945 (1-1242, translated) 414 residues
 VQLPLTTGSI ALDKGEHTLV IRAEDEVGNR TEKTIITFST DENPISGDYA PSNGATVGVG
 DVKLSARASD PSGDTVMKTF LEADSPKLDS GRVMSSSGTV EDAGSVSRAE AKMLERGDOVE
 KLSLSDGLGM EVTSDAALPY QLFEVDAADA LAADTEVRLN WAGSADGRAQ VIMYVFDGEA
 WVEVDRLTGT DELEEFTLQG VVNAEKFAIG GTVTVLQHS EGFAGADHST RNSDVTAAHP
 DDVARSEYDF PLANESDTQY YNEEFHEHOT NIHDYVLAER ENKNIQFMFH TGDVDVDDWQ
 PAQWATANPE YQRLDDAGLP YSVLAGNHQV GHTSNDYTEF SRHFEQGRYV DNPWYGESYQ
 DNRGHYDLFS AGGIDFINVA MGWGPDDDEE AMWNEVLAKH PFAVAILNLH EFML

> RXA01957 (1-462, translated) 154 residues
 MTTTRTVSTSA PHVTVNNTA HNKTRTVTNG ARKNTAERK SCISFRVGPPE LFDEFKATCI
 DNDISMTKAF EKELRTWDE HNAGATKRN TRHVTYQAPV GTVATSSISIP LGLFTVFKKSS
 SDQMWYDLES SPLTAQEPMS NMDMHRNGSF ELHL

> RXA01958 (1-507, translated) 169 residues
 MSKKRDHLTV IPDLERSRTH SRSTQPPPTL PAPQLTIITA FDKHQPLRV VKNTTTPSSV
 QPSPINYSFT DPVLREAHYA FQHSSELARPT VLDGHWVRA QEEFDTEHNA AYYRAADQLL
 SPFDAYILDN GDVYTKTPRA ISAAEQEEIL EHLHEHHICW DEEAEEELLR

> RXA01959 (1-381, translated) 127 residues

MPHDVYDVEH IISKQPFCSI FQQLPAAALK PTIQKAATNR DLTKLNTQEI AENLQRYLDT
YSVMSSHQVST IEEVTHVRNP HEPDYEFSQ YGAHISLIGE SYAVNTATNE PYATDSEGHF
LALYFEM

> RXA01960 (1-318, translated) 106 residues
MPQHFSQENY RKAPVIMSAP LTIHDLSTN SKLNLKWLTC TVLNSPNLPE PCITVSVNHT
EGMSLVSFEG GHGLTEIANT QLVPVLELPK FNPFEALAIH LEAANN

> RXA01961 (1-480, translated) 160 residues
MTDNADNNTD NVTNNSDTNL DYSFDPLPDE PYAYGFELVA ADAHSDSTTT STDTPETVAV
ALKTREDITIN WVNTPRAEGK PDEIRINNPI RSERIAEFVH EMIMHRLGLVA CMEDLAILIK
NRKLTQLLEAE NAITAWHNLT KESLQGIMGL FYQYVENNTK

> RXA01962 (1-570, translated) 190 residues
MSDNTQDNPF SIRYAPDHQ LALNELVDTA DLPAPTSYMK NPWSGDNTPPI AEWRREIRITQ
WQRTETIIVNQ RDDDDLHVS FPKLGQHIQL NTDDILALVA ACVTPTANDI EATIEENLHS
YPHDTVIMFN ADDLDDLGL VVAVKDSASGE HSPRAVVRTN TDHGALDETE LARLILKFGG
SFDDYGVQLQH

> RXA01963 (1-684, translated) 228 residues
MKNRRKIMST LITVCAVLGI VAAHPFHASA VIGGSVPSTD SVANAVAKIG PGALNCSCGM
ISPSWALTAR HCVDDINILG DIDTITPITP GIHRNEGNYM GEVYRAPSGD LALININGVH
WQRTETIIVNQ EYPLGTAAQS VGFGGGGVNI RTAESVNMIL TDIVSVRSGK FHHGVRGRSHY
LLFYDASAET GRIHKGDSGG PIFIGDEVVG IMSHGTINKN DGSFDDDES

> RXA01964 (1-1326, translated) 442 residues
MTSAVNQVQK TQKVLKPIN TKNYSATDAV QTGQHGSALG SNIGVYTYTA GLDIGNGYVK
GILEATGDTT GTSVDVIDMP SAATRMSRPT EVPEPDATV AVTGADFFNH IDTNFNSPMV
KGNRYRLCGT RSLSARGSLG EFDLVGNRSK AEQELSKVLV MAVLAAKAVK DFVAAGHRIP
QVAVEGDPGV LRVHTYLALA LPINEYVGH HRGYKAQFMGD GAANPAVHV TVNNFETPAT
VQLLIFERVE IAEGASQAQYA ITAGGEVLMN GMLADVRSKG LALEGVTAGD VLQARHTIGV
DVGEETVNFY VFTDGRFNHD ASRAYDKGY TLESIAIQAM DDAGLAHNFN SRKQLADLYLQ
RPPSALKRNF YTRVEQHVQD AEAFVVFQDVA AEFARVLSDV GALTEVAFVY GGSGLPLRDR
LHEALLKAA EMGSEDHFFV LY

> RXA01965 (1-561, translated) 187 residues
MAQKQDTHY SEDDAPWRNV RMRFPETDAI VERFLETQGA RGISLAMRQL IYLFVAEYGD
VEVATVIGLK LIVESLQAGAE GSDLFAQLAA GVADVDVAVT RKKAPQQIAP PSTTTRAPDQ
VNEFVAEAE QVEESVVEA KVPKQQVAPQ PAQKPEQKPE QKSAQPAQSE PDDGDFMDVV
MGQAQFGR

> RXA01966 (1-657, translated) 219 residues
VSESENNTP AVAARDRLV WVDLEMTGLD LKRHVIVEVA ALVTDANLNV LGEGVDLVVH
ATEELAQMD DFTVNMHESG GLTEQIRESA VTLKEAEDAV LALIEKHCDP AHPAPLAGNS
IATDRAPIRE HMPRLDEALH YRMVDVSSVK ELARRWYPRV YYKQPEKGLA HRLADIVES
IRELDYYRRS FFVAEPGPTS EQCADDAAQA VDRFAPYFD

> RXA01968 (1-1158, translated) 386 residues
VLAIGSLAT GCTIERSDAQ EQSSQQSTEV EAEFAQAPVI SVDDGDEOVD PSESVIVKSM
GDGLSKVTMT NEEGYEVESE LSDDGRSWTT AETLGYNRTY TIKATDKNGE TATASFSTAT
PAATTNVALS PLADSVVGVG QTIGFRFGSP VKDRKAAQDA ITVTTSKPKVE GGFYWLNNSE
LWRRPAEYWD PGTEVTVEAD IYGKDLGGGV WGETDNATNF TIGDKVEAVA DDATKTSVY
KNGELLRTMP VSGFRDTSWV ATPNGTYIIG DRNESMIMDS TTPGLGYEYG GYRTPVKYAT
QMSYSGIYVH AAPSWVGAQG SYNTSHGCIN VSTENAQWFQ EAVKRGDIPT VKNTIGETLS
GYDGLGDWNI PWSWSKNGA DQTSAW

> RXA01969 (1-474, translated) 158 residues
KCQRRLGSLD PLYKNRNSLL TTQKWFSPRQ QESLEQLWAY DKAYGALKLA WLAYQAIIDC
YQMGNKREAK KKMRTIIDQL RVLKGPNKEL AOLGRSLFKR LGVDVLAYFDV GVSNGPVEAI
NGRLEHLRGI ALGFRNLNHY ILRLCIHSSQ LVHKINAL

> RXA01973 (1-582, translated) 194 residues
 SAMSKSQDDR KIAELEAQFH SLGLNNTELV TLDDAASLLG VPAGIHQIEA EVMLNVNFGDG
 ADGMGGDDTK FLHYQPDSEQ PYVWVMKRVY SFEAMKKLMV GLFTGLCLIL VGGFALGLML
 GGFIVGLLGL CLGTSAMIV GPFGLMRMKA YPPCMDSPWF YMSQEQWRTA MGAAQQTEVS
 FVEHWDNIYG DNLH

> RXA01974 (1-1452, translated) 484 residues
 MTQVVAGTLV GESINREIDE DKYPYLSSYA APVAVPVREI IGREEEVNKI MAALMRPEIS
 NVMLVGPAGS GKTTLVQQAL VKDPERNYIE VDVAKMVADL STPAQMAARI KGVFEDAIAI
 RKHEGHELVL FYDFEHQIVQ LSNAAVEAIK PILAMSGVLG VRVIAATLE EFHEHIRPNQ
 ALTERLQEIIR LTPTDQKTTV AILRGMDRY GVSQDFYDDH VFEQIYSTTE RFPSSSVQPR
 KSIRVLADAM GWHRLSGKPM DMDLLGDVLH DAIGVDIAFK VDGTSIKDKL DEKVMAQSLA
 TTVVADRLQL VVADLHDKSR PLSNFLTGP TGCVKTELVK QLARVLFGDG TGRILRFMS
 EFALESSLDL FRSELTRRYA DQGNAILVLD EVEKADRAIA RLLQLVLDG RLSDOYNREV
 SFLNTYIVMT TNAGSEIFET ISNYATDDTG DGRAIKDFVK NIHTSIKNKG FPELLGRVD
 EIVP

> RXA01976 (1-1521, translated) 507 residues
 MTQTLAGERR IVTTAELKAM LARGDKVFLP GVAARAPEIL DNFDPADRAR LDVPAADNEI
 VSVFESRRDT VQCISIADRD HLYITDDMTI THNTSNIIFL KSTDEMTIKT LDVSGGERHV
 VRRNSKVTTR ALQQLVMRTE GKVSYSATSE KEPPVSYNDL NTLPSQNAIV FRAGQYPVWS
 RNETIWMPSF MLEFANQIQP GREYSLQITP TLSSANEFDV NQNAPEFMAM LEKRMASQIR
 TQRAVDIYKK ATGLDDSDIA RLDMOVYSAE IMDIVDTMIA KDEYDDTPDY DEGDSEVMNA
 RDEMESEYDV DDEFEDSAQG GPFVATGTEK KKKSLSEAE VNDEFIHDQE NAEHKLADMR
 LKRYAEGKVS RDMLADQFGH ILQDSLELD TAAYDESLHA FAQDFNFRVT ANNGLVNAVD
 GTVLIEALSQ EDIALMRAQA GVEQSRVSE GEEALSGTED DPLSAMGRYK TTRAFRIMLV
 ELPHWRDLAQ GHFDKEVARA FRRIEDA

> RXA01977 (1-576, translated) 192 residues
 MLRTILFVRKI RALLLVLMIA PTPLEVEGLTS TAMIIVSVIL AIYMAITMYR VVHGRHEFAH
 IARRMALVYN KTRSSRFSVVI AYVVLIAIYA LLIPLVYSV TFGFIVPSTP NTFSDAPAWI
 MCVSLLLIIV ASFITSIMDD FIDGILTDFY DEDNADSPDS PAEDIATRPV ESATTSALAG
 FAVGYICGRF NR

> RXA01982 (1-1158, translated) 386 residues
 MATTSPLPTTI TPDSEETVEK RHLSTPLILS LPCESVPYAL AAGEGQQHQL GPYHLTVMSR
 PEDNGGIFSL ARVSAGKTPA TRFFSVAGPT FLYMMEGRIT LWFADGRQEI IAGGSATIPT
 NTPWSFACEG LVNSALVYYS SSNAFLHAAE KLGTSSFSHT FRVSQEVGTI KYEELEDGCF
 TFYERDHLAE LGPHFDRLPE DMKAFALNDG EGRDLQEFQ INSFVCRPRH TGNQFLAMQT
 KGAKTPYIPR FHRHLHTENF ICLDGRVKLH VNGQEILSR GDYVHAPAGT IHSFAFAGHN
 TQMLGVLTE VFEKFFDYIN TPTNARVQLE DGGKPPFPPE AFAKVQAELE VVVGFPPRIS
 TLDVVTNSRF EPINRTITYR ALDANQ

> RXA01987 (1-213, translated) 71 residues
 MTFPAQSRRL ARSTTDKWIG GVAGGLAETY GWNPAYVRLA FVASVLFPLP GSQILFYALA
 WLIIPSRENRF

> RXA01988 (1-318, translated) 106 residues
 MIDPLTPVVP ITTGTSVAEI YADAREHLDN GATQVMIPVI SPSNLTLSV ALGNQEVLDAL
 GHSEQQAVHS LLEIHTPKRS WPLSELYIDD NEGLAQVSRG FARLVG

> RXA01990 (1-999, translated) 333 residues
 TSDHVAQFGM ATASAAATLPD SIVTSVSYTL NGLSFSDPVE LGISDNDKRE ELLGDITKGE
 LRLQMEFISV DSATADEEYV FNLTGDLGRF ENSNDRTPVP RNDAGIRVAD LLVYNGGTRG
 TLTNTSSDAG TTSRTAALDM ELYGWVSSAQ QTGERPIQDW TVGKTGQEVV NKVVRIVGAV
 HPWIIISTVQH TWVKSTQTVS HFRSEQDWKI NQPPAVDMGA LAYAAPLGVV VGHANVVISN
 NNGAGFRGAL VNTTPTTRDV ILNFTAADGA TLRERSGGGF EDDFVFSSEVP RVEETSTRIS
 YSYKNSEFED EVFAAFPEYR RSCVGTNRV FSG

> RXA01991 (1-795, translated) 265 residues
 MTNLLPHFSP TDVAWEPTV VYSADKTTAT ATFKNIPSDI SFSWTGIEAL EPFSPGKTFE

HKVQGSVGEP AGAFTRDNYF TEGELYKRRH ADDLLSGDGL FGPNTDGDG NLPSVDDGKD
 GDDPGDGSVD RDGVVAIDVV DNADGTVTVT LSDGTTFTLD AGQDQDGLD GLDGTGLTLE
 SATPDEDGNI TYVLSDGTEF TVRNGVDGSD GKDQKDGNGV TDGVDGSDGK GLVEVSRVTN
 DNGSVTIITYE DGSQITTKPT PTNWL

> RXA01992 (1-450, translated) 150 residues
 VYCPFCQHDH SKVIDSRVID AGSAIRRRRE CSKCEGRFTT IEKAVLLVVK RNVGTEPFSSR
 EKVVGVVARRA CQGRDVSDDA LKRLAQQVEE TVRSNGSSQV RANDIGLAIL DPLRELDEVA
 YLRFASVYKS FDSADDFEKE IRLMRRRGRD

> RXA01996 (1-537, translated) 179 residues
 MSKLTGTWTL DPAHTEIKFV ARHAMVTKVR GETEYTDSD VVDAENPENS SAKVVIKTAS
 VTTGNADRDH HVKGDDFFAV DKFPMTFEA TSFVIKNENE GTVTGDLTIR DTTKSVTLVDV
 EVGGVAEDPF GNTRLGFEAS TEINRKDFGV DFQAPLSTGG VLVSEKIKIE IDGSAIKAA

> RXA01999 (1-471, translated) 157 residues
 MTLPTPTHST KGSSGRMKRM ALIGSSLIIS MGLITACGSA AAEPEAPAPT VTETVTATVT
 TTAKASTITS TVTETTSAD LAQEIVKPA VEEYSEFQVN TPQQFAAIE PAPAAPAPQT
 YYANCAVRA AGAAPLYAGS PGYSSKLDRD GDGIACE

> RXA02001 (1-549, translated) 183 residues
 TRDPIVAAVG IQAEFTIVS RNHNVPEDLV VSVTQIHTGS ADNIIPETAY INGTVRTFNK
 DVQAMVITRM EEIVAGQAAA YGVEATLTYN RNPATINDA AKAAIAAEVA GEVGLGVNPN
 GSRGMGAEDF SYFLEKRPGA YLFVNGGDSA GLHNPAYNFN DEAAPYGASF LARMAERPLP
 LKG

> RXA02004 (1-207, translated) 69 residues
 RVGRLMRQNG ILIIRSRKFK RTTGSDHTFN IAPNLFQQDF MASRPNQKWA GDITYVWTRE
 GLGLSGRHS

> RXA02006 (1-495, translated) 165 residues
 MTVAHKRSLT WIKRLSATTF AAFGLQIQLVT PAHSIENTTQ IPESELHNLG LTDEEIQEFN
 QYLIDESLFG ETVETSPIVV SDNEDAAQDP GFGLFTTNPV KHTDEHIGAL YFSDLPGISN
 LTCTANTYIGG KEWTTAHCV EGRSRFVGTI EQSDGQYAGI EHYT

> RXA02007 (1-429, translated) 143 residues
 GITANYAFKG KKVVAWKDLA GIGFKGARTF ARPTSDAEVT LPGVTFNSLP RLEAASHGRI
 PDAITASKEA ADGKVVVVQE DGYSVMSKSE EYLERQKALG KPVQLNFDDT TDGNTTQTES
 VESQETGQAA SETSHRDNPA SQH

> RXA02009 (1-123, translated) 41 residues
 MTMYNAAKTL VPQIVAFDDT AIIALDQAAE DEFRAKNYPE V

> RXA02011 (1-318, translated) 106 residues
 VANDFIEPND APDAPDNGDS GSSGFVDEAK DKTRSAQQLG GYGALRVGFG TAALAANGAR
 SMGNLARNLW TPMMLGALSA GTGISAATGG MITARVGAML AGTGSA

> RXA02013 (1-549, translated) 183 residues
 MTESPDLAIV FLAAFNDIEA HLRTQLRAKR SDSFRWMMVRI AEKQHLISKE QAETLDAFAE
 LRNAISHGQY NDLRPIADPR PDTVDITIEI RSLLLNPPPIA LNVLPQEKVR SYSLEDPVSR
 ALEVHHTTEI SQFPIYKGE YVALLTNTI ARWVASDLHD NAQLDARSIK EVLDYAESSD
 TAV

> RXA02014 (1-396, translated) 132 residues
 ISLQLQAIST FPTDPEGVWT SFNQLLFDRG LGSLLVPALAP ESLDDLPEDEV SALRRRTTEKN
 TTTLINLAKQ HGLVHHDIAF GTYIVGLITI SRPPIALAT ISENSHKALL GLYLSGLKHG
 MMANIGEHGD KS

> RXA02019 (1-492, translated) 164 residues
 AGTKVEASDL GLQAIPTSLP PSTSYDSIDD VVGLVAASLT SSGEIATKPR FVGTELINSI
 ATNVTDSSSLV EEINMVPLSL AEPSPVPLQ HGDITISVVSQ DPDTGLPENI AAGGTVILAG

GTDPSITILIA LPQSIAEKVA AQLSNTPLAV VLTGDRANNY TTEE

> RXA02021 (1-948, translated) 316 residues
 MSNIRGAQA VGIANIADMG TILDWYEP QIFNPQWAE RYPLEVGTTR LGANELTPRM
 LQLVKLDQDR LVEQAVVRTV IPDLSQPPVD AHDVYLRLHL LSHRLVRPHE MHMQNTLELL
 SDVVWNTKGP CLPENFEWVR GALRSRGLIH YVCVDRLPRM VDYVPPGVR ISEAERVRLG
 AYLAPGTSVL REGFVSFNSG TLGAACKVEGR LSSGVVIGEG SEIGLSSTIQ SPRDEQRRL
 PLSIGQNCNF GVSSGIIIGVS LGDNCIDGNN IVLDGDTPIW FAADEELRTI DSIEGQANWS
 IKRESGFHEP VARLKA

> RXA02023 (1-768, translated) 256 residues
 MAPKQTPSPE KNRNLVGPVL QRRQTEGTFD QRLLEMRADH NWKHADPWRV LRIQSEFVAG
 FDALHEMPKA VTFVGSARIK EDHPYYKAGV ELGKKLVAAD YAVVTGGGPG LMEAPNKGAS
 EANGSLVGLG IELPHEQHNL PYVDLGLNFR YFFARKTMFL KYSQAFVCLP GGFGLTDELFL
 EVLCMVQGTGK VTNFPFIVLIG TEFWAGLVWDV IRHRLVEEGM IDEKVDVDRML VTDLDLQAVK
 FIVDAHAGLD VARLHN

> RXA02032 (1-570, translated) 190 residues
 MPFLQISLLS IGVAADAFAC SVVRGTAIQV NLFKRALVLA GIFGVFQAAM PLIGWFIGRF
 FAGITFFIAEI DHWIAFALLG IVGTKMIWDA FQPEDDETIV DDGRVQFRPA IILGLATSID
 ALAVGMGLAF VEVSIKVAL SMGSITFALS LAGAWIGHHG GKGFGKWATI LGGIILIGIG
 ANIVYEHLSA

> RXA02036 (1-381, translated) 127 residues
 VHIFPGHLAD TVSWDCGGGS CATNDLVSLF MPAAFMSTLA ACVFGAWAIG LIAPALFIAV
 TAWAFRSGVQ AAIAADGYTSA TSVGFEMTVS LILFIIAGLC FLGWIPMFIN NRQVARKVRE
 RAAGLSN

> RXA02039 (1-810, translated) 270 residues
 TSTSTTAPLG LVGTLVWLAV QAVMHDGELY HVEVPTIALV IGFGAQLLIG VMSYLLPSTM
 GGGASAVRTG THILNTAGLF RWTLLINGLA IWLTLDNSWL RVVVSLLSIG ALAVFVILLP
 KAVRAQRGVI TKKREPITPP EEPRLNQITA GISVLALILA AFGGLNPGVA PVASSNEDVY
 AVTITAGDMV FIPDVIEWPA GKSLEVTMLN EDDMVHDLKF ANGVQTRGVA PGDEITVTVG
 DISEDMDGWC TIAGHRAQGM DLEVKAAPN

> RXA02040 (1-528, translated) 176 residues
 YIPFVWISDL GEAAEENFA RFWSWLKSRK DKARQQGQTF GVFCYASNGE NHWMLSTARR
 FFGKVKGVDP EQEIRSFIS DQWNDMFAVA RSQLVGPGGL GLKQLAPAAG FHWEEDFAG
 EDSLHAYLIA STAAEPEAEA ARAQLLSYNG DDCRATAAVR HWRQAGARTA PVLGNI

> RXA02045 (1-261, translated) 87 residues
 MNFATIFGSI FEVTLVGILL GAGLPALFAL GIRFAHSPSS NGTNALGKIA STICFAIIAV
 AIIAGIWLVT KATIIQYSGF DIFGTEG

> RXA02046 (1-264, translated) 88 residues
 MKETLTGTLT HQMTYIIVPAN RTVPHLLPEA AEFETMPDVL ATGYMVGIIE WACMELLRPH
 LDDGEISLGT HVNFSHAAPT VPGSTVTI

> RXA02049 (1-447, translated) 149 residues
 VRYLTLATII AGLSGFVVII IAAWALGDSS QLSEFTAYW GLFFAGTGVL TGLTQETTRA
 VTAGSRGSSR GGRAGSVVGF RPFLLSFVVA AIVLVVLGAS APLWIGQLLS NLQGVGVGLL
 AVGLASYAIQ ATISGIFVRL PIVEKSMRP

> RXA02050 (1-372, translated) 124 residues
 LAIVWAVGLV GAGLAWLVGP WILDVVLQKE LFAVPGWLLA MLTLGATTTA SLMVSGCAAI
 AFERHGIYLT GWVVATVVAV GFLLGPFDDL VAAGLALIVG FLCGLLVHMG AFVGGDRNRV
 LTAG

> RXA02051 (1-498, translated) 166 residues
 MVIRALQREE EIVLLSAGAL GIHEKTVERT IRGKRIPGTQ KTVHVQYSYT GKLGDASDV
 EIKSAGDNKL SITIPFIFI GYDDLKFKTI AEDDGWISFS TDDIDTAEVV SEIMSQENFV

EQVTNNREML EDQAVDFYND LLHEFTEKLD TDRYEDTKIE LEFEFE

> RXA02053 (1-579, translated) 193 residues
 MSLSVVEAIT NRRATRKVTD EAPTPELIDK IVDLAEAPS AFNAQGREIV VITDPAQKQK
 LYEASHQKQF LTAPVTFIAV ARVENEPEDL EEILGTERAE RVAGFINGRS IQQAREATLR
 DASLAAAFLL LAQAQGLST SPTTGWDEEK VKEAIGLGGR EDRAIALVIA TGFFNEQPEH
 PGRLQNNRID NSY

> RXA02057 (1-531, translated) 177 residues
 MKRIKCAVAIS SVLLSGCSS TSTTQLEGFD GRSAQEIIIE LDQTPVADRA TNLMASIRAD
 ELILSDQSGQ LSIMPADEF YISAAPYTTT THECFYHSIT TCTGELANTP VKVTIVVADNG
 ETILEEDTIT YKNGFVGMWL PRNIDATLTI EHDGLKSTQP ISTGDDAPTCT ITTAEALA

> RXA02058 (1-552, translated) 184 residues
 VQIVSPNGEI ESFVLGKLYE TALVERGRSA SVQLIDGDL EQLSMLRDDS TDLVIACSGQ
 LLEYNPDLA SEFAVEYANQ TAFDKNSGEW REKVYDALQG SLPDSIVATD PSNAIGCKDD
 TSLPQNIVPI YRKNFLDRDN RDTLNEFVGS LGTSDLEALV KDAQTTGTTS ETALDFLLSK
 GFSR

> RXA02059 (1-495, translated) 165 residues
 MTQPRPDAA SLSLEKKRPEG WPGVGSFETYP EAQAAVDLLS DNAPFVTELT IVGVDLIEVE
 RVTGRLTWGR VIAGGMASGA WLGLFFGIVM ALMSGWFSS IAAGIGMGLV FGIVGAAVFPY
 AASKGKRDTT SSTQIVAGRY DVICSPERAR EARDMIAKLT RDLRQ

> RXA02066 (1-492, translated) 164 residues
 MFNSDTTANL QAKSRDRAGS KAKSRSPFSD SVARDVLDVR TKTAQVKNKA KEFSSVDHLS
 ADAAMFVDN ELSRGAMHRA RLHIVHCAEC REINRQRET VDYLRSECKN EEVSAPMDLK
 ARLASLATEC MFGPGAENLA MQRPESEFVAK VESVVRVAVNK NQGR

> RXA02067 (1-456, translated) 152 residues
 VGWGEIFLLV VVGLVVGIPPE RLPRLIQDAR AALLAARTAI DNAKQSLDSD FGSEFDEIRK
 PLTQVAGYSR MSPKTAITKA LFDNDSSFLD DFDPPKIMAE GTEGEAQRNK QAADNNANV
 ERPADGSTAR PTQNDPKDGF NYSGGVSWTD II

> RXA02069 (1-579, translated) 193 residues
 MADFNRSELD SPLFGSRKRF KFDDDTIGAY AEKVAREFFT QGYLFWQTIF VVVWIFLNIG
 GWAWSWDPYP FILLNLAFST QAAYAFLIL LAQNRQEDRD KHTILADRRR AEETKADTEF
 LARELAGVRL ALGDTVTRDY LRHELEDLRG LLDRIEAKLD DEAAASRIADR HEQHSGSGPQD
 LSDPTQGDVA DEF

> RXA02070 (1-1098, translated) 366 residues
 MTQVTESAVR SALS RVDEPE IGKPI TELGM VKSVSIDGSD VQVEVYLTA ACPMKTITVT
 NTEAALKDID VGQGVHVTDD VMSDEQRRAL RVSLRGETSE FVIPFAQPGS TTRVYAVASG
 KGGVGSKSMT VNLAALAKR GLSVGILDAD IYGHVSFPGML GSDQRPHQVD DMIMPFOAHG
 VKMISIAHFT EGNAPVVMWR PMLHRAIQOF LTDVFWGDL ILLDLPPGT GDIAITVAOL
 IPNAELIIVT TPQAAAAEVA ERAGTISVQT NQKVAGVIE MSAMVLPDGT TMDVFGTGGG
 QKIADRLTAV TGEVVKVIGS VFLDPNLRIG GDVGNPIAIS EPHSPATAAI NEIAEHLAHR
 KVSPTK

> RXA02071 (1-453, translated) 151 residues
 MSNSPTDVST SAPRIMIAPD SYKGTATASE AAQYLGEGLV EILPNASITL APMDAGGEGT
 SSVFGGQVIT LPTTNAAGRL TEASYTLDSF NTAYIDIAA ASGLPAVADD LVPTTGDITYG
 TGVLIADAVT RGATRIALGL GGSATTDAGS G

> RXA02076 (1-534, translated) 178 residues
 MKSPFIDVA ALLRGSALPE HLTQSGFSPPT RIGFEMIAIP EGGKVIVEAQ IIPLGGGLAV
 EADIEAQLLG QCSRCLREL TPTKTLHVSEV FAADPDFVTG EDAADDEDEL PMVNDQDIDL
 LQSVIDEAGL TLPFNPVCEE LYGACQDDE TPAPDGVSEE VEDEEKVDPR WAGLEKFL

> RXA02080 (1-807, translated) 269 residues
 MSIEWLQIVE LGAIFGAGFL AGSNIVVIGA GTEVLSFPIIV FLGLPLPLTAT IANTIGIVPG

SISGVVAYRR ELHAHVKTIR FLLPASILGG ITGASLLHFF SADVFTAVIP WLIGFGTLLV
 IAGPSIKKHV GAHTSGGISA GFRQLPFPSP TTFIVSVCGA LLLMGYGGYF SAAQGIILLIA
 LLGITSTLQM QELNAIKNLT VAAVNLIAS VFIISPELI SWPTVALIAL GSGALGGYIGG
 RYARRLRPSV FRAFWVIVGI TTVIVMTIG

> RXA02081 (1-1629, translated) 543 residues
 MTLSGLELLE FERRTAMET RLGRHNRGAG GAFPEAVVSR SVLPLFVQA RNFLNNQQIR
 AQVHRRILEQ LPTGEIEVLL GHSLGSVIAA DLLRLRPPEL TVKGFTVTGS PLANQGFNVD
 DLFKLRLTPL SNVSWWNWNVF SGSDPVAAGR GSVVAVPVWL DFRVKTISLVP GPGHSSREYC
 ANDAVAEIAG FGLFGSRKE IVLAEKNLQI PLNDAEIFVL QALRYCYLIL QRLKGDEALR
 YEYALRETQD RLIEEIKSRN AEEGRPIKE IARLDFDNGD PNAAPVPGL SPFMPEQAI
 ERLLLEIQGN LLLPFEIEVP EKIQREALRD FTAETQLGSL VGADIFDALQ MAVGVVSSGA
 KSNWRKMGAF GVGAAALTA TGGALAAVAV TVAGVATVAS TLAAGFGPGM MGGVLVTAGLT
 LTVGGGSLTA GVLSSVNTTE EIEALVVQKL SLAILWQRHE IDRTHVEWEE FAEAEHLIVR
 EHTRVKNVSD SSSPILKAFE QQRSTIERAL KYLSDHGMPE GFEELEPPA PTFPLKLRAK
 KTD

> RXA02084 (1-345, translated) 115 residues
 VIIIASVVFL LVGAMLANAA AALFSASEPF GRISYLIQLP NEDDFVPYSL RFVAFFPLML
 SASMAASFFG VWAVLIIPFG YFPSLMMVHK HNKQVQRTWD SVTVADFYED STPLV

> RXA02089 (1-471, translated) 157 residues
 MSSIYSATRY AAHFKSVFPT ALDDIQSMRM HPRSLARAIP TWRPPSIPLP SLPGEDPLTL
 TLSRRHAPAG ARQIIREFGE QREPAYLITI RITSPEGFKV STRLAEGNIR AILSTAHSQT
 VHQLTDEPAP TFCWLVDHAF DVPVRSPLFL EYKSAA

> RXA02090 (1-801, translated) 267 residues
 MSFFEDIAAG LDSGIESRV NGDTMFVPIT SDLEIQFVEI DSSLPAANVY IAAANVDEDD
 DEFEAVILSV VFSVEDAVAA VAKHVATDQV VTLVRLDLEG TDERIQDLEF FQDAVNANLV
 RAEVQGNSEL QVLVEVEDGV PTATVNFIAI GESFEDLIDQ AIEELWESDG DAVLSDEDQ
 RMFADLTSEL EFVTEVDL DL GTFTDFDRLE DILSLADQQA EDWEAQLVPF EDEEFDEPDV
 YDLFVDDSEE DDDDLDDDED DEDDDDED

> RXA02091 (1-651, translated) 217 residues
 MSIWKRLLVQ YRFADTLTA GQPITLEELA TPEVILEAVA KGQEIFGIEQ PKHAAQLWFH
 SLCTAIVLGP VTAMVEFDVI PSLDIRRGQL HNIDGYWFGF RPEEMLVDAS LHLSTQFGE
 STRVVIALDC AATDLRPAFL WAVASDALGI AASGAGVEAF EEEHAREVAE ALIEGMNSVN
 SVPSPRFNDD DYFIRAGCCM IFHSPRADFC TSCPQKR

> RXA02094 (1-717, translated) 239 residues
 MAEHNAIITD AVHSDPAVLE DNAGFSGKYL IRALDKAAHM QTGAIEGYIS WLRKHNPEKT
 PAQLQVLVDQ HFMRLATGSG AGVGMAAAVPG GIGFVTGALA VGEASLVLFD AAFYPTMASA
 HLRGIDIRHP ERRRLILV LLGTAGKAI R DAGVGLSKK NRRAGPIAIV FNIGGLMEVN
 GRLMRYAVKE VSKRFRSALI GKILPPGIGA VLGTMANRKI AKRTVGNAYD SLGPLPTFH

> RXA02097 (1-3372, translated) 1124 residues
 MPAGIADMTD SLLGWASQTE LDLNQRLAGV EYFPQQLRH DELERIHRFY GTFLSRQVGA
 GASLGDLFEM TPLCTVTTLV SRASRISDPA DFFGEYIGGL GLSAEHAHAVV EGLTEKFLAQ
 AGLLVPEGIA SPLELLSIHA GISHNEVAHV LTEVENGTE YPFMFDAVL R LPEVAQTLI
 GGVQELIEFA TTHRTSWSDR QRESSLPAMI DEIVVAELRE R PVGTADREN SVGVALREL R
 PRLILDAERR KVCLRLPEQR VSDDEINWRV SLECTTRIFS TRAWGDTSG YSEALDITVE
 RQIRETTVTD TSNQITWVVP VVDFNDPVLV FSARGENLTD KVSLLHQEYI VLAPAEAKLE
 DMVTGQPVVP IEQFLVEGWN SWVCSRVDR GLSSLKVNKE VRCIDPRRRV AFHHPAELVP
 HVRSLIGLVP HAQSLIAEPF PTLGGQDETWP MLSISAFAGV GAAGEIADLV LPEVPAODGG
 LFAIFDEPIY DAPVWGEYLV RLRGPNRESF RPEFAIVEDM TTEFEVASGA SFRIPTTTGL
 SEASLRVRSR EKHFTEAPRL VTVEATDPNA SFVVTDEGD QMPLRFVPPQ IAIELPLTLI
 PPTWRVTRTV CGPRDLGAG ELRIRTGVVD GPKVSVRNH HGSPLRTVKM VTPDNGRTWI
 ASMKEIAST FVMPRGSI EF EWTDRKVD RR VSVTIAVIDK TENFTGITIE DGKLVFEELA
 AGRLQAAWVW PQTAPWWSAV ELAVTGEPEL LPEVLVAGAN LIVQLHTADP FTTSPVPLSP
 GKAAVTEVEQ GYSSAQTEEY AQLSAFFGGE VEEPPISDAV VPALWDVSHI WTEQNGTEHL
 PVVHAALRSS PAAALKGLSA SLVPAQALPG KVISSGLAAS PFTTESPATE VHRTAWIGTL

QLLGALPSAF KEAEEELGNRT PLLPILGQLE EVAGKNILST LATGRDSTLD TACIDQSTVA
IAGMNETQQK ALLDMFFSNA DIVPGPLMED NTRLMMAVFT FKKRDALREV LQTEGLIKTA
VELLRAMRG T QRLYSSARI RFDKLDGVNT DNPNMMWALT PVVSLVFALS SRLHAHELIG
KTRTLDRASA GNGRIADLVP DLVTGDLISA EAMVLGARNP GLVD

> RXA02102 (1-1158, translated) 386 residues
MTSPHSFSVT PIRTMADGTI KQIHPTGTG VMTVPGRGNR PLSHPASTIV ELSAHDHTSY
CAFCSDNNMLS TPPEKSRIII DSSGDFDILP GALPGELSET TPEFRVRPNL FEIVSFDYWH
QNEFGDMDS TAMRMAQYLA IPEGREHVLA IVRTRLASA EDPAHMTDGE LLEKAPSYFA
GGHDVITGR HFVDVATTSD QLASSGTLTV KEHEAFIRLT VDGIROLYHR NRYAPYVVA
QNWLPKAGAS FDHLHKQLVA IDERGLIAD ELHHLRGNPN MYNELAVDYA GYHNLIIAEN
DHAVAFAGFG HRYPTIEIYS KSAIPEPWLQ SDEEIQAMSN LIHACHAATG ADVPCNEGWW
HKPIDVDMPM PWHYMIKWRV STLAGF

> RXA02103 (1-396, translated) 132 residues
MPKIQFDVLV PDTDSIALAG RFTVVANLLI EKGLMDHGVV VHDPAKIAE AVEEQLRQTY
RDEHEDADLE ESSVNRYLIE VDGVGKSVNQ VTMIFARLIT PPAPLKPDAF LLEQELAYEV
PAVYPWTVEI LR

> RXA02104 (1-420, translated) 140 residues
HACAQLEVDG TKPGMGAAAGG IAIGLTWLST LMHGNDQQIH ILPGAPLIAR SNGIEDALPE
TDLLITGEGR LQDSQFTGKV VGTLLHGLAKA HDVDLAVAAG IVEGGIPDDF LAVEMIKSSD
VAAQLRDAGR RIAQEYVAQN

> RXA02107 (1-342, translated) 114 residues
MDLHKVAAA AATPLSTKE FPFGEPEHYV KVRGKVFLLT TILNDEPIIT LKSDPEIGAS
LRSGFPPTQA GYHMNKVHWL SISDGERITK DFIEGLVEES YELVISTLPK YKRP

> RXA02108 (1-435, translated) 145 residues
MTIYAPRSVA HSIPEVECHV EHGRNFTVGS LSVLEVLGSEH AMLTHSMPIA ENVGYLINGR
VLHPGDTFQP IKDVELALVP VNGPVMKMLD VEGYLKFFFP KRFIGIHGDI VNDRLGAINK
KFLTHLGETY GSEYSPLEEG ESLEI

> RXA02109 (1-921, translated) 307 residues
MLAVLFGVVA GAIMPFTQSV NNRLRQSVGA PLLASFISSL VGTFSLLVAT WITSGHPYPA
LGNTTGPQWW IFTGMLGVV LLTGNIILFP RVGSVQTVIL PISGQIMGL IIDTTGLAHS
PQAPLTLFRV LGAAAVLVGS LAAVGVFSKK NIGQTQSQGA SIWLWLRFVW VMGMCAQATV
AVNGYLGTVL GPSIESALVS FAVGTTALFI LLLVTRTKWR GINGAGKKNP WMMWCGGVIG
ATVIFSTAYL GPIIGTGVTV VVMLLGMMLA SLMIDAFGIL GSPPRHIIHA QLLGLVVIIL
GVTMIRI

> RXA02114 (1-486, translated) 162 residues
SIGYAWTTAF HALTPGLGGI AIGIWLGGV LGGLVIRKPG AAIFVEVVAA CVSAALASQF
GISTYISGLA QGIGAEIIFA LFLYRRYSLP TMLAGMGAG GGAIFLEMMF YGNLAKTMSF
NIITYTTVLI SGAILAGLLS WYLVRLART GALTDFACGR EV

> RXA02117 (1-474, translated) 158 residues
VSTDPEEFQD AETLDQLAYE IILLTRYGVQ NTPTNKREAI MDRSALILLT RLDAQGPMTV
NELAESFGLN VSTVHRQLKA AIANGLIEV DQACPAKHL RPTELGKEKL QQELLARQQD
LTRLHWDWE EDIKTHAKLL RKNHESLEEY LDMKWPRP

> RXA02121 (1-705, translated) 235 residues
MITSPFEREL KLLNEGELGI VQQLVESSNI GFIVDLELDG DYGWAVYKPE LGEQPLWDFP
PGLYKRERAA FVISEFLGNV IVPPTVIMHD APAGVGSQVW FIENGEHYFE PLFDTADLH
PQFVRMAVFD LLCNNTDRKS GHVLLDGDHI WGIDHGLCFS VEPKLTIVW DFAGCTIPDD
LVTDVQELLE DPPEELHQLL HPAEIDALQR RASRISRLFF LPQAKSHRQF PWPLV

> RXA02123 (1-1371, translated) 457 residues
VKGYSLEPNV QTVGELKAAG HIYRPLRVEI RDNLAKLRS GEDPWPGLHG LNYTVIRQLE
VELLIAGHDIV LIGERGQGT RLLRTLITLL DEWSPPIIPGR DVFEHPLAPN VEISDDQPIE
VWHRDARYTE KLATPDTSVA DLIGDVDPMR VAEGRSGLDL ETIHYGLIFR ANRGVIAINE

LPDLAERIQV AMLNVMEERD VQIRGYNIRL DLDVLVVASA NPEDYTNRGR IITPLKDRFG
 AEIRTHYPLE LDDEVAIRQ EAELVAQVPD ILVEILARYT RALRESSSVN QRSQSVARFS
 IAGAEITYAAA ALRRAAVFGE DEAVARLVLD EAAVEVLGGK IEFESGEGER EWEILDYLLR
 TATAEALRST LRSLDLTPLI AALDGSITVS TGTNITASEF LASLPDELGES TLYDDIAQAF
 GATTFSFRAM AIELALEGLY LSRKIAKDSG EGETIYG

> RXA02124 (1-1956, translated) 652 residues
 MATSHSRPRR SRYGRYTGPG DPLAPPVDLS DALRDIADDV MAGYSPEQAL REYLRRRGARG
 QEGLLDLAWR AERRRELLS RNNLGGTLAE VRKLDEGLI LERAQLARDI DMDDTDRAFR
 EMQISNLPES TAAAVSELNS YDWQSQEARQ KFEQIRDLLG REMLDQQFSG MKQAMEGASD
 EDKAAIAEML RDLNDLLSKH REGTDTPTDF ANFMAKHGEH FPEQPRDINE LIDALAARSA
 AASRMFNISV EQRREIMKL SAQAFGSPQL QELLGDLGN LQGLPRDLNW DGESEQFSGDE
 GMGLGDGTGA MQDLAEIDLNL AEQLSNSHTD LDIDAIRQL GDDAAVSAGT LAKLERALRD
 SGLLRNPDG SLKLSPOAMR RLGLALLDAA SEQLSSRPGS RDSRLAGANG EATGASREYV
 FGDTQPWVDV RTITNALQRT AGTDTEGPLR INLDDVEVIE TEARTLNAVA LLVDTSYSMA
 AEGRWVPMQK TALALHHLVS TRFRGDELAL ITFGRHAQNM DIEELTALPP VHEQGTNLHH
 ALLLAERFFA RHPSMKASLL IVTDGEPTAH LEADGHAWFN WPTDPETMFK TWTQLDKVTK
 RGTHHTLFLRL GHDQGLEHFL NQLADRVGGT VVAPDLDLGL AAVVGEYLRH RY

> RXA02125 (1-801, translated) 267 residues
 MVATSQFID SEAAQAVRAA IVAGYRNIDT ALAYGNERG V GEGIRTAGVP REELFISTKL
 AAELKDYDGA VAAIDESLAK IGLDYVDLML IHSPQPWSDF RGGDYSEGNR EAWRALEDAY
 KAGKIRSIGV SNFLEADLEN ILDSATVAPH VNQLLVHVG N TPSELISFCD SKGLIVEAYS
 PIAHGEMLKN QQVKAIDKY NVSIPQLCIR YTIQLGTVSL PKTANPDHMS SNAQIDFEIS
 EEDMAALQEV TARYDGEHSG FPVYSGK

> RXA02129 (1-234, translated) 78 residues
 MKIIFKMASN KEIDNKKGLA MLVFAELVME MLDQPPEQLH NVRGVAIEKR EFLKALTADF
 TSRLKQAQTD KILVWDF

> RXA02132 (1-639, translated) 213 residues
 VHNFSFVDVE SYAKNNNEIL RDAKRLQISA LCLGLILGGG AVAVYLFNSG AVMMWMIAIV
 MVFLALLSFI MIPVIPRQMG NAQTLYDDYE LAPAIAEVN PRDVLALLV NRNVNPEAKP
 EWALATRTIV RVGAHERRLG ERIPSAITG RRTVKQDDHW DEISPMPTW GTTDKDIIRE
 AEKTIPELHW AKLEKNRGL EDVKKTPNNL FKL

> RXA02137 (1-798, translated) 266 residues
 MVVLIPFNDE VCTPIPDGG FPCSLLSVKL PWDKNKNNEG ADAAGQDASS TPETATPDAT
 EQKLKPKHTA PKGRPTPKRR EVELERGVVG QSLAPTDTY AQQRQKRKEF KASMTKEEFK
 AYKQKERDAR VKRQRETQAA MDRGEDAYLM DRDKGEVRFF ARDWVDSRRF LSNFVMPVAI
 ALLVVMLIGN FNPSFAATSS VMAMVLMGLF LIEGITTGR VNKARTRFP GTTETGEGLG
 YYAYSRTIQP RKWRTPRARV EIGA EV

> RXA02138 (1-342, translated) 114 residues
 MTAPSTNTGV ILTESAASKA KALIDQEGRD DLSLRIVAPG GGCSGLRYQL YFDDRTLGDG
 KEDIVGGVRL VVDMKSTPYL LGAQIDFADT IEQGGFTIDN PNAGSSCAG DSN

> RXA02141 (1-408, translated) 136 residues
 MYGPTVFMAA MAVIYIFATM HVSDGGSVKL VEWVGSVALV LSAGLTLMLG VYLHFTEVRV
 DVLPEWDWEEA EVADKAGTLG FFSPSSIWPA AMSGAVGLFA FGVVYPHYWM IAVGLMLLIF
 TITKLNLYQG VPKEKH

> RXA02146 (1-627, translated) 209 residues
 VGKHHRRNSN ATRKAVAAASA VALGATAAIA SPAQAAEVVV PGTGISVDIA GIETTPGLNN
 VPGIDQWIPS LSSQAAPTAY AAVIDAPAAQ AAPAASTGQA IVDAARTKIG SPYQWGATGP
 NAFDCSGLTS WAYSQVGKSI PRTSQAQAAG GTPVAYSDLQ AGDIVAFYSG ATHVGIYSGH
 GTVIAHLNSS TPLSEHSLDY MPFHSAVRF

> RXA02151 (1-1188, translated) 396 residues
 MDWPDIAKGI SILGVLLHV SLAIPGGQDT MSHSLNALID PLRMLPFMV SGFFAVKVLN
 QSFGELEFRGR LWFYLVPLYL WTPVNLVYLR LEGTVFTGRA PGTWEWYSGS MLSATNMYWF

LYFLVIFNLF LWATRKLPAP AIVALVASLW LLMPAYSEIE ILRKSIIYLP TFLIGAYFRP
 LISRFABAAAT RPKAIVFAAV LYVSGLALGV ISNGLRDSEN HGASVLWLMN LRDTFAHALG
 GNLTGFGMDH LPGMIIRIVS LPAGIVLCVW LGRIKPVGEF LKLIHGRHTLP IYIGHATGLS
 LIFGFGRLWN FMEIDNFSDS LWHHTNTWMV IAFACAMLGG YLTYLISRVF VLGWTLVPEPK
 LPEDPKTPAK AQADSHVKAQ SAKPMNASTS SKTYGI

> RXA02152 (1-402, translated) 134 residues
 MAIYRKLAAS AAAALASASL VACGDS EDTT EETSTTSSST TSSSSSSSSS STAATSEESS
 AVEEPVAPVAP VEEAPVEAPV EQAPVVEQAP VEQAPAPVQE APAPVEQAPA PVQEAPAADA
 PPALPGGGGG HAGY

> RXA02163 (1-753, translated) 251 residues
 MAVATFGTIT DMLETGKIVS NVGGTDTIDL GALLNETQAG TRWSELSPNY QSNRVVQIST
 TDVRTSNAA MYLSMMSWVK NGGKTVSSSTA EADAIPELS QLFVGGQGYTS STSAGPFDEY
 LSQGMGSKPM VMIEYAQFLA EQNKENSRI S DMELVYVPS TVYSTHTAETS LSDVGAETGE
 LLETDETLQQ LAVKHGFRPK NSAMIADAGM TDRMPNNLNVD IDPPDYDFLE RLIDGVGASY
 SATPAEEDTD L

> RXA02164 (1-1575, translated) 525 residues
 MKNLVKGTAL GLSLVLLAGC STVSDSIDSL GGGGSGSSET LKIVAATELE DLQPAIEQAS
 DDLGFDIELS FFGGTLNSNQ ALMDGAFDQD YDATWFAFNR YVDLIGASNK LGETTAKIATS
 PVAFGVKTSM AQELGWDQDQ PTWEELGQAS QTQDFTFGMT DPATNSNGFS ALVAMATAYA
 DTGQALTTND IPATAEFMST SLSGQITSG SSGWLKDTFL EQPDRANAI NYESVLHTMI
 SEDGADITVV VPAAGVVSAD YPLSTITGSG QGEHVAELAG WFAEHDPALT DTYRRPTAN
 ATLPAELSSG TIEAPFFGS KTVTDALIDA YTNQFRVPEG TTFVLDVSGS MGLQRITLLK
 DTMSDLISGG ATTDLANVL RDREKVSII PFSFGHEVIS ETLAGVGSFS RLDTQQRVEA
 LQADGGGTGIY DAVLAAYAES AGGDYIPIV LMTDGLTAG RTYDQFLTEW NALPNSIRSI
 PVFVILYGEA NVADMEQLAA TTGGETFDI NGDLDEAFKE IRAYQ

> RXA02165 (1-612, translated) 204 residues
 VPTNNGSFF FSRNKLAGIA IATLIALHL VIGLGAFWVP VAIAGYGAAV ALTPKNPPKK
 ELPPVQATPE LDSGPLLAAR SQELVTRTMS HGAAPVIEA IKRLDSSQL VTGNWTSLTN
 FPEHQVTIRS IINQYIPGII DAYLKIPTRN DPRAVEDLIE DFDLLNSETM KIFNAIQEQG
 LNNLEDHGRA LRMQFGQLPE EFRE

> RXA02166 (1-177, translated) 59 residues
 MSLDPQLLEV LACPKDKGPL RYLESEQLLV NERLNLAYRI DDGIPVLLID EATEWTPNN

> RXA02168 (1-2814, translated) 938 residues
 VSISLTPHL SFKEPAILYA QQASAWQQVI ADSSDHITA THRELLSRS RAKTAPFARQ
 ITAIVPGSLA RLEELTREDA QIGADIDAQP AVSIPGILL QIAATRQLRD LGLDVAAAAR
 LGHSQGLLV EAVDNEEDVL APAILLGAAI SQFAGKGAHM LSVRGLSREI IQDTIAGVDG
 VEVSRLNRA HFVVSQKPEA LKKAAMALQR AADVYNEDIN EKRKGGS LAE PKFDYLDVAI
 PFHSSMQDA ADLAVEWATT CGLNVNARAL AEAILVNPAD WVEQIANLKA DYVLSLDAGV
 SRFTAPLLDG RGISLVPAFS AERDNLARP GFHVPTAEDW SEFAPKLVLK PNGEHKVLTG
 FSRLTGYSPI VLAGMTPTTV DFEIVAAAAN AGHWAEMAGG QOYSEEVFTK NKEKLVSLLK
 VGRSAQNSM FFDRYMNNLQ FGAQRIVSKA RATGTSINGV VVSAGIPEVE EATELINDLN
 ADGFPYVAFK PGTVDQIRAT LKIADANPET KIIQIEDHG AGGHSWSVNL DDLTLTYAE
 LRSRKNVVMF IGGGIGTPAK AAYLTGEWS TDLGFPAMPV DGLIVGTAAK ATKEATTSBQ
 VKQALVDTGP VDPHDAGGWW GRGDARGGVY SGLSHLHADM YELDNDSDAA SRLISSIDSD
 DYADHREELI EAINKTAKEP FGEVEEMTYA EWQRWVELA YPTQDPTVRIE RFLDLVHRIE
 ARLNCAEHGA ITTLFPDHAS VENEEAEVEK LLAAYPQARE IQVSARDAAW FICLGRKHHK
 PMPWVPAIDA DLARWGLDT LWQSQNERYG ANSVRVI PGF VSVAGIDRDV EPVALLGRF
 EAACVDALDG EPEEIFARLN ESKNEREFLL ATPHIVVHGN LIDNPAHLVN EGAFELIEED
 GYWVIRILAD SYFDDLPEVQ RPYLVQHVDI PVELGDAG

> RXA02169 (1-846, translated) 282 residues
 LDMQINRRGF LKATTGLATI GAASMFMPKA NALGAIKGTV IDYAAGVPSA ASIKNAGHLG
 AVRVYSQRRP GTESWMIGKP VTLAETRAFE QNGLKTASYV QYGAETADW KNGAGAATHD
 APQATIALHVA AQFNKNRPIY VAIDNDPSWS EYTNQIRPYL QAFNVALSAD QYQLGVYGNV
 NVINWALADG LGFEFFWMHWN GSEGIKHPRT TIHQIRIDKD TLDGVGIDMN NVYADDWGWQ

TPGNAVDDAI PTIPGNSNTG TGTGIDADTI NQVIKILGTL SS

> RXA02170 (1-774, translated) 258 residues
VSTVLLAGV IIGGIFTLPQ KEEVKVSELQ PQASAASIPS SSSTAGKAVE ESPLTQFVEN
STGSGITYMS LKDDFHTGTS TERFARFALS LSKLYIAEYV LEHGTNNKES LAMEMIKDSS
DVSAAIILEYA YPESIEEIIAD QYGLLSTRGD AHWGYSVTST YDLVKFVSAL IIDDPDPSIL
EAMRNASAVA ADGYPDQWGT AVLDEAEGSK WGSWDDMLHL SSVTFGEYDV VAAAVTGSKE
DLTQLVENQL GEVVSQHG

> RXA02172 (1-339, translated) 113 residues
VNAEQITQGR RQPTAQEFRD MQASPEFGEL RSKFRSFAFP MTVAFFLWYV VYVLVASFAS
EWMAITPVFGA INIGLIFGLF QFVTTFTVITY IYVMFANKNL EPRQAIRQK MEG

> RXA02177 (1-933, translated) 311 residues
MREIFLISGD STESSLVFKT SEEDGAEFF IAVTDELHAI LAGHSEIKSA PEPEEHKEVP
PPVLEPVAAV EEPREEKEID PRISAPLTMS PREIQIRVRS GATIEELAE IGVTEARVEP
YAHVPVLLERA RIADLAKQSH PIRENGPAKL TLWEILATAF ATRGHDLTTA RWDAYKDATN
QWIVRVWDKA GLSNDYAEWT LNLHNTSNPT ADERTPVAAD LIDPEFIQPV RTLTSVNSTQ
EQYDDDETDFV DTVPSDDAP DSESDAVAEI TNDNEPEVDA EGPRNRRRKA VTPHWEDVLL
GVRANTKRKP K

> RXA02178 (1-870, translated) 290 residues
MPSQLGENAA IVTLWFSAS DPQSIIRSEP RADRGYGRKL LAQLNPTWPI TPIGQFALNR
SVSPASANEFY IAGFFGITII QTVELDVTSK SKLNPRLLRS VPATDVYIFA VNEETLGGF
AHIYNGEIKR SFIAYEERVF EDNGIPGGFT TPYWAGKKGT RKTALSFPFN PIELVHEAQR
AWLGFDTATS PDINNVAYAT DGRPEPRIAA PRIINSEEV RSAVEKLGRL ESAFYDDYEE
YEAPDRVVSK RITSNAKKA SAAQKFGKSL WRASREFGNS MAERLHTR

> RXA02180 (1-1458, translated) 486 residues
MTSGKSTSTR GADRLFKIS ERGSSIGTEI RAGVVTFAM AYIILNPLI LGTTPDVEGN
TLGIAQVAAA TALAGVMTI AFGLIARYPF GIAAGLGINT MVAVTLVSGE GLTWPEAMGL
VVLDDGVVIVI LAVSGFRVAV FRAIPASMKA AISVGIGLFI AMIGLVDAGF VRRIPDAAGT
TVPVTLGIDG SIASWPTFVF VVGVLCCGIL VVRVRVGGFL IGILGTTILA IIAEAI FDSG
ASFENGEANA EGWSLAVPGL PDSFGGIPDL SIYGAVDLIG AFSRIGVAAA TLLIFTLVLA
NFFDAMGTMT ALGKQGNLVD DEGNLPDIKK ALVVEGAGAI VVGAFSASSN TVFADSSAGV
ADGARTGLAN VVTGSLFLAA MFLTPLYEIV PIEAAAPVIV VVGAMMMQOV TEIDFSKFYI
AFPAFLTIVI MFTYSIANG IGVGFIMYAI MAAAAGKAKQ VHWLMLWLVAG LFWVVFALDP
IMEAVG

> RXA02181 (1-678, translated) 226 residues
MVDGHIRNLQ GHIDRLAANA PTASQFHRI ITQLREAPGS VQAAVTIENN HYNVELRPFR
KNSLVLTLDT HGHDRDLHP KIKGHDIAWQ NTATANSRRQ GADDGLLVDE SGQVIMAINA
SLLAIGDGTV FHSHTPRSLP SVLESTVIAY LQEGGCNAKP REQGFINDL RSSEVWLVDSS
LSGIRRVAAV LEYGSKFPVS ETRPVAAFPV TFSVNDYILW STAQQV

> RXA02183 (1-525, translated) 175 residues
MASRKTARKN LIQLLSLIVA VLLVILSVV FQQWNNRPE PLPQEISISA SSPAGEIEVF
PFSMCPEPGE CEENEVPTLE VGADEELHLT IPEAIHDHW YLLTIYDDPA ANDEPYHTSY
DATEATVPGS VDPTEGAER PRLVVVEVSA VMIGEDENGE ESPYTVTWSL STMNE

> RXA02185 (1-579, translated) 193 residues
MGRHSTKTSS APTKLAASTI AFGAAATIMA PSASAAPDSD WRDLAQCESG GNWAINTGNG
YHGLQLPSAS TWAAYGGQEF ATYAYQATRE QQIAVAERTL AGQGWGAWPA CSASIGLNSA
PTQRDLGATT STPEPAAAAP AVAEYNAPAA NIAVGSTDLN TIKSTYGAVT GTLAQYGYITV
PAEVESYNA FVG

> RXA02186 (1-219, translated) 73 residues
LFPEFERMYD MANVEKKHFV DPAWPEHNPA DGHVVTELIS KVAGASSPWG DDKEFPVSAE
ETGYVHPYTR INR

> RXA02187 (1-2199, translated) 733 residues

MKKDSPIPTL KGWLOTQSDQ QLSTILNRNP DTVLPPLPPNL ASLAARLQLR ASAIRAVLKL
 NNALELGVLEA VANLGGELHP VTAPEVVEYL HVALAEDLPA QDTIGAALAT LKNFALVYGD
 DQMLIAQETM AALPVHWRLL PEVSDRGQSE EQVRESVDKL SDRHRKLLHT LAASGGFGLT
 RDAAPDADPS RPIQQLASG LLARVDEQTV RLPAWVRRIV EGREQLPAPV RPIPTRTAAG
 SNDGGIAAGL EVVRHMRLLI DALSHVPAPT LKVGALGVRV VTRLSKELDL DETELARLLS
 LQMGASGLLRK GVFPDPLMDD DGGDYVAPTE LADEWMEYDL AHQLGLTMSG WWKQYIAPWL
 VGRADDKDKP IHVLSKTSII DSLPDARAKI LSSLRVLVD NLHADLAFHY PLAASRMNPD
 TITQLVQEAQ WIGAYSQGVV AAGQALIDGE NPTEVIKAPA PVENFIVQGD FTMIVGPELT
 PAMQKTMDSI ASLESFGLAS VYRLSEKRSI HALDLGLTTF EILEFIKEHS MTDLQPSVGY
 LLSDIARKHG TLRGGFALSY IRSDDFALLH SAVEAGADVA LRQIAPTVAI AQAPLLQVIT
 VLRAAGQPPV AEDGEGASLN ISPSPARVPA ASPPPVVPAL DESRVQAQAVK AIRRENSASQ
 GTVSTQPTLS VLQAARVGQR TVTLGFVDQK GVAVHRVVKP LTVNAGQVDA VDEATGAVHR
 FMLHRITEVI VDN

> RXA02199 (1-570, translated) 190 residues
 MTDSTPQGST PGMSPEAILN GTGKPWEWL KLLDDVKATS WTHTHIAKHI VDNFVDSGWW
 AQGIAIGYEV ERGMKRPGMT SDGFAANASK TLNLPVEKVV KLFQDDDLRA QWLDPALIEK
 TSASEPRTFN AKWLADDSRV SVNFTSKGDN KSSFGIQHRR LPQDSIPVM KAFWKERIAA
 LVEVSKQFSL

> RXA02203 (1-378, translated) 126 residues
 MTIRATPQFS VDEFIISTLEE FATGSYLKED EKEFWDEPFD VKALPDLRFI LENYLDLSLDK
 LGEAPDLDAV NAAQAQSTLDE LEKFNTKHHG AVVEPEEKKE ITKLMFDAK QTGADDLSAE
 APPEFE

> RXA02206 (1-936, translated) 312 residues
 MVGSSGLRVS RLGLSTSTWG SGTELAEGD IFKAFINSGG TLIDVSPNYT TGVAEEMLGT
 MLDAEVSRSV VIVSSSAGVN PALPLGRRVD CSRRNLIAQL DVTLRALNTD YDLNLSVGYW
 DEGTTPPEHVA DTLDYAVRTG RVRVYAGVRGY SGWQLAVTHA ASNHAAASAR PVVVQAQNSY
 LLERRAEQEL LPATQHLGVG FFAGAPLGQG VLTAKYRSEI PHDSRAASTG RDAEVQSYLD
 NRGRIIVDIR DTAACKGLGIS PAVTATTWVR DRPGVTAVIV GARTHEQLSH LKAKESVTLK
 TPITQALDDV SL

> RXA02207 (1-759, translated) 253 residues
 MRRRSRVSRL LPATALLAST ALLLSACTQG VTDSPDMGKA TPAVSPAAAN PDGQVIEFNG
 ITDMEVTVSD ILGVRTEDEL AIGTVSDFEA GSQVELDVOK NCGLDLTATG TFVLPACADGV
 YLIDAKDPDL DELRATDKPV TAAALTSDDQ LLVNGEDEEE LTIYREGEEP ETFTVAGPNT
 QLIAVPVIDR HDGAVVRTWNE NTTIQDVDPY NDREGATLVR GLGVGQMAGG EDGLLVVSDE
 MGGQIAIYNA DDV

> RXA02211 (1-453, translated) 151 residues
 MYSVLLIQPR QGEAVAAER RDLFQATGLK PQELTSRMLD TTTSRIGSLE GFDGVIVGGS
 PLNATNFEYS DWQRHVHREL SLLINHLPTF IFVCYGNFTL TFFSGGQIGR THFPEDSGATT
 VLLTDAGKRD VLTQDLPDFS TSFTGHTENS V

> RXA02212 (1-498, translated) 166 residues
 MIPENIDLKQ LASELGDGDA AMGEHTGNQF PTELEKDLIN VTDAKESDFG SLGVVILDET
 PVMTSNLRDI AQELLITDLD DTVVVRAPMS AAVVSDVHSR AALESQOHL LGTTDYVLGT
 ELLVQDVTE TVGNIDWGQL LIWGLVALAI AVVAGASVR RKAISL

> RXA02216 (1-306, translated) 102 residues
 VAPAPGHVVL ATGPTCPIQM LRANKNTWSV QFHADMDAVG MKNRMDFYSN YRFFSPEDYD
 RIIAELPSVD SIYANRVLRN FVEVCEGIRV ADGAHQPLPK LN

> RXA02217 (1-663, translated) 221 residues
 MTNKRALLI GGHGKVALLA TPLMIDASVQ VTSMYRNPDH RSEIEALGAT TLERDVTLLS
 VEDWADLLKD FVVVVWSAGN GGKNGADATY AIDRDAIAS IDGAASLGKE APRYIMVSYI
 GSSTHTIDPS ASFYPPAESK KAADEHLSST NLDYLLILAPA ALTLDEVNGV EVIADTNEAA
 AGRTTSRVLV AEVITELVVR DFPQTRVLFP VDGESPVSSI S

> RXA02218 (1-267, translated) 89 residues

MFAIMTVTQG DHTGIIAAVS TALAELDVNI HNVSQTIMDQ WFTMILHVGF DESVLDIATV
QERMKPFVEKE QGLVIRIQSE ALFNAVNEI

> RXA02219 (1-1386, translated) 462 residues
MDDFSALISGF TDRSSRGILD TIEMIEKYRL DIRVTMGIS LLECARSGME ETATAVYDRV
TSQAARLVEV CEGIERELGI PIVNKRISVT PIALVTAGCS GDPVDVARAL DKAADKVGVN
FIGGYSALVE KGGTTSDIRL IRSIPEALST TDVVCGSVNV ASSRAGINMN AVNEMGKVVK
QAAELTKDRS AIACAKLVVF ANSVGDNPFM AGAFHGIEEP DCVVSVGVSG PGVVSRAIIGN
LQCATLDQVA EEIKKAAFKI TRTQQLVGAM ASERLGVFPF IVDLSLAPTA EVGDSVANIL
EVMGLDQVGT HGTTAALALL NDAVKKGGMM ACSRVGGLSG SFIPVSEDKG MIDAVRTGAI
SIDKLEAMTA ICSVGLDMIA IPGDTPAETI SGMIADEAAI GVMNHKTAV RVIPVPGTVPI
GDEVDFGGLV GYAVPIPVNT VGNSEFIHRG GFIPAPVHGF RN

> RXA02221 (1-1362, translated) 454 residues
MFTASIPTYE LGSFSKGSYV EIKGTYFYFD TLNLTFRNSG AKDNEEFFVD VTLVPEPDNP
HSTRGHAISS RWNLDVIGHI ASDMTEKEFQ VRRVAASGYD ARVSARIWTN NYNKEERDFW
VSVKLPDPDF LVPLNDPPHD GFTLLPYGTA IQVTKESDHM DVLSEFVPPS GQGQILVSLH
IINAGVRKEW DGIEVRLDNQ RIGELTKASS EKFAVPVVRHF DDLGLSTLCR ALIKGSSILAA
EVTLYGARAH ELSSEDELEPK SSSPLRLVE YQSNPFNYQV FNRWGEQNGV RAPKSKQSSS
SFFAAYRGPS QPSKSLTFPV AQTAPAQPSD RFLDWDSSLQ PDGTPRATPF QRGVTRGLIG
KHFSNQKSPR IDFATVQCCD AILRTFEGPT DKLYKDGRTS WPLWALMAI VTLVMLNLN
IPGIGPFIPL IGLVLGHGF WTRRKLNPFF GRSK

> RXA02223 (1-420, translated) 140 residues
MSTYQDDRFP GPDYPAPLGE KPSFTLTSTD LENGAKLAE QLGGTDISPQ LWSWDLPEGT
KSLAITCLDP DAPTGAGFWH WAVFNIPITV TEIPTGAGE TLGGIEGVVS LKGDGSKGRGF
YGAQPPAGHA PHRYLFAVHA

> RXA02226 (1-1056, translated) 352 residues
MTENQTPSSS SAPKPGPRPG PRPGPRPQAQ VAAKKAATV PAPIAKTSND PAKFGRVEAD
GSAYVTSAG ERLIGSQWAG TPEEGLAHYG ARPDLDLATEV ELMEQRLISH PDDATSIRTK
AEELKATLPT IAATIGLDGV EARLSKIINN SEANERAKE QAKNKEIRAV KAEKELAVEA
ETLAENSSDW KVAGDRIRAI LDWKSIIHI DRKTDELWK RYSRARDSFN RRRGAHFAEL
DRTRASARKL KEELVERANA LKESTEWNDT ARAFRDLMTF WKAAGRAPRE IDDKLWAAFK
GAQDYFFDKR NAVAKERDQE FEANATAKQK LIDEYDAQIN PEQGLDGARS KL

> RXA02227 (1-618, translated) 206 residues
VEDVNTLII MPGSPALVPE LAPADAAGAR LLASLRAVFD AELANDDRPI ELVGSRDEAW
FTKHAGNLRA WGAPSVQVSD GHYLPAILQR VALGGFESRV THVRDLRGSV NDMVTVLAL
DGPTGLTTRA PSALVPQGAN IDAWCSRLLS GKGPEVPSTS TLIDASLREP QLWLDSAVA
TEASTAQLLD SDTHGVGRY VARWTF

> RXA02230 (1-537, translated) 179 residues
MGEQLPFPANG SRSNKLPLIV IGLCCIMLIL WLKLPGVLLA TIIGVATMSV MRMTSTPET
ASLVTSIRLS ANEDSDVQHE WQFLTSPEA DALADRTLVR PALADPDGCG KAEKFHYEI
SNANRFLGRL DARLQQNLV SELETLLKVT DERALELRET WLDARKAAQK LGPNYNRES

> RXA02231 (1-756, translated) 252 residues
MTSDLTKTGM DPAKWQDAVE AAIASQRLEV TGEVRGQQLI QFSDSDSGAQI NILAVEPFAT
FAGFNSATVA YGHVSMINDV LSLVDIIDPF GTPVATITCN LAQGPILLVE PVQRWQQIRI
TALGIDVEVH DNADAYIRNG GETVGMVLSE GAEKIASGSG AVIPDASAEF SARVLSAEYR
TNTLTGQRFI HATVDGLFAF DVCLPDAPEL PARDSVLSGK VMLTAAVIPT EVTGCGSGSGG
GCGSGSCGCG GH

> RXA02238 (1-285, translated) 95 residues
VTNVSNETNA TKAVDFPPVG ITAPPIDELL DKVTSKYALV IFAAKRARQI NSFHYQADEG
VFEFIGPLVT PQPGKEPLSI ALREINAGLL DHEEG

> RXA02244 (1-1533, translated) 511 residues
MSLEKSGGFR SRTPKAQQEP AKQKPQARKS PSKAPARGQ GQSQGQRQQQ SSGKGGGNRK
PPAQAREVRA LGVDKPREIA FEVLDRVRGT EAYANLVLR LLKSHNLSSR DAFAFATEITY

GTLRNVGLLD EVIKAASGRE LSDIDPEVLD VLRLGAYQVM FTRVEDHAAV DTSVKMVGGL
 KKFQATGFAN AILRNITRKE PEQWLKELEP AEELARVAFR TAHPRWIAQS FSQVLPADL
 EAALAAIDSP PVVHLVARPG EISAELALI TGGDEGKYSP YAVYLEGGDP GDIEPVKDDL
 AAVQDEGSQL IARALVEIPV EGTDAGRWLD MCAGPGGKAA LIGALARMDR ATVDAVEVSD
 HRARLIEKSV RGLPVKVHV GDRNTINTGG YDRALVDAPC SGLGALRRRP EARNRQKQSD
 IVELNTLQYE LLESANVKVR SGGVIVYSTC SPDLRETRGI VDKALGALEI EEELEAEFMP
 GMTDTGDEKS VQMWPHRHGT DAMFVAVLRK K

> RXA02254 (1-681, translated) 227 residues
 VIAALTDLIG TSQHALDQIA QLAGAKGRII PVCAEPLDLE AEVSGGLSDSA RVMRQVRGVQV
 AVAATPGQVR RVRIIPDNPE PNPAIEAIL DADVLTLGPG SWFSSVIPHI LVPGVINDALA
 QTKATKTVVL NLTSEPGETA GFSAEERHIV LRQHARNLQV DQVIVDAKTL SSQTERNHVE
 RAARTLGAEV SFHDVQAEDG RGRFTSIHDP AKLCAALLAS FAGARRR

> RXA02255 (1-936, translated) 312 residues
 VAKNSVRAAE VSAILRFAGE MQAVGGKLV I EANLDSMQVG MRLQEFIQGL YNSRVDVHTV
 NPTVSRKTTPR YLVRIIDNAD EIARRTGLTV RSGHVVKGLA PSVVSQTISD AEAAWRGAFL
 ANGSLSDPGR SSSLEVLCPG QESALALVGC ARRIGIAAKT KDSRGFDVRN VRDAEAIAGAL
 LTRMGAGQTKR MLWEEKRIKR ESRTPTGTGLA NFDANLRRS ARAAVAAAR VERAAMKILGO
 DYPEHLAEAG QLVRVQHRQAS LEELGRLADP QMTKDAVAGR IRLTLTMADK RAEDLKIPDT
 NSVVTEDLLE EI

> RXA02266 (1-513, translated) 171 residues
 MTQDEHPDQA DSHFNMLLPD GNENAHQLSV ALNQVAHLIA YDADSSIHRP DGLSLASYRI
 LFLSLWTGPM SPLOVTDKTG MKKSAISNL KPLLAESLIV QVTANDRRS KVLSSLSEKGT
 TYIQKTATRQ NALSEWFGT LTDIEQDLLE SLRKLDDSN RASKVRKNRS N

> RXA02267 (1-873, translated) 291 residues
 VOKWGLSFE RIVIVNNVQ FHRFFDDSAV YYPFCFVPLDR AIGEHFDRQN KPSMRFIGTL
 ILPLAKLEEA AQYGTDEVLR VSAVISTDGL ADLRRDFYEL PNIDIASVEI KLVGAALINT
 AHLGSDVEKLI QQHRNTEFVVV EIPTALVTAD IVRKLHMGCA GLKYRTGGDR EELFPSPQDL
 VTVLRTAIDA ALPFKLTAGL HRALRYRDEK TGRHLHFGFLN IAAAVATLRA KGKEAEALKI
 LEGDDAAPLI HALQSGENWR DSFRSFSTCN VVEPLNTLID LDVLAEGBDVH P

> RXA02271 (1-558, translated) 186 residues
 MSFLNSAKTK TVALTATFVG AATLATPAIA SADIVDNALA ALPSGEISCS QAEKYWTTEA
 DYNKVAQAN ALAMFDSRGP QIQAALARVD EAAANRCGLKG GTVAAQAEAT EAAPAAPAPA
 PQDNTGTSQT APAPAAPAP AATPVVNLAP AGSPTFTIEV PGVGVQLPDL LYQIVQQFLA
 QFGIKI

> RXA02279 (1-1404, translated) 468 residues
 XARATALVDF LESQTVQQLN NPDVQTYLTE AELIRDDLRS WAVIKSNGIG QHRSCSIRRG
 NDEPLAIARK IIEETASHPE LRFENLEAQF SEFTILLAQS PENLDVARYQ ELRTQGNFVQ
 ELALDSIFGQ HAVVDGTGNG EAILDETIGY MIGAGMRETT ARTASQFAQL YSFVGRQERS
 IEMARLAFEE LQAAGLPHRE EELRLGMQLA QVEPIEAREI LEKLLLPKFE QNLTLDLELT
 EALLPLGATV AIHDPPQAAAA ILRHARENA GFGNFELAVQ AMTMITDVLY TQNMHEQLE
 ELNHSPIYAO MLDDQHQAEI KLLDSIAIV ADLGSTEALE TLGTAMGLAE TTAQKLKYQE
 SLNRAYTFPA RPEDCISGAA DASALAMQND DPSNAAQLE QCAQYLFQLG HETDGASLLE
 SAFRVEGIPPT EQALYYANAL SSIYEDFGDS AKSQYWEQQA QEQKQLLE

> RXA02280 (1-753, translated) 251 residues
 ADLAETMLGL LTLTSSRGRI SIGEITTLISI TEDVSIQLAT TLDDFRQLNT IARPDTLIIN
 GGYITHSDLA RLIPVHYFPL TVSTADLRES MDLMELPPLQ DIEKAKALDA QVTESLKDFQ
 IKGATRVFEP ADVPAVVID SKAQSARDN ETQSATTDRW ADILATVDNT LSRQATNIPQ
 DQGLSALCLN WNNSLVRKLA STDDTAVVSR TVRLLYVQAL LSSKRPLRVK ERALLNDLSLA
 DLVSLSSDD I

> RXA02285 (1-729, translated) 243 residues
 LVLDERWVGW GLVDKWDEGG VEKRLFAAVL CVVGAGRHHV DERGEVRYGG AEAAKLSLEG
 RVVGVEVEDG GHEVFAVGVF LEAAHEVRNG HVEFLWAHGW VYKQQLTDVN ADGARLIGHG
 ALQHFEHLTV RYPTLHREQM CECYVEKVVA GNAQAQALHV FFAHRPIEDA LVIGIGGLFG

RFCGNWPAGD LRVVDLHRQI STLDQANLNA RPACVDALAA ELRQVLDCTE GIGKVRLLQHN
SGF

> RXA02286 (1-549, translated) 183 residues
MKNAKLFLAL ISAPLILAGC SSTDTGTAES TISSETASAV DATTSTSSST ATSAVIDDDP
VFDIIDIVLA QYPRIITDI DREDSSDQYE VDVVVGQEVLEL DVTTSQGI HTDDRDNDDD
DDIREAHAAT VTAAQAIGLA LDQYFDGIID SVELDEDDGQ LKWKIDLDDT SGNDLADVEI
AAV

> RXA02287 (1-552, translated) 184 residues
VYSISETIAR TLMRPTDHVF DLMGNGNAWF VDALERLGRG IITVRPTVET VAAADTYHRV
TRRPAVATT YGAGFTNTMT TLADVALSRI PLLLVGTAP SAGPRCFDID RQGLARAVGV
ETFTVHADDD AAVTLQAWNN TPENTHVILE IPYDLAAATA TDPTVTITYLL RPFQFKLFMS
PTLS

> RXA02294 (1-375, translated) 125 residues
MAKTKLESIS ERNSDDPLSY PDLTLAIPST TVTVVVAEDT PNDNFSLELL GAAESTRLLG
LDLHIIAPS VHLPALAVAA ADIAHHLPEK FQFCEAETCT HLHPDDDTYL TAESVAQLGT
KLKSA

> RXA02295 (1-780, translated) 260 residues
MGLELAASGW GILIAGAAVA GWIDAVIGGG GLVLIPLILA VMPQLAPVTA LASNKLAAVT
GTASAAFTLV RRVKPKDKLL ALYVLVAAVC SGAGALAASL IDQIMRPLI IVMLVVGLI
VVFKNFEGTG ESKALPTGWK RWAIAVAVGL IAYYDGI FGP GTGMFLIMAF TALLSQNFLS
SAAMAKVVNT ATNLGALIVE IIGGHMWWTL GLVLAVANVA GAQLGARTVL GGTRLIRYA
LLTLVVVMSV YLTWQQIQGM

> RXA02296 (1-489, translated) 163 residues
MRNQTIAAVA ALVLLTAATP AIAATPATAG NGLYSIDMG EQKLTCLVLD EPSTEAHVVA
SCAATFPVTV KLLDGAHEQA AKLEITQAQD GELSVTASRQ FLITTMIAPT SITKPTVNR
LVVVGGENEV RFYATDPDVL PVLITPDSYE VLTDSAAKVK ATL

> RXA02297 (1-1137, translated) 379 residues
LSDKEPDPEH QIPEKPSRKV IALRWCVAP LSLAVGWLEF MWGVPAAWIL GAILVAGVCA
LTTGQDLPM A KGVHVFGRSI VAMLAALPLI SSSGSELVRF LIPGLVISFF TIAGVIGVGL
LLARSRPEIL PETGVLSMLA GGASVMPILA RELGADFRYV ALTQYLRLLV VSMTPPLVTH
FFVPGGADLG SPPEKWLVDL SLGEFGTSIS VLSLLVLFGI VLAGEPLGRL LRLPAPVMG
PLILTVLVSF VIPDDLSQLP PTVFKIIAFM AIGWMC GGPL NMTALKVFSEK QLPATFLFIF
ALLAVCAGAA GLTTWMLDIS FFEAYLATSP GALETVLALS SEGSGAPVVV TIQIIRLLAI
LTIAGLIPTL LRRILRRDR

> RXA02298 (1-1659, translated) 553 residues
MTLQSSDKRS PSLLDASSEV FVHDLAALSP TDATAWGISG FEGDLDQFSP DYWNAIAERN
RDMVADVDAF DDGTDNDDE EDFDDVDRVT ADVLRDRVCL DALHMQGET LANLNNIDSP
VQTRIDFTLI MPRETDDDEV NLRERLSRVP DALHGYCESL AEAASQGHVA AVRQVEEVVS
QCEDLADSDS VLQHLGLDEN DPVVVEAQEA FARVAGWLAE QLAPHAPHVD AVGRDRYEMF
SHLHVGEFVD LDEAYQWSE QLRDIDAQQL QVAQQLYGGP TTIREAMKKL NADRYLIRG
TDALQEWQMK TADQAIADLD GVSFNIPEQA RQVECLIDPA GTGGIFYTTP SDDFSRPGRM
WWSVPKQTEV FHTQELTTV FHEGVPGHHL QISQTLVEKD NLNRRVACW NSGHGEGWAL
YAESIMKELG YHEDFGNLMG YLDAQRLRAA RVAIDIGIHL NKRNPCTGL WDASYARSFL
RENTSMNEDA LYFELNRYLG WPGQAASYAI QQRRLWNLNR EATSQQQTAL QFHSKALSYG
SIPMGILRDQ VLN

> RXA02300 (1-333, translated) 111 residues
MKTYAVLIAV AGLALAGCSS SAPGIWRATE PADAYLEIAD DGTLSGTGCG NRLFGGWEKD
GSTITFGAIG MTEMYCEGVN DWLSQMRTAT VTDATMTIFN EAGSNIGELK R

> RXA02301 (1-717, translated) 239 residues
MDLALAQVDS TSVGLYDALD LIGVLLNGII GGTIARQRGY DIIGFLFLAL FSALGGGMIR
DMLIQGGTVA AIDNQIYALD AFSGALIAM VNFKGRVWEL FKVHGDAIVL GVWAVTGSVK
AMNAGVAPLP SIFMGVLTAV GGGMVRDVAT GQTPTIFGGG TLYAVPATLS ATSMVIFHSF

DQVILGMIIS PFLGIALAVT AYWCGWVIVP NTDFAPVNLT VSQLRAMLSK AERKDKDQK

> RXA02302 (1-765, translated) 255 residues
VATNRTSSAG VITSVLASAL FGAIFFISGA IEAKAETIVA WRVLLTAACY LLALLHPAGR
KVFKEFWTRL RSQPRQILYF IFLVVLITLQ LWLFSWSPKS HALDASLGYL LLPFLVLVIG
RFFFFADYITR LQWIAVGIAL IAVTLKEVIS AQLSWVTFAI AAGYALYFAL RKYSGLNNAF
AYGAELVALS PLAFEMLATV EDPLSNAMLS MVILAGLAGA LAMALYLAAS TLLSMPMFGL
LSYGEFILLF VAALL

> RXA02303 (1-720, translated) 240 residues
DPPDPADRYIA HLPDRTHHTA MIMLGSLGDH SMPGVAFIGG VSVDDVPEVG GAIFHPSNPT
GRWAVSFHSG GWWRGSGDAL EFQWRPEVMA AELSGTTLT DLDYPLAPGH NLHDMNEVVG
KAVGYARHHN PVSITGWGYS SGAALAAINA SLFDALVLTF PDLGSVEKLP AEIRGDVAVP
AAAAMPPTTFV QIAAQDEIAE RPELGDDATV KEYVSRHRIS TPKVAREKIT DVAEFLKTVC

> RXA02304 (1-891, translated) 297 residues
MKTPRLLKIL SAMVAVTGLL IPTVVPMAA DAAELSDNVP DRTQIAIINP DGSVQESDNA
EESRPALSLA KLYLGYYVLA QGAEEEDIELV PDMIRYSDDF TADYLESEYP EAIPEVIDAF
DLEDTEWAGF WGNATTSAVD IATFVAALID DPTAQPLDA MSDTAEYAAD GYAQNFGTFT
LSDVTGTFKC WSDSLDVHSS VSGPGGFVIA ANTYGDAETL TEDVQDSVSS LYPEEVTTAI
EEQVDQQLCEC AAETTHLGMH TGAELKAQLE GTIYGKTLFS LPNSAPAPAF IYNLLAH

> RXA02307 (1-390, translated) 130 residues
MSGTAIMYDT TVVPSKKEIA QAWTGYVDLQ GSYRLVDTVD GEVGVLEVLI KDERGRLLOI
PFSYSAEIN PEQTLSTLEH GVLGKRWVTN ALGDPVAVRE FIRTILTGDG GAARSDGVKG
YLDIKSGSDA

> RXA02308 (1-429, translated) 143 residues
MSETQSNVS AVMPAQLPPG PAERTVYSYG VRAGDQVHIL RMEAFDSAN IVGERDIEAH
AEQVFNQLQA VIEHAGGTIN NIVSTTYLA DVTDAPVVNA ARSRYFTGEV LPTHVTIGVA
ALARPQFLVE ISAVAYLGDL SKD

> RXA02314 (1-441, translated) 147 residues
MEWYQVRRRA RQLLIVLFIA AMLGAASMVI GPFLNDRTIE GNSGRALAQV TNVGSYRTTV
DFQDENGIIY SPATGLLFPT GLGEGQVRVW NYAKSDPDVL KVEGRKWTL S IIPALSVAAV
ATATWSVLWL GVGREGRRSD DANETTV

> RXA02324 (1-1086, translated) 362 residues
MATTTPVIVL SGFLGSGKTT LLNQILHHRG SRKIAVIVND FSEINIDAAI IASEGHLTRG
EDRFVELTNG CICCCTLREDL VDSVGLASS DRFDHIVIES TGISEMPMPVA ATFQWQDDG
TRLADKAPID TMVTLVDATQ FIDILIRKNTS LTEADMGATE DDERTIADLL TDQIEFADRI
YITKSDLVDR TVLEQTTRALI ASMSPRARID LLIDGLNDGS PITDDILGAF LYCDIATRAY
EGYTEELNP HTPTEEYGI SSVVFRSDRP FNKDRLLQVL RSTTGLVRSK GYCWIAHDNL
IVQVWHQAGP NLSIRPAAWV ANSEITPGTE LVLLIGHIDG PTLALLQGA TLTDAEVAAL
VL

> RXA02325 (1-870, translated) 290 residues
MMDHAHSDCS PTLRRDLEVT GQLQPEKAVD LAAPHEGKVA NITKVTSNM EHTITQASKA
KEVVVLIGH SLPTEQDLEK DILHFQAGNK GRFSVAIVDP DRSAUVARF RPKQIPVAVV
VKDGASIAEF NSLNKEPVAQ WLDHFVSRET IPNEKEGDVD KQIDPRLWRA AELVNAGDFR
AALALYELQL QDATVKRAHA AVSVLARMSV ADRGEDPIEK SRRDPDDVNC ALAAADMYVL
MNQPDOTALH LAALLPKPEA ARRIVELLNL FDPDLVLALE IRAQVGNAMS

> RXA02331 (1-366, translated) 122 residues
MELNGGRFYA RKLTSNDRID DVPALSILA DAAQFIADAT TAWHEDTEYT WAICEQTSVE
LLALARLDPK QRTLEVVPAG DPATQLPNDF VLAPKTIGDA VAEGRDTITR WAQGYLEISL
TD

> RXA02336 (1-180, translated) 60 residues
MKDTEINWQ GYADGTAIRES AVIHSIEREV SAGEQPTPND LKFLGLGFQHR AGYVGLSITG

> RXA02337 (1-924, translated) 308 residues
 MSKLYAGARI NALRRTHQLT QSALADKLDL STSYLNQLEN DGRPLTATVL LQIMKVFDE
 ASYFSPDRGT ATATRLAETL AMNQGPTMSM DDLDFADRF PQLAQHIQF AEVDPTHSSA
 HDFVDRDYFAT HKNYIDSLDR LGEELATAIG QPGLRVTRLA QLLDAEYNTI VFRAFPDITG
 RRHFDPPQSRQ ILLRQDLSEA QCCFLAEEL TFLAAEELD TLTTDQPLP SEAAATRLAKV
 GLSQYFAAAV VMPYTRFLEF AQDKHYDIEL ISEAFVGSFE SACHRLSTLQ RSGASGVFF
 FVRSDRAG

> RXA02338 (1-480, translated) 160 residues
 MKKSIYVFEV EGGSDKHFDG HRKDTMPIVN SINDAGWQAE VVYRPFWE TEGLFEYVSENF
 DGYISRVNPG NIPGGERGYF DLLTRLSEAG LVGMSTPEEM MAYGAKDALV KLSQTDLVPS
 DTEAYYDVET FHKVFPTSL FGEARQAQKT WLHRLPHLAR

> RXA02339 (1-492, translated) 164 residues
 PTDNLFYSPA QRYDILLTAF EVRIGDMVQI NDMLAPPEVK LPEDPALGAD PTLTSTAIAH
 PDSPLVWAYR AENLIKASN DEEKIQAYAF ARTGYHRLD RLRANGWKGV GPVFPSEHPN
 QGVLRATIASL ALAAKLIGED NEYDRRCRQML SDADPESVAV LLDK

> RXA02340 (1-639, translated) 213 residues
 ERVLKQNRGS TGSGIWRVQL VDKELAASIE PGTALEPDE IKCTEAVDNH TEVRKLGEFM
 DFCQYIIGD NGMLVDMRFM PRIVEGEIRI LLVGPHPVFV VHKKPAEGGD NFSATLFSGA
 KYTVDKPEQW QELIDLFAA RPVIAEKLGG DNIPLIWTAD FMLGDVVDGK DTYVLGEINC
 SCVGTSELD MGIIQLVASE AIKRIEEFAQ LTV

> RXA02341 (1-411, translated) 137 residues
 MGNLSLEKHTA EGDRIHVDTL SPLSAMLFPF FELIVITGIC WMGIGFLDQL PGIDGTFNAD
 SFPEGTRNLL VGVWAVLAAR RFGLPLIRQR RLRVILSDRK LLVRRAGLRT GFDSIPLSYI
 QRVRRRNTL VLVGGH

> RXA02347 (1-321, translated) 107 residues
 MDELGVGCQC CEKDSITGKA PHPVNKPLVT KSIIRALGDV PDVMSNQDIS LVVVDLWKFD
 TITPPIAESL MRSVAKVNGE MHPQYPTATA MAAIKHSNT FDQINA

> RXA02349 (1-390, translated) 130 residues
 MSTAYFIARG NDTYRPTES SGAWRDELH LAPVAGLVH HMERWRREV DGLVFSRFS
 LEVLGQIARD DVTLRTEIVR PGTIELIET VAEINGRVTI RARAWLLKTS DLAHISGDTF
 EALPSMTELA

> RXA02352 (1-555, translated) 185 residues
 IYNTSSTLNG FIADKDNSLQ WLFVDPGSDG ASEDGNGFLS KAGTIVMGST TYEWLLKDL
 FISDPKWDV FHKVDRPTWVF SSRNLETPEG KPVKVVNGDV ADVLPAILEE SPENTDIWIV
 GGGDLAQGF DAGALDRILL TMAPVFLDEG QPAMPRIIES NLRVTNVRE VQGFTEITLE
 TIKGA

> RXA02356 (1-996, translated) 332 residues
 MATVTFDKVT IRYPGAERAT VHELDLDIAD GFLVLVGPS GCGKSTTLRA LAGLEGVESG
 VIKIDGKDVQ GQEPADRIA MVFQNYALYF HMTVAKNMGF ALKLAKLPQA QIDAKVNEAA
 ELLGLTEFLD RKPDLSSGQ QRVRVAMGRAL VRPEKVLMD EPLSNLDLAK RVQTRAEEVAA
 LQRRLLGTTV YVTHDQVEAM TMGDRVAVLK DGLLQVAPP RELYDAPVNE VFAGFIGSPS
 MNLFFANGHK MGVRPEKMLV NETPEGFTSI DAVVDIVEEL GSESYVYATW EGHRLVARVW
 EGPVPAFGTE VTFSYDAAQA HHFPLESGER IA

> RXA02358 (1-291, translated) 97 residues
 MVSYSVHGAL DIDGSLKLT LDFLNKLATN PASPGLHIEP IKNSIDSRVR TGRVNDQFRA
 VLFEELHDEFD HHFVVGGFIE MMFSPRQEK SALKSTL

> RXA02360 (1-2433, translated) 811 residues
 MRGDVQKITK VYDGKHTLE IPVYQRNYDW TEKQCSRLFD DLSEVVKENH RQHFFGAVVG
 KPQGSWTVWV IDGQQLRTTI SLFMLALVHS LRASEVEEGE FNAGYNIDLA TLIEDDYLR
 GNENGLKFKL KPVKNNDNEY QKLFGESEF IESSNLTANY RYFRNVLKAT DLTAALQLEWA
 IEKLRVVMYLD LEEFDDPQRI FESLNSTGLE LSEADKVRNL VLMDQELKTQ EKLYEQRWNP

IEVCVKFDTD NFIRWYLTLLK TARTPRKQDV YEEFKKFIRN SKLPVEFILD DMYEYAKLYR
 DLLGATGTGFI AADRCLKRFV PVMGDVLPFP LLPVLKDAKD GIITESDFLG VLKVESLYLF
 RRFVAVGVASN ALSKIFSTAY SDIKKFWTPG QSYSSLLAYI LKRDDSGSRF PSDSEFFRNF
 ATKNFWNHNN ENRRYLFDCLE ENADSNVDNR IQTSLDEGSL SIEHIMPRSL NDQWRAELGP
 EYARHETWII NRIGNLTITG YNSAYSNSSY ERKRTMENGFLVSPYRINNF IKKQKHWSSEE
 QLIERTELLT QAAIDYWLPL KETFPQPOAV LPATESLSDSL SFRGREIVAF EYEDYKETVT
 SWADMLQSVL KVLNQSFQRE LIALTNEEIC LATSNNSNSS LREIDHGLFV DTSSTSSVKI
 GFLRRVFTQL GLEQEQALVFT LRPLANDVEP RDDLEVEVE KKYSDLTKEFI PQLEEAENLE
 GADTEVIFPL SKLKEQLTAF SPENPQAALG GLPVPEFLKQ NVIEQLSAEH ILAVLTQHFHN
 IASMMGDDYL LEELRSGRLR ELLQRLLEED S

> RXA02361 (1-651, translated) 217 residues
 MELLSHLLAL DPASPRLTIVY NESTGARLDF SAILTDNWNAS KVGNNMLLEEL DLEEGSLITI
 DLPVSWQAAM IMLGALATSV EVSFDDPEAD AIFTSLDKRS HYKGDSDVLI VSEDPFGRGV
 VEGGGELPNG AIDFGPTVRF YGDQFFQPTR TLPEIIQHSF VPGARVLAT GWSDIESFNH
 QVLEPLAVGG SAVIVTGLAD IERNQIATN EKTTHRI

> RXA02362 (1-3699, translated) 1233 residues
 VTISRRLKQE RSFADDLQDL KTLNDQLRFT NAKLQARISG IGNDGKKITR PTFLLALDFQ
 LTVEYETIIL AILVEAVGGN QSKPAILKDL FIEYPLVFLA ALSGTAMDLA QEGFWPAFWK
 RTQVSVPHEV YDAIRKELVN SIKRNGLETFLADLNRREY VGLIQHSGSL SAKMDALIVK
 FIDHTRAEHQ GWSGSEDFAS YAKSVFSSGD NLLTTESLKQ LVTHIPARSV DFIARVYELT
 NWYRDLLKDLN EVEAFVGTAG LPELSKFLL ECLSGEAEQI AEKTKAAPAS LENLEPPHLY
 LDPOQSFTSL VEPALSKTAA LQIPAPEWTV IYDGNISIKVR PEQDWSYGGF AEYRLPLDKP
 LSSLRVITLT IMLGLILIEGF GHKNPIMFFK NNGQPYANQE MLSGNVAITAI VPAAIIRAR
 MRASKTFNYQ DLGPLSGWNK WVIRSIPLKR AESITVSHGG FRKELEPVRRK VDVQWITEDL
 TIENLQGLDH EPVFHTSPRI EFPTSGSNWV IQYSQILPDG SLEMEDYRV EPENGEYELD
 LFEESDDPWV GQFLVITLLKD EKVYETRKFN LAEGLDLSLT DFGGCGPENRF RYPSINQOQT
 GLTKTFARFS SNSEKHIFP DEIIGLDAFT SQKAFNIASG DFPEDYNLDV FITPQLHYQ
 VPVTHSQTKW ESTKTTLDNF DFADGNLQIR FPNVEYDPM LKIKMVAYK PESSEPKYLS
 KIGSSKYVSI PMDRIKELMD DDAQFLILAE WFAESKDQHR EKIISAKRT GKISNAALKS
 ARPQQAASSH IATIEKKPLL AAEEIKLSTV ELEGHRHTSK RLEGWAWASAL PLDIPPIKRV
 FGQTSGLSPD THFVVGPLIV EVREKEFLSQ WQPKVPSVKA VVANDPSFEL DQFQDFPFLTH
 RWMFAPRSKG VLLPQEIRTW WDAREFNMRHV LAQRENLHVYK SIQDFDDATS TYLTSDPRVA
 LDELKKSIPP SNSHFESFIR SGLAELSFEV DDTAGDIHRV FWTGLQEMN DLRLILQIQGY
 ETEERATERR NSQSYIREIG GSELWNILKG NSEGLSLAQK CAPQATEINV IRNSGLEAMR
 NGLGADQFSA EFISADSRRL AQLEWLENRR ELNDLGQLPT LPDFAEKYEY LIDHLGDDRI
 KYTARELSTL ASEHRRGNAE NWLYAPYVSF IYSLNRMIA HEVIRPIAQI NYSRHDWANA
 ARLIPRLTGF DLVSAAEKVL SAINNNNIIP TAI

> RXA02367 (1-609, translated) 203 residues
 MSNAINFVDE YEINNHAFTG ALNPQCEGDA NVEIITSREV PLGGPRAMIV HRTLPRQRQS
 LIGAWCPFVD YGPDVSLTG GMDMAHFHT GLQTVTWLFE GEVTHDSSG NHAUVLPGEV
 NLMTAGAGIC HTEVSATSTT ILHGLQLWTV LPDKDREGPR RFDHYAPEEI TLEGGARVVF
 LGSFLPGTSP VHTFTGSSCF RVH

> RXA02368 (1-675, translated) 225 residues
 MIVLAGATRV TYVEFWLAI PLFILAFAFI LIPFFISKTK GLRDIIDAWKI HTTQGDKKRA
 IRQLIIPATA LAIDIIGLPT LFNAPPLASA ALFGGVYVAS LAWAAYRAQD LPRIRTKERL
 AELSQNASLD DVRSDDLVL EQPESRELVR CLLAHGAMDG TRVMARQVAR VLDTEVDEVH
 QVARSLEQHG LVSRSTIMFG GDPOKGVFIEV SLKGISAIFA LESGR

> RXA02374 (1-621, translated) 207 residues
 MSYDFVLFEF DGDGSGARIS KTPLTRIDF LPTSTTPVLE SLSAGLAETV PDTVKLEEDA
 IHLSGDRCLY VVTNNYSAEE AAEWLTAIAF DYGLGLADMN ADTILLFGE DSDAVVQIDD
 WFSFASAYG LPHLLVEVMR LKDSKTPYLR VTLAADDSEF IQTLYETDNK QWLVESSST
 GTDETHVKTI NDVLERIETW FNQETAV

> RXA02381 (1-1023, translated) 341 residues
 MSVTNFRRLF AGIAVIAACV AATPTAQAS SGSSGSGSSG AGSSGLWDL LFPESHESFIE
 RLTDPLDDSH ISIHFDLTPD LYEVEFDPQ IGECPAVVAV VARGSEQNLQ IRPARYSEES

PWTSNGFEK NFRSFFGRME KHYRESTGES LMKDVYVMGL NNIEYPASLP LSSEGSSAIE
 LGTSSISGRD NVISAI DRFE SATGCTPKYL LAGYSQGVLI VDGYEELIA RQQLGTLHI
 ANPAQQVDDP TLVGHEVTTG GLASSVEPVE DNPFKVSYCL PGDIVCDRSF EQFSAGSSSI
 AAAQLSTGNI RPRGVHVQYF VTTQFWDEQI FDEVASWIEA A

> RXA02383 (1-603, translated) 201 residues
 MPVRVIVDSS ACLPTHVAED LDITVINLHV MNGEERSTS GLSSLELAAS YARQLERGGD
 DGVLLALHISK ELSSTWSAAV TAAAVFDDDS VRVVDVSSSLG MAVGAAAMAA ARMAKDGLSL
 QECYDIAVDI LKRSETWYIL HRIDEIKWSG RISTATAMVS TALATRPIMR FNGGRMEIAA
 KTRTQSKAFA KLVELAQIRA D

> RXA02387 (1-678, translated) 226 residues
 VVWCLPTWIK AGQDAVDLAL SAAVDPSPGT YLIVMHSGGG RSKSMVKKLE KVAVVHDAAK
 LKDRDRPGWV KQEFKNHKVQ VTPDVIHALL EGVGSDLREL ASAVSQLVED TQGNVTVEKV
 RAYYVGVAEV SGFDIADSC AGQMSKAVAS TRRALQLGTS PVALAALISM KVGQIARLYS
 TRGRINGRKA AKELGMPFFV VEKTAKVARN WSGDAVSEAV ILMADL

> RXA02390 (1-669, translated) 223 residues
 VEWTAFTGLI LLNLVGSLSF GPDTFFLLRL ATRSRHAHIA GVAGIVTGLT VVWTLTVVGA
 AALLTTYPISL LGITQLVGGT YLSFIGYKLL RSASRELEDA RQFRFNADAR PIPDAVEALG
 TRTQVYRQKL ATNLSNPKVV MYFAAILAPL MPAHPSPLVA FSIIVAILVQ TETVTFSAVCL
 IVSTERVKA MLRAGPWFDL LAGVVFVLVG VTLLEYGLTG LLG

> RXA02393 (1-282, translated) 94 residues
 MAESLVIINI DEKSAKLLID AARHHIPTRF TGPNARPLSV IPIEDFRSRP TLHPDHGWMW
 PLSPFVVDL LGGGLKIGET ELESTNIAFI VDA

> RXA02395 (1-732, translated) 244 residues
 LITMAIPSEI LILAFITFGG TAITMKNRENV DGFDSGSSKE QVLFDMFSNL PLYSITPFIL
 IFVLAVFFVT SADASVVMG TMSSQGNPAP NKLIIVVFWGL CMMGIADVML LTGGGSEALT
 LQNLTLILAI FAFGLIVMA IAFIKDLST PAAIRQRYAK AALSNAVVRG LEEHGDFEL
 SIEPAEEGRG AGATFDSTAD HITDWYQRTD EEGNDVDYDF TTGWADGWT PESTEEGEVD
 AKKD

> RXA02396 (1-279, translated) 93 residues
 MATTASKIST IRPAQQDALW SVREDLHARF DGLVDPVQVD AILDHVASN R EAKITVFSKI
 FIAREATAAL QQIAGNVNAD LLDFIALNRG MAA

> RXA02398 (1-1530, translated) 510 residues
 VVEVKRNLL VAPLTASLVF CNLAVANAV EVEAESPVVI NEVESNSDPV GDWVELANTD
 NNNSIDISGW SLVDDKEDLE NALVLEPGE IESGGYFVVI TDSADYVPTN NTFGGQEFYFG
 LGKDDTVTLK NAEGEVATY SKWDLGEHAE NTYGRIPDMT GDFANTGVPT PGAKNVAEAG
 SGEEGVAVAN AQLPFHNVET TPIHLGGDFT GEDMSGVDFD ANSTAWIANN DIGKIYSLAH
 DIANNVTKLT GEWETGYGPE GGEPAEGIV AATNGDIYLS TERNNADKNV SRPSILRFAT
 PTGKTGVQNA VQEWDLSEFV GDIQPNGGLE AIAQLEDNFI VVGVEETGDV IVDVLSADQP
 VLVQRYESSF DGVMSLDYNA ATKQLSVVCD EACDGLSEIL EWDGEKLYKS KDKIYERPN
 LGNWANEGFG TYTSELKCN GNTVSVTSYL WADDAATNEG TSLNSAQVIN GDCCGVNIPG
 ESSSDNSSSD FATGSIAGAF ATAVLAVVGI

> RXA02403 (1-765, translated) 255 residues
 MTTFTITSGGL EISPAHAHIV HAESPEGELL FVSSASQYGE GNAIRGGVPI IAPWFGGLLG
 LDPAGHWAKR SAWDVTEHDG QIHAEYGRDG LLLDIRANST KNGFEITLRA YNDTDEARTV
 QLAHPHYFKV DDVEKIEVRG LDGVDILNRL NNEVETQDGP VTFDGEFDR ALGTVPVRI
 DTDRIITIEG DGHDSVTVWN PGESRASTVA DIGEGEWRDF VCVEPALLGA DQKGRVAPG
 QSVTVGMQVS VEKRA

> RXA02406 (1-549, translated) 183 residues
 METLAAQART LLEKVGAVPT HASFVESIAK AIPILSILLT LIVTVNGISS GNPVQPPALE
 QVRTDVVNKI NYERNLKLGLV SISPELELHT AAQTIAQRNA DSDSEKVPD PEGTLLVQQ
 NLPYANANAD TIVDRFLNSP DHVKLLLAND YEAGVGVAY KGDHAWIWE FTVPADADSVE
 STE

> RXA02407 (1-306, translated) 102 residues
MNRQNQLHYP QEVKAVESVE SSLNMSSPSA PLATPDVELD VHTLSSENLP WLCIVWDDPV
NLMSSVTVYVF QTVLGFSSKKR ATELMQVHT EGKAVVSSGE KD

> RXA02408 (1-828, translated) 276 residues
MLIDVAGFLL GHVTKGDTGC SVVIAPNGAF AGVDVRGGGV GTRETDLLEP HNSVQQAHAV
VLCGGSAFGL AAADGVM TAL ENRGIGFPVR PEGPIVPIVP GAVIFDLIVG DPNKRPTAAD
GEQAVENAF A GTHNGSGSVG AGTGATAGRL RGGFGQSSRR VGKTTIAGV VANPVGEVVD
LTTGALFGRP EVMGVGVDKL KSAATLNTT IGVVATDAPV TKAQAKRLAL VAHDGLARAV
RPSHSPMDGD TFFAMSSGDG SGVTPVELGE LSAHAA

> RXA02409 (1-414, translated) 138 residues
RAQSVPKDPL AEMTGMTSGH KEAPTDPALA RLLPDFQHEG DEEYDGNDSF LRSLSHEGDT
RAKLENLRVI NDALGPDGNV AVTASEEEAH AWWAALNDIR LYVAGSDVGR GEAAEEDREN
LVQWLAYNQE SLLEAMMN

> RXA02412 (1-480, translated) 160 residues
VAIIVIAFVL LFNSLVAPNN SSSPVASPT SESVEQTISE SPESPSATED QPPSATETP
RNRPAQPSLP AGASPANDAA ATQTDAGN LN NVYTGSA TS AGFAQAVRDA FVNHYLDTNE
LSGRVTATSP VTGNYTMYNC EDNGEYVTC GNNAVVIYS

> RXA02417 (1-2124, translated) 708 residues
MDMNSSRLA LRTALEKLSA SATAMASASN DIKDLVARLD AQEMSLIDAN PAPTAPTAP
PEAQLEPQPL VYATASTAPA LADVSGTNRI PRFVRHRLAD PASEGWPLGV EKQKQAPAY
PHFVRPAPPA KPPTMSEKI MRGVAITGGGV ITVAGVILV SVAIQRGWL G PLGRVIGAYL
LAVLLGAHH YVRKRGTRVE ALVALTVTSQ IAPLATTSAI IFLEWWPPG LGSILVALIGN
IGFLIVGRLL SLSKTEKSAA EGHTVVFVGA AVSGFSAILF ALSADAWWPI FSIVAALLLS
YRISTNIIRA SMAAFVILQ FVLSASWQTM EWPATIVGTI TAVLLVALTL WDFPKITATD
SHDIALEEYV RSFETNPVST WVGAVSPVLI VFITTSMFIA VDWPWLALIP ACAVAALGIF
ALRSSDTASI ENQMRSLIA VVGLALIAET FVQLFYGDLP TNPLLVMVFL IAGAALFMWL
RMLPPQRLG VVPVAVWALIA AVAMTGVLRL NVVSIPLWL TDQALQIAL LILVFIATII
QVRRSFYGHK LWLQILVGLT LLTLSAISIV TITTFIGRLI AGNAGMMLG LIGHATVSIIL
WMVIAAALML NRKLLDAPGA LWTGVGLAVA GTFKLVFFDL VALSGVPRAI AFLLSGIALL
TIAAMRGRRR SENKADVARE QVARHGATSH KNEEPSHESP SSSPTTTL

> RXA02421 (1-810, translated) 270 residues
MTLLKPIQL AAGINPEDAL AMRHVFISIH EDTNSNGITR ESKDEEILAY TASQSSDPRR
FPLNPPRFWM VFIREGGSQA RLWKVVENHG EVTNDGVRRV FNLTEIELMD DLGRLVIRW
NSPRKWWIK TTAALYVDT IADAEPIPPF GFDNLVLSYP FLQEVMPREPA YASWRITALGA
VKGIYLTID RTGRHYVGKA EGTENIRQRW NSYATNGHGG NVKLKQLKPD TFRFSLLRVF
DPATPTSIIN AAESHFKIAL DTIKHGLNAN

> RXA02423 (1-216, translated) 72 residues
MIRKLARPML ASVYVADGAE TVLNTSAHVE GTQVVLDRIR YVLPRKYAKR ISRDPELVTR
VIGGTVCVAG SC

> RXA02425 (1-630, translated) 210 residues
PGAFDELTSV WGEKGGSWAA VIGFFGGIAL IAIIDRLVPT AINPHEPSTV GGAVEGFERR
NRMKMGVLT ALAIAIHNFP EGFATFLAGL SDPMIAIPVA VAIATHNIFE GIAVPVPLRE
ATGSRKRALG WATLSGLAEP AGALIGFLLL MPFIFPEALG LCFAAVAGVM VFISVDELLP
TAISSGKHH ATYGLIAGMA VMAISLILLI

> RXA02427 (1-387, translated) 129 residues
VDFELGKRCP CGTGLTYGEC CYRFHSGEWV APTAALMRS RFTAFAVNGS QYLLDTWDEP
TRPSLGLDM GIDFYRLDIL ETTGGGPFDS TGTVKFQAFY KGLASGVQEE DSTFRKVNGA
WVYSTGDVD

> RXA02428 (1-1134, translated) 378 residues
MAATLDLPTD DEPIAYAMFAH CFTGSRFTPA AARVSKTLAE SGVACLRFDF PGLSQSEGDF
SKTTFNSNVD DIVAASQWLT EHYAPQLLI GHSLGGAASL KAAATKISCLK AVATIGAPFD

PAHAVLHFAD RICDVEDDQGA VTLQLGGRDV TISREFLEDL AEVNPEDHLR RLKPLLLLLH
SPTDQTVGVG NAQLIFRVTR YPKSLMTLDK ADHLLTKDGT AQRAARIAN WVEPYLVPEN
VCEDLPEFVA EASTIKASKY GAAIRTGHHN FITDRDKSQG GKNLGFPTPS LLVSLAALAN
SQTIKQAAID NRIGKLDVVK VTISQEQSAD HGQIKLRRKI SLIGNLSAD SASLRAASNS
CSITQLLAQG IVIDDEVN

> RXA02430 (1-186, translated) 62 residues
MSPVSRRAHE FRINEGEFEV VDVGSLNGTY VNREPRNAQV MQTGDEIQIG KFRLVFLAGP
AE

> RXA02433 (1-600, translated) 200 residues
VKLFKATAVT FTVAALALS ACSSDDSSSS ESSTSSSTSS AASDAATQYP TAEELNAILA
VATDPEAPIE EKVTVQGSSE NAPELFETMT QAKVESGAEF QVVGSVLPGY DPTSEVLTV
MFQLPDRAEQ EAEGVFEFVNT DGNWQLSQDW ACILITNTVA PEQVPAMCVG TDASSAGIEE
APAEEGAVVE EAPVEEVFVQ

> RXA02437 (1-810, translated) 270 residues
MSTIGNKLKV VDGARKAYGT YADYRDKVS ETYDALSQAA GEYAPKAEQA VETARESAKE
FYTESRKDGA NWTAKAARAL EKALAEADQK ASGLKDKARE SGKLNRRKAR RKADKAARAA
RKATEKKESH WVRNLSLAAL ATSGIVAVAY AFLNKTKKET PGTPPPRVEV QLKKAVEQDE
PEVVAEAAVE EPELVYSTES PETTEAPAEA TETPAETTEE EAKTEAELEA ELEAEADAQ
EAAEEAEAEA IQAEFFDKNA PORTQSEKKK

> RXA02443 (1-954, translated) 318 residues
VILKDFNNNG ELFGASSAKN FRKLLAVPAV AASLAFGITA CSAVDDTPDI VVTNNILGDV
VSHVIGVSDA VQVLMKPNAD PHSFGVSAQD AAAMEHADLI VANGLGLEEG LQSNVDNAKS
QGVVPVLEVEG HIDVIDYSPG VPDPHWTFDP ARMLAATEVI EAELIKELDP LTESITQSA
QHYREELVAL DEEVEELLSSG VAPENRKLVT NNNVFGYLA RFNYTVIDTI IPGSGTLAAP
SASDLNDIST ALEDNVVPAT FTDTSPPQLR AEVLASNAGI DVGVVSIFTE SLTDADGEAP
TYISMQKINA ERIASTIS

> RXA02444 (1-1278, translated) 426 residues
MKNSKLLLIA AVSTASILLA SCGTDDSSADT ATASSSATAS SEAHDDHGHE AEGSSTAVEV
SSPQARIVTT YDGGIITLDA NTLEILEDTE LAGFNRLNSA GDGRHVFFST GGGFQLFDTG
AWTEPHGDNT HSYTATPELT DITYSTDKPG HVVNHAGKTV LFGDGDGKIQ IFDTASLLKG
DEVEPELKNA LKAHHGVAVV LENGDLHLTL GDSDSRNGAV VFNAAGEEIA RNEQCPGVHG
ESAALGDAIA VGCEDDGLIY KDGEFTKQVA PDSYGRIGNQ SGSDVSPVVL GDYKVDKAD
LERPERVSLT NTGETELTLV DLGTSYSFRS LGRGPAGEAV VLGTDCALHI IDANTCAITN
TYPVIDAWTE PEVWQEARPT LFINKDRAYV SDPSNNELHV VDLANGNILA SATLPPTPNE
LTGVSG

> RXA02452 (1-180, translated) 60 residues
MTPAGPAQLL IVALVVIVFL GSNKLPDVAR SVGRSMRIFK SEIKEMNKDQ IEESDQTLKN

> RXA02454 (1-813, translated) 271 residues
MHLLNFYVGD VLSLNTLFRR DAETYSAYLV DAETGEFQPN LSESRRLYDV DIARVNIIGE
LMDLQAGECL DKSIDVIALG GLVESSYLEV WTELTAEEVS DASEYWRLE RIDRLNQLGF
DVGELKVTKD DSRQVVRIRP VVVDPGHYRA ELLSLTGLSV EEHQAGRLG SIQAQVAEC
GPHVGLTQAA HLWMTNEYEP TIAAVPVEML OKLEPAQIFH EIVDHRWFIA QERGAVATLP
EATASYLESV LPARRDEARL LSTNPSEDEL S

> RXA02457 (1-1110, translated) 370 residues
MFYFTVNNPQ DPLSTEIVET NRRDLAFWHR LRPKDDDDLA TAINKICVRT GLSRKLIAAC
LFSICFLPYL PNFHKLVEKL GHLDMARINA ITKAGEKVPS EKRELFDAYL VDYLTPEAE
QCLPQASSIS AMMRKFAQH CPDDKASSAT NDGSIRYRRN NKGGISITVD ATASEVTEIK
AALEQMSKDK DCTPGTSLH IIRGLPTKVV LNTYGTCDSP EYLEGGTWS KEQSEFWTK
TSSSRDMDAA HFSYTTAYAP TREMRVYIKG LRTTCSVPGC SVAVENCQLD HIIPWEGGGP
TTFWNIHPLC VFHHIQKTEG RLQCYPLPDG TVLFLVDGIP VFSIPDGPLS KSNKTWGTKF
GKYMERRIAA

> RXA02459 (1-735, translated) 245 residues

LARRSYDESD VVRVPGKGTR PRTKDRPSHE NALVGMVVTK DRGRWGVLD GRQDAIVTMR
ARELGRTAIE VGDRVGVVGD TSGRPGSLAR IVRLEERTSV LRRTADDDTP FERIVVANAD
QLLIIVSAVAD PPPRAGFVER ALIAAFVGNL QPVLCLTKSD LADPAEFAAE FEALEVFEVV
CGVDDPLDPV LEVVEGHITA LIQSGVGKS TLVNRVLPEC RSLNWCVRGG WQGSAYVDVA
GRSCH

> RXA02460 (1-504, translated) 168 residues
LRVYIPATFS TLRGLNESRV ITARSGYGFA VTPALLDFYT DGDEEEIAHA AFQDAAEASI
RLLAIGDEET FPYRRVVSV DVDDSVVYQ PENGESVVKL SPAHINLDDV AAIHIDVEAS
EADTKKAIEV IDESDLGEED AELTVGDAQD NFMAMYDPEE LPFLVELL

> RXA02461 (1-408, translated) 136 residues
MRGLIVDYAG VLDGTDEDQR RWRNLLAAAK KNGVGTVILS NDPGGLGAAP IRELETNGVV
DKVLLSGELG VEKPEEAAFP AAAADAIDLPM RDCVLVDDSI LNVRGAVEAG LVGVVYQQFD
RAVVEIVGLF GLEGEF

> RXA02464 (1-507, translated) 169 residues
MGTFPDDSRP PEITQDIEIT DGRIVAIGQS VAAVYTNDFS PRIVSYNDGD ELVGEQAVDE
VEFPDPFPQS ATADLPHHMS WFNQDGLVLF SPTQLNVRQS FNDALGTGIA LNSGLLYPTA
EGITVANWDT GEVQRTIPVD RAGYDGEVAL GVVQGVIVEK RGSEIVALG

> RXA02465 (1-399, translated) 133 residues
MPASIRWGGI VALIQSTIGF GYAFFLIYRE ATGETDPSIV YETDNANTWV GYGTAFFII
VEGTVVAGAI NMMKGHRWGR GAVVMLNLI LPAAVYMFIE GRFSWAVTG ISALFVLGAL
FNKRAVLWAN NEI

> RXA02466 (1-87, translated) 29 residues
VGEQGEQTFY YVIEIEDGVN TAAYGGDDA

> RXA02467 (1-225, translated) 75 residues
MDIKIGFADT ARELVISSAL QQDEAAAKVS EALANDSGVL DLSDEKGRRY IIRNRIAYV
EVGTSAPRTV GFAGA

> RXA02472 (1-291, translated) 97 residues
MSFVNITALT PFAGAEKEIE QRFAARKKAV DTAKGFQEF LLRPQFGEDR YFVVRWDSR
EDYQAWSAR PAGNHADDEQ RGMSEVVLGF DVPVLEG

> RXA02473 (1-741, translated) 247 residues
MVAEYPDGSS EIFPVTLNLI PEDTLVYDAV YKFSIRTGS EDQITFFVSN QFDVFPFAGT
SFTLTGYEIE QDLRSAGWKE ELNPVTGELS VTPVISVIYP DGSRDNTIAT MESVGPDDSE
LFKPDPLDIP KSGDYIEIG VLAPGLPAGT EFHLDYYALP DRFFDLGGST SLSGNGKFSL
GVPLTWNDLD QLPISITFPD GSHTVENLHV DVTANFAGN PIDEPKDDXK DHPQAPKPS
GSSFGSS

> RXA02475 (1-1155, translated) 385 residues
MLGLSRKKFA MLAALTAGIV GVVATGCSTP AEPETIDNPV FIGISIDPIK NLSPNHAANL
FALGDSGGG IFQELAPTYF PSIHRLNGF IAPDRDSLTV VDASLKEYVR HEVARLGVMG
QTSARSPHLH KSVAFSFNEG TAEAPYRHRI VSATEKTSAS AMTDQHRFAL TACDDGSTRW
VEYSPDRGME DPMGPGSARI VTLQADGELS EIDVEWNFPD RPSAPIILSC EDPSAIVSE
EDIIVVKDEV SPAESIGKLE AYEIPDRARF DTVSGEDYFA FSTTGMRLRI NIPQAKIVYA
QSIDLYGKHP VSITFDSDBA YVVTSGDSGE SLLEIDLNDP TCTSDQLSLT GFNKLTLTARK
PKPEPSIIIE TILPIDPNYS LGCKS

> RXA02478 (1-1236, translated) 412 residues
MRTSLIARGL YRIPALVDQ GLLTLFDARL SVDDLPAPIV VVSARSSDGI TWTTPPAIV
ETEHRGVGDV CLVTGDLCHF GLSNLAGFFE DPTDLEPLA RRDVSGWTSI SMAHYFADVD
AAFASSGTGL VLAAGRWIQS FVVRRGREIS LRLLRSDGHI TDIAGNGESA MTQLPSGRIV
LHSRGVGHRL SSVSDDFGET FTFLEVPVEL IDPGCNGHVF YWKAAGMLAA TLADPDRLR
HLVLDLSSDE GATWAHRITI EREEAAYSTA AEMPNGDVAV VWEAEGTIRAI KCTVISVNDI
SLRIDEPISD AISLRHVVIN DDHDGIEVAL PDASQWGEV FKIVSNPDAS TKQIRTRGKL
ARQTLLEIGDE LVFDIRKGGE VAYGVTPYD GRSLGKLNRI LEWGCGRGFA VL

> RXA02482 (1-810, translated) 270 residues
 VGVAKSKKSA LPKVLLTIV ILLLLVLVAE FGLRFMIGKQ LKDFEQAQAS SQGISATEEP
 SISFGASPLL LGIARGSINE VTIDTPDSVS ITNQDGVPSI SGTPESTIQL QGDLIDGDRDN
 PVADHLTLTT LATQDDFILAT IQQMAEATG GNSTSGQFAE QLIQELIKVT DTSDAANQT
 IEVETFDGAA RASLHPITVN GQLGFEIVDS QLFGLGLPDE ISQMLTDALQ SSINEVAGGL
 QIQSLEVVDA GINVTILTGDN INIQTLEAAQ

> RXA02483 (1-813, translated) 271 residues
 MADHAHLNRA SFRKGANGKQ KEIGVITRGT TGVNRLRRFD RWCFFHHPKIR SLLDATSLAL
 DVGYGASHTT TVEWGRWLHR LQPDMDVIGL EIPNERVLEP QNGVSPFELG FELAGYTPQL
 VRAFNVLRTT DVDQVEAAWE TVTSRLAPGG LFFEGTCDEI GKRCWTITLN SDGPGQELTLA
 WDFWGISSTPS DVAERLPKML IHRNIPGEKI HALLAAADLA WDYCAGWEPH GPRVRWEKAR
 EMLLDQGWPI AVSRRRVGDS LLTVPWETVA P

> RXA02484 (1-501, translated) 167 residues
 MATRTENTIT INQPVGKVHQ ALTTEAYWAY IAENLSPEAG EVNEFTAADG GATATLFEVL
 PLEVLPEAVR AMISQALKVK RVLTVPALTN NATTVEYNAD VKGTPVDFKG TIAINGDDAA
 TTFDYSNEVS VNIPFMGPAI EPKVADALGE LFANEGALTE KWISENL

> RXA02486 (1-636, translated) 212 residues
 MTEFSDVPGT AAPLHRALEN AGYSTLESLD GVPYKTLIAL HGVGKTGLGR IQAALLERGL
 SLGETKGAT IPTGHTGKVA SDIKTHITSV DPVAYVDGLE GRRVAHGHLQ LSIFGRVTGA
 EPKMWGPMSI GYGVSHVYSH TGREGDWFCQ GFSPAKSKIC LYGLKDSPRG EELLQKLKGY
 TEGRGCVYIN KEPIDLDLVL EAMISESWAG QG

> RXA02488 (1-369, translated) 123 residues
 KLTATGVDVDM GTFFYPEGEAL APITLNLNTNE VVCDEPETEV EPEVPVEPET PVDPETSVDP
 ETPVDPETSV DPEKPGDDNK DDCNSSSSNG DILGILGILA ALGGVGALVY NFLVASGFLLA
 AFK

> RXA02489 (1-624, translated) 208 residues
 MNRFPSSALL ASVAGAALAI PATSAHAASE ICTTGDVGVW NVRDSFNLSYL LGNIANGSAY
 KYKGGLDVRD QATQDNGNKT PALTWVPVDSV TSSKISTSGG AHWTGHNLYP GDDLADEVNPN
 FTLDLDFSNI TVELSGSTGR LLVDYTSREY INTHTLGEFQ TGEQAEALATI TFAKAPDLTS
 NSNVNTGDVA LTADGVVEFG GFYTAGEE

> RXA02495 (1-2568, translated) 856 residues
 MALTYSVSVL GTAFELCGSLI LTHSLERTFS SIVDAGVEGV DVGVIAQQNN PDGVVFFSVIA
 EIEQYQVEVA VNIIGDGPGM PSGTMTGQS ALILTDSGDN PLQAGSSGTH FLAIYPOGEW
 VSPPTLIDG HFPTKPDEVV VNASAAKRGK LSLGDHLTIV TPTERTDATL SGTFFESNTDV
 AGWVGVGFTF QRYVELLTNG TDASQITIAF NDGADPMAMR NRIKGNHRDL LPILLPEQIID
 QTTGDTDRQL EFMTYVLLAF AAIALIVGSF IANTFAMIV AQRTGEFALL RSIGVSTFQI
 GFSVIMEAVF VGLIGGFIGI AVGFGVVNAL VQVINQFGDT LSSIDITYNA GSFIFVFLVA
 VTATVLSISS PAHRAGNLPP VQAFESSDAR SDALGRIRFL VAAVMTLTGI SLTIAGAVVS
 AINGDEFKTE TRLAFIGAGL LLVFFSLSLG GPALMVATSQ TLGVAMSPSF RAVGKLAQRN
 TLRNRRSAT TALAVTLVSVG LVACVGVIGA TTRASVEGSM ESTIKSPYVL DSGGTMIPG
 QPAGGSRSLG MSAAVAQEI A QTRGVGVKGT LMTGSVQVNG WDNENTTIFD GDLSQFLDLA
 VRSGDAFDDE TPGVMISTTY ADQSDLEVGD TVTVNPFYGD DGRVPIITGI YAETNLVGH
 MVNAAATNRR LITSADTYHRS QIFVNGDGST TNEELRDILV DAVAPPLIVQ VSKKDEFRGS
 LGTQINQLLG IYGLLALAV IIAVLGIVNT LFLSISERTR EIGILRATQV QRQCIIRMIT
 LESVILSIHG AIHGLLLGTF IGWAIVSCLR TRGMAPVEFP WTQIGLMLIS AIIIGGIAAL
 IPANRASRIS PLEAIN

> RXA02496 (1-807, translated) 269 residues
 VNRSNSSSVF LGFPSSPAA ASIRAGEELP LDFPREWYEF TDPTDIEHVF SIDLTWLESN
 WNCTFGTPOC LGDISENADV GCCGHGAFLA DETDRDQLYD AVAQMPAKYV GLRPASTDGS
 LASDDTDIE PWLTDWELDD EDGNFEPALK TTVNGACIF ANRAGWETGA CQALHGWGVN
 ANEDLTIVKPP EVCWQLPLRR LEAWEERPDG QEILRTTITE YNRRGWGNGG EDFDWYCTTS
 PRCHTNAEPM WKTQETELRA LMGPNSEYV

> RXA02498 (1-804, translated) 268 residues
MSEELTKVAE LMAAAKEGR STDAPRRRRR RSIEDGGVSV AELTGSIPAV KEKPAESKHS
SVPIDAPAEF EVVEAPKEP AEEVEVASVE GDVDKQETPE RPAPSNEETM VLRIVDEKDP
ISLTITGAFFV VPAAVAKPAP VVRAEKDADV ETAVKADFAE VEVDNDDTTQ MAVVEEVDEE
PEQENKMSVF AIINMAIVGV VLGVVVFLGF EMLWERLNKW IYAVLAVGVT LGMVGGIHAL
RTSRDGSFVMT LAGIVGLVMT FGPLAIVMT

> RXA02500 (1-99, translated) 33 residues
MGSVIKRRK RMSKKKHKRM LRRTRVQRRK LGK

> RXA02505 (1-171, translated) 57 residues
VAGTHAYVNE TLSENEFSMC RKNEPGLVIE LENISIDRIV ISTDPAHRYA DELMAAAV

> RXA02506 (1-882, translated) 294 residues
MHLNQLLEFFI AVAQHGQINR AAEELLISQP ALSRQISALE KSVGAPLFER HSRGVSILTGA
GEILHEEALR TLSRMQSVVD EIQSGEHLIT SINIGVPPGI PIDWLRCOLI DLGPETRISL
IESPTDDQLK LLKQRELDIA LCRRQSEAF TTVLHEQELG IYVRKNSELH QKVAGKDNAT
LEPDLGLRVL AHSRGEVRIQ EEILKNAMLA AGVNATWIFR KFGQYSSLLA DLVQADVALT
TEESARTNFP SWQWVPIEGE DASGNDLVVR TWITWNPQPT PAVKALIQKF IDGN

> RXA02510 (1-636, translated) 212 residues
MDSSDSHVQG DVYVDQGLGE PDRLERLWAP YRMSYINTRS GGKQSTTAKR DPFFIEVPKMS
DEDDLIVARG ELVYCVLNLY PYNAGHMMVI PFRKEKNLED LSLAESAEML LFTQTAIKAL
KQVSNPDAVN VGLNLGKASG GSVGDHLHVH VVPRWSGDAN FMTVIDGVKV LPQTILRQTRA
MLAQAAGTID GAGPTVDPTL TSAIRTAAPK EV

> RXA02514 (1-837, translated) 279 residues
NSHNPTPVTI TVTGKGEVGT SFGAISIEVE AGADAIVALQ YVSGSHTADN VEFIVGDNAR
LTIVITDTHWN ADAVHLSNQL AQLGRDATLR HTVATFGGVE VRIVPRVRF APGDGAEMNL
VYFADGGQYF ELRLVDVHA PNCRSNVLYK GALKQDKNSD KPDRCTWVG DVLIRSNNAHG
TDTYEANRSL VLTEGARADA IPNLEIETGQ IVGAGHAATV GRFDEDEHFY LQARGIPAAE
ARRLLVGTG NEVINKVPVE SIRGELDNVR SSELAVLGM

> RXA02518 (1-411, translated) 137 residues
MSEHTENTTE VEDQNASTFE AQSSERPEQS EADLAKASDV EYMRDVIDP ELGINVVDLG
LVYDIYIING NEAHIDMTLT SPACPLTDVI EDQARTAIVG NGIAEKMSLN WVMPPFWGPH
MITEEGRAQL QALGFVAV

> RXA02519 (1-1806, translated) 602 residues
MFSAFLRRMM RVTKDEQIQP NSNAPENRKW FPRAPRPLRQ FLDTLPRIGT AGSRSATLHV
EDEQSPGLAT FLDVATGASS INDRDTSASG LEPEKIRFVA WRLIGHTMGA LMIAFGALGA
GALPVVNNPY VDFPGGNFMS RMLQTSSMIV LIGVGLFLVA WVLMAPLVGI PFKRSGNRTA
SVSLSMRLRT FGAWVAPIML TAPLFTQDIY SYLAQGSVTA QGMDAYAGGP LELLGPDNHL
ARSVPFTWAQ SPSPYGPVAL SIAASISVIT NDSIVGVGLA HRIASLLGVV AAGWAIMTMA
RRCRVSEESF FYLGVNLPLL ILHLIGGIHN ESILLGLFLLV GLELGLRGTD RIQTLGLWGA
WTYIALSGVL ISCAGLVKVT FGIFGLFVGM ALARAFHARG HRHVVAIGVA GLVQVAALVI
TVVVLSVITG ISLGIWITQG GAATIRSWMS MTTNIGVISG FIGMNLGLD HTAAMLVVTR
AAGIAVAAAF MYRMLFATYR GHIHAVGGLG VATFVLVILF PVVHPYMLW AIVPPLASWAN
RLFFQLGVIA YSTAFSFFVL PRGLALPVGT VFSIYFGAAL GFSILLLVGW WSLRRNPFTG
LH

> RXA02520 (1-684, translated) 228 residues
VGDDVYKNDTA HTGGDTRRK ILLILLERAP VIASDIAEQL QLSTVGVRRH LDNLVEENLA
EAANPRQNPY EPKMRGRPAK TYRLTDKGRS IFGHEYDSLA AAALATLREV GDDDAVRQFA
RKRIETIVEE ITPADVTDQS IEDTAKSLVE AFSRHGYAAT VDATRNLGLQ CQHHCPISTV
ATEFPPELCEA EHQAQVSELLG QHTQPLATIA DGHGICTTNI ALTPIKHS

> RXA02521 (1-1443, translated) 481 residues
MTSATTNPGV NEPLTDDQII ESIGPYNYGW HDSDDAGASA QRLSEDVVR DISAKKSEPE
WMLQQRKLAK SIFDKKPVPT WGADLSGIDF ONIKYFVRST EKQAQSWEDL PEDIKNTYDK
LGIPAEAEKQR LVAGVAAQYE SEVVYHQIRE DLEEKGVIFL DDTALKKEP EIFQEYFGTV

IPAGDNKFSA LNSAVWGGGS FIYVPKGVHV DIPLQAYFRI NTENMGQFER TLIIVDEDAY
VHYVEGCTAP IYKSDSLHSA VVEIIVKKGK RCRTYTIQNW SNNVYNLVTK RTKVEEGGTM
EWVDYTSVVG VTMKYPAVWM TGPHAKGEVL SVAFAGEGQF QDTGARMTHM APYTSSNIVS
KSVARGGGRA AYRGLVQINA NAHSTSNVE CDALLVDDIS RSDTYPYNDI RNDHVSILGHE
ATVSQVSEEQ LFYILMSRGLA EEEAMAMIVR GFVEPIAKEL FMEYALELNR LIELQMEGSV
G

> RXA02524 (1-690, translated) 230 residues
MTETTPQPPK PEPPLPKFSL NFERADILF IALIVMGIFS LCMIPRAWM LTQPLAYILI
VGGYTSVAVG GANASVENGI WVVYWLCTLI GALKFMFVYV LMGKRWGMFV IAMSQYMPR
FHRMFKKSV DSESTRLYAMI IGLIPLAYLP GPVPGTILNA VAGLVKIPFW IIMAWNACIV
LSVNGLFMFL GTTFGEQVLD IVNVVNRMYL WITLGLLALM FFRARKQFAK

> RXA02525 (1-378, translated) 126 residues
MTTMREVSTD LNILIVPSEW EKVLENLPAT LSESGFVASE IHSQIVDLTC EPDNNMLVTQF
SQLEGHPPIV EVLHRLVING SSDLELKDLT KKVVGALPQG TYWYGTSLG ATEPGVNASC
ANQHRG

> RXA02534 (1-804, translated) 268 residues
MNSPNADIIL VVNKLSKFID IENIMLVGAR CRDIHQKQYR DQTAGRRTKD VDFALALESW
DDFNLLKQKF SPTGNAAWQGI TIGNIPVDLV PFGNIENPPG EVLSRKGHLN NVAGFKVEFVE
QAEILYPLNDA IDIKLSTVPG LTALKLHAWL DRKKNINAKA SDLALILSWY EEDVETLWNR
FYALENQGYI GEPEAMAAEL LGLDTGRILG HKETQALLDR FNEQSPPPEL QFAESLEAPP
EHSHPLEERR IQVEALLGGL RDSLGYDE

> RXA02537 (1-462, translated) 154 residues
MLAKSSSELE GIATSLTAVA GALHESNTDR LQSWQQLEMT TSASSLIQGF IKLVYDNRPT
VNIVQMHKT ASTLFNTADF LRTLEGYVDV LEQADKKSIT LTVMLRYIAS LSSLLDLMCA
REINALCTAI TFEPLKHLGD FGTLPPQQST SFIW

> RXA02538 (1-672, translated) 224 residues
VNAPPEIRAL AEAPHDMQIL EAGDGLSLVS FGDIDRATTV TTIVAGVGSS NPEGWNTYVD
RARTVSASTG SATVLWLGYQ APASIPAASV GAAANRAAAD LQRFQALQS RNPQRKLVVM
GYSYGSTVVG KAASSGELSA DALVLVGSYG AGVSHSSQLG APVYATGSA DPIGFAGTQY
DGIHGTDPTA ALFGATVWDS PSTHSGYWNQ QEFLGNVAEV VRGK

> RXA02540 (1-438, translated) 146 residues
MASTPKKSNQ EQQPRVDFQ GEVFSIVSAA ELAGMHAQTL RTYDRMGLVT PIRTRGGGRR
YSRADVELLR ETQHLSQEEG VNLAGIKAI ELGEENRNK ESLRKVTAEN EQLKQDLRSG
RPRGELVHVP RSTAVVMWER RKGRSK

> RXA02544 (1-1428, translated) 476 residues
VSHTCGIVIF VSTESGNTPK RDDAKSTIPP KDLPTDVLDA IEGNFEPPLN TQKSAVPPNA
EATVADSESG TTDRSVILGR DGRWLSGWAL RFIVLVIAVG IALRMLGFIW VGILLPVVLA
LVCTVLMWPPV KWLREHKIPT ALAVVITILG FFALIGGVFA AIAPSVSSQT KQVVDQATVG
IEDLMDWVQG PPFNLDISQF EGALNDLTSM LQSQSSTIAS GVFSGLSTAS SVVTLVAVML
VLTFEFLKDG PRFLPWMRGF TGENAGWHLT EVLTRTWNTL AGFIRAQALV SMVDAIFIGI
GLLLGLVPMFA LALAVITFFA GFIPVIGAVS AGALAVIAL VTNGVNTALL VLVLLILVAQQ
IEGNILSPFL QSKAMNLHAA VVLLSVTVGS TMFGIIGAFV AVPVAATLAV WVYHSEMVA
LRAGEITSDD IEIATTKGSP TSLNGQETLA AIRSRFAILG RKKPTSATAE KADSES

> RXA02545 (1-558, translated) 186 residues
MTETLFFVSAT TEEAVYLPDG IDLLVTGIGT TAATMILTKE LATREVLPAR IVNIGTAGAL
VDGLAGVYEI EYVLQHDFFS ELIAEMTGKP CNGSTLATS GHFPVASLAT GNSFIADSET
RNHLATRASL CMEGAALVG VAKHFGVPIT LLKQVSDSAD EASGSWFDA VDAGARQALAE
AVKEFK

> RXA02546 (1-1104, translated) 368 residues
MPLFFIDDLH RSKKYFHAHL SELLLGEFAT LSLPLHPTTA AKAADIDAT REFIRQWEGR
DDVEYARINW SPVGLGKTEV FVRLTLMTTE ELVVFAQVED KXSHHERFS QLSGFTAEEV
AKHVSILWRS SNDDLKAVL VVDNFKHPN SGLLKRAVAV EGVHTKWLEN VRLHETLVA

DKRGEFGRAD LGLGDAEARV RLRHFSVDAP AGLTDIEVPL SNLCELQEPQ VILMVENLDS
FLALPTWPGV TIAWGAGYRA VDIVRGPFYS NGRLLYWGDL DLDGFKILDG VRSHVPHTES
VLNMSETVSR WRYLGVADRE FKAESFDNLH DFESDALDLL ITDGLERIEQ ERIRLDVAVE
ETIEKVIRG

> RXA02549 (1-1326, translated) 442 residues
TLTAISSETW PIMLAPWVCL PLLSRNVDAI AIALSLLPAA CMGAVNATAT MAALIPAALI
LLYRGLFLRL LLWGMGVLAV NSWIGPLVL LGKYAPPFTE FIESSSVTTS WLNPEVILRG
TTSWTPEVDI ERQAGYLLVN DALEVTLISVL VAALGLIGLT LMKHRGLWAF MIAIGLLILG
SAHLTAQVEF LDGPGGAALRN IHKFDLLVRM PLMVGVAAALG SHISLPLLLGT TALTSQGGKH
HTIPLPLQKR QAAGLLVVII AVGALAPAWS ARLLPQGTWD EVDYDYWEAT EFLNQATGT
RTLWPSPPSR ARQDWGWRD EPAQPLLDVP WAVRDAIPLV PPEAIRGLDG LDDLGLTGTG
LNDEALKRGL IGAVLVRHDL EADPDIEVDL PGEKHTFGSQ GQVDVYLTD PDRNMWITSQT
SKQLPTVAGG GEILSLDLTI NG

> RXA02552 (1-795, translated) 265 residues
VGKHAHEETP PKKNSPWRIG LLTFLISSVV VTLVGMVMLW PDSDDVVLAD NFSQTFAGNH
EQVDGTTITLV DNSACNSPDT GRVFAESPIT SAEPATLECV RALVDITSGA NEGQKTQLIT
YAQPGDFEFS EGDKIRMVET PDTNGEIIYT FADYQRPAL IIVGVVLIVA MGAFAMRWG
RALVGLVVTL GIVGIFLLP LASGHDAMWL ALVCGAAILL IIVPMVHGIN WKSAAALAGT
LVALLLSAVL SWASIVTTEF ARTGR

> RXA02554 (1-624, translated) 208 residues
MSHTKPSIAI LGAGRVGSSL ARSAVAAGYE VKVAGSGAVD KIALTAEILM PGAVPSTADQ
AVKDAIDIVFL AVPLHKFRSV NPATLEGKIV IDTMNHVWVPV NGELEIIDQD PRSTSEIIAE
FFAGSTMVKS FNHIGYHEIE QDAGTGRAIA YATDDVDAGA QVAQLIKSFG FVPLNIGALE
NGRILEPGQE AFGAHLNKDS RLELVNQR

> RXA02555 (1-603, translated) 201 residues
MGEQFPGDKN IRVSDTERSA ALAALGQFYA EGRLSLEETD DRCEAVADAK TRGDLNAIFY
DLFNPQIAVY DRSQCTYTAT EVaelHRKGA RPRAGILGLT TVLAITGTAA FASTAFATV
LLALIPVFI MLYVMKIGPE SWHAPTQRQL QRKRMIELRE KEKLDMELK AQRKERTHAL
TNRALDAAET AFNTKPKWKN K

> RXA02564 (1-675, translated) 225 residues
MAEVGAEPAG SAQSKTKQEV VGTAARVITA IAAFFSIQSA SGGEDIRSNM TLIAPAAAGG
GWDTFQREQQ QSMRVNKIVN NIQVVNIPGA GGTIALGKLS TMTAPNTLMV GGTGHIAAQI
QFDTPAKIDV VTIPIRVVEE FDIITVPADS PYNTLEELIE GWKADPAGVS WTGGGSFDQL
VMTEIALSAG IDPKQTTTIF SDGGGEAIIQA LLNGTAKAST GGFAD

> RXA02568 (1-1359, translated) 453 residues
IPAAFSAPGS AIPTPGTAIP VFGSATVPEA PGVSAPGASV FSIPVPGSVT PPAPGISAPG
GALPTPGSAP PTPGGALPTP GEALPVPGAP GAPGASGIPS PGLTPGVPT PGASLPVPGA
PDAPGTPSIP AAPGQAPGI PAAPGAPAAQ AAHAKPVFQD AEKRPRTDEA GNAKKLEPLR
VRLAQPIITRK QWAMTLGVVLV LGAIIVVAAA VVLAKWAFTT EWLQDFEVEY PGKYDNPEGA
PVGIPITLSW QHFNMFMMV LIKTGIEIN RTRRPKGYNT PKKGKKISL TLHLHLVLDL
LWIINGAVFI ILLFATGQWM RIVPTSVDVF PNALSAGLQY VSLDWPTEG WANYNSLOEL
TYFFTFVIAA PLSIVSGFRM SSVYPKNNAT MNKLPIGIFA RALHMPVMVY YIVFICIHVF
LVLATGALRN FNHMYAGQDV VNWVGFGWVF ASL

> RXA02569 (1-750, translated) 250 residues
MSRSSKISVA FGGLLIAATV LYLVLVRPTD WESVGGSTEA LITLVGVVAG TIALLVGVLP
TLPARTIAII PVALVLNILL GQVTGSFVIP LYLDVAGTVL VAALAGPSAG LATGALLSVV
WALFNPLALP FAAGSALTGW LTGVVKKGA FKNIFATII S GAVIGLITGA VAAPVAAVY
GGTAGVGTGA VVSLFREMGN SLLASVTWQS FISDPLDKAI VMLIVFVVVK SLPKRTRRAL
VQRPVEDVA

> RXA02570 (1-642, translated) 214 residues
MNPLTWIIGA FSMWIVLVG NKLGLSIAVI IIAQVVAMIR VRNVSVLAST ALLSVPALAS
MALIHMPYSS DGWLIATLT ARFSALMSIF LLAATATITP ELVKSLYRWP KLAYIVGSLR
QMIPOGQKTL ALVRDANALR GRSVKGFPVA VKYVGLPLIT HLLSAGAARA IPLEVAGLDR

PGPRTVLVEV VEGRVEKHCR WLLPLLAVGM AWWL

> RXA02573 (1-444, translated) 148 residues
MTNKTMLVAF DGSPESSRAL EYAAKLLQPR TVEILTAWEP LHRQAARSVS LITLGVPEPD
PAHSAALKTC QEGVELAQSL GLEARAHMVE SATAVWSAIV DAADELPRDV IVTGTRGISG
WKSLLWQSSTS DSVLHHADVP VFVVPPLD

> RXA02575 (1-1158, translated) 386 residues
VKNSGKNSAK NRTKGILIGV LVGLIAIFAG IYAVDVFLNK DNIPRGTTVG GVSISNLSAQ
EARTKLETEL ANDVVQPVTV TAGEQSTTFD FVASGVGIDM DATIEGTGEQ SNWPITRFVA
LFKESSESPF STVDPAAFGP TLDMMVGELY RDPISGNLHI DAGTLVVDNT IDGQAVDRTI
LEQAVTENWL NPEGVKAEYP VVPAISQDT IDKLAEGAGA KAVSSPFVVR GDDGIEGTIP
VERMGEVVSF PEENGITIRD INAEAAATML AEGLKETEIE PTNAQISFSS GSRVVTPEVT
GHGINWEETL ADLPNNLTGD GPTIDAIYE DTPATFTATD AQNATFNEMV GEFTTGGFSA
ASGTNIRLTA QMVGAVVSP GDTFSL

> RXA02576 (1-1422, translated) 474 residues
MTPTRRLLW AWTTVLLGSL LWPLAAPGEL LLRDMSVVDH PALSLNALGF GDLPSRNAPO
DGVLLALLGLF PVSWIVRMTL LVAGFAGAWG AMRLGPSKFL AVTVIAINPF VVERLLQGHW
SLVMAVWLF LVLVALRRHP WQVVAIWAAS LTPGTAVVAA VTVGASSKRK RTTLLCSFLS
WLPWLIPALL ATPTSGGALT FAIRSETYAG TLGTALGLGG IWNAGAVPAS RELGFVAVGI
LLFAILLAGE KNCPPWLALL AVVGFMGAIG FWMMPNLFTW TIAYVPGAAI FRDSSKLLML
AIPAYVCLAA GVKSPLSWVA TGLALLQIPD APREVSIVRP SSAHVESVEA LAEIAADRDI
LIIQGGLPVT REDGIPVVDP KTKALSUVES GELRVDDIIT DAPSQRWTEA TQAWAAGDIE
RLIEGLVGWV VDGDTITETG APPQHGWKYY LGRLVTLVWM ALPLGLLFRF KTKK

> RXA02577 (1-885, translated) 295 residues
MGAYDWDWII STCEFSGKVM AVFMKRSATV LIAGVLFLI FAFTVPPYVT GQARTIPKDL
DLTLVSESPQ GFVTEHIVT APTEKVDEIA THVDQTVTDV QGKTVAEISD DVVLIGHSRV
FVIKPTATIS PVKADSSNV REGLYHFFPA TILNRNSPPY DIVLGEDSPV DYVSREGNTY
TFYQHLRYV LDDSHYTSVE RTLKVDREFG IIVAKDEAMT FHGPDGDDTV EETYTADTLK
LLQDHARDID KRLSWAKGFD FFSKFLGLSL LAIGVLTGI FKRQQLMSTR NKLR

> RXA02584 (1-351, translated) 117 residues
MSLLCDSIAI GLFAFLFARVA HQSADMPNV QGWFFTWLFF LAGVFIAYLV AILPAKLFPSE
RIRPAEPTVM LLAIVIGLVI WGFNNGGVPH WSMFIVATTA SAILVLGWRA LFKVTMR

> RXA02585 (1-981, translated) 327 residues
MGIQOIRHVS PVGVALTMVA LVLSFVAMAR VMQIMLKAGG SPATLKATTA LTFAANSWSA
TLPGGPAFSA ILTYKVQRSW GASAVLCSWF FLLSSALSTV WLVALGVIAV FYMGASLNLW
SLIATTFMAY GLSGAVYWAA NNPDLSARWV RKLTKNRWG FVEKLLGSI QLRSSVSLTGP
QFAASTAWSL GNRILDAISL WICIAWVTGT APMFEPEPNN TTIAGVLLAY TTKATAGSIO
ATPGGIGPIE AAYIAALVAT GMTAVEAAGA VIIYRLCSFI IMAIVGWVIV FIYFTPGQLK
ANESLDVEQD TINDSDNRQS AIERPDT

> RXA02588 (1-684, translated) 228 residues
MSDVHEVIHS YNPDKKEGPE SVLLVVDAPL DMGLGAILG GRPTAAYRPR FDAIGRWLLA
RAGRRARHEL RHIEPEATVF ANITPGGSDV VRPWEALRN VGFVFAKPK IGEDSDVDPD
KLIRHRRRYE EGVLRGVIVA SADQGNFRET LELVAEGIP ATVIGHFEHA SWAVAHDTIE
FVDLEEIPGV FREPLPRVSL DNLPDGGAWL QPFRPLTALL SNRHSQEQ

> RXA02591 (1-1830, translated) 610 residues
MTTAAIRGLQ GEAPTNNKEL LNWADAVEL FQPEAVVFD GSQAEWDRMA EDLVEAGTLI
KLNEEKRPNS YLARSNPDSV ARVESRTFIC SEKEEDAGPT NNWAPPQAMK DEMSKHYAGS
MKGRMTYVVP FCMGPISDPD PKLGVLQTD S EYVMSMRIM TRMGIEALDK IGANGSFVRC
LHSVGAPELF QGEVWAPCN DTKYITQFPE TKEIWSYSGS YGGNAILAKK CYALRIASVM
AREEGWMAEH MLILKLINPE GKAYHIAAFA PSACGKTNLA MITPTIPGWT AQVVGDDIAW
LKLREDGLIA VNPENGFFGV APGTNYASNP IAMKTMEPGN TLFTNVALTD DGDIIWEGMD
GDAPAHLLDW MGNDDWTPESD ENAAHPNSRY CVAIDQSPAA APEFNWEGV KIDAILFGGR
RADTVPLVTV TDYNEHGTMV GALLASQGT ASEAAGVTL RHDPMAMLPF IGVNAGEYLO
NWIDMGNKGG DKMPSIFLVN WFRRGDGRF LWPGFGDNR VLKWWIDRIE GHVGADETUV

GHTAKAEDLD LDGLDPIED VKEALTAPAE QWANDVEDNA EYLTFGLPRV PAEVHSQFDA
LKARISAHA

> RXA02593 (1-213, translated) 71 residues
LKIAHFDDN PADESSYIFA RSLAEVDGWT LEFGVAGVKM TTIIVSSIDDA ITTILRWMMG
EDIRDLNWR A

> RXA02594 (1-324, translated) 108 residues
MEAMATTITV FSPTHSPAQI RETILSAAKE DDVDFGLVPF THPRNVTIEV DDELINDCLG
WLDVVALASG LGIQYNDEV LRYGDEDISFT VQTKNDDAR IGASRLGL

> RXA02598 (1-591, translated) 197 residues
VTTDONKRSI SELAARIVSE ICAPWVLNIG FFLILGVTG AWTILGIVAAI GTGIVPMILI
LGLMKLGRVG NHHVTTNRQR GLVFGVLIIVC VIIILIFILRA LEAPQLIWDG MFSALIFVLV
FAQVTLKKA SVHVLGWVCL VMFLGLTVSS WLLGLLFTF VTAARMRIK HHTMSEIVAG
VVTGAVATGI CYALLA

> RXA02600 (1-1398, translated) 466 residues
MQPFPLSLTN SSVAGIAAGA LLFLSVPFAS PVHAQTILQD TLEVTVLDA DELAPEDEDF
LSTETPKIDF PDSVTAVRYI TLTONTDKIN DDVENYLRAE HPEWIQTNSF APGEVIAVG
FDPNTMGAYA GNDVAAETGI AEQDRIDGTT DAMRPLLDQG RIALGMLGA KSVADTSVVR
ESSAPSGGVI AAILGGIAAL VAIIVAWATS YANKKKAEGA REQDFYASRH YGEVAQQLDG
INVRHSLTS PLADDELRRQ WDDVNSRFL EVDIFGRLEG LTSTSENKAF RKALPDIEKA
HTAVTQMEIA QKNIDTLYDM EHGHEDETRR ELTRLADMQ EARQDINDKO AVVDILRLT
IQRTETIAPS APDFMDQYAR LIRDYAVALQ GVEKNLEQVK QTTERNAPAI YDDNWRVGTG
YNSWVPYYMI SSWHAADVSA ASSASSSSAN TTFSSGFSGA GGGSSW

> RXA02601 (1-1989, translated) 663 residues
MKGEDTMSA TNLAVEQLQR VLLPRRGEPA DVRSLYLLEA ESNKERLEWE DRFSVSVPAE
AEVSPQTYFN APFAPSYNRW SQLDSVVLKL KVSGEARVDL YRSKIDGARI GITGSVVKDD
FIEFEVSLAP FDEGGWIWDF LTAETDATIVE BAGWYAPHAP KAQIMPDGSE VGFPEARATV
GIPTFNRPAD AVAALEALAS DPAVDVIDT VIMPDQGNKH PADEPGYKAA VEHFGRDFEE
FRQNGGGSG GYSRIMFEAL GGVGDKGEAG AAKSPYILYM DDIATEPDS VLRAQLVARY
AKSPILVGGQ MLNLQERSHL HTMGVEVVGH DFMWTAAPHV HYDHDFAHP LHDGRKFDDK
PDAPNSRDLH RRIVDVFNW WMCMI PRVVA EQIQQLPLF IKWDDAEYGL RARKAGFPTA
TWPGIATWHM AWSDKDDAID WQAYFHLRNR LVVAAMYHQG SVDGIVRSMP KATFKHLCL
EYSTVAIQNE AMKDFLAGPD QLSIILDTSL PRIAAIRKTY PDAVVLPSAT ELPRATGAPG
VPTKIDIGRL APIKKAMWLA KGLKHSLSKE DASHHEVPOA NFAPIEARWF LSRVDOGATV
TTADGRGVVY RKRDRDKAKE LGKEARALQK QVAERFELS RAYRNAHPEL VSREAWGKVF
DEQ

> RXA02602 (1-504, translated) 168 residues
MSNKEVQILV AIQDQLMDAP GVLPTARGLS LLGEHAAGWL ALGAGGAVVD KKRRRSWAGL
FIALGSHAA SVIIRKVRAR ARPHDPAIRI LGVTSPKLSF PSSHATSTTA TMVYLARITK
SPVPLLGPI MVLISRMVLGV HYPYTDVLAGA LLGAATAEAV HKIERATK

> RXA02604 (1-2076, translated) 692 residues
VLACGLMTFS QRPPEFETGK QPDPETEHAG DFEETSSSA PRAASNGSSG PNYTLITTF
AALTAGIFAF WAGTRKRKWS DDGLIVLRTV RNLLAGNGPV FNAGERVEAN TSTLWQYCIY
LVALVTDYRL EDIALWLALL FTAAASIIGV LGTAHLHRKR IAVLLPAGVI GYFSLSPARD
FATSGLEWGL SLMWISIOWL LLVLWATSGK TSGKKASGAK TSNPIVNAGA ITYALAFWSG
LSWLVRELA MYGGLTGVL LTPAPRWVW LGILVAALPL PAAYQIFRMG YYGMLVPHTA
VAKSADAVW GTGWEYVEDF TGPYNLWGL ALLLAAGALT VWTKDKHLAT PKRGLGLRPL
GMAIALLVIC ALVHFLYVIR VGGDFMHGRM LLLPLFAILL FVSVPVNVV DRGQDQLVAL
VLVTFVWS TSVVFVQGHQW ENTQHVVD RDEFWDTNR DEDHPPYAE DFLTVDSMND
YAEVMRDQTL VNPTGQQLNI LASSDPITYS WITTPRVEG EAGDLANLSP TVFHVNLGPT
SMNAPLNVVR TDLIGLATPL AARQPRIEGG RIGHDKLMDL EQQVAESATP LAYTPGWLDT
QKTYEARQAL RHPELVHLFG TYREPMYSYR FVDNKYALT TGRTEISDN PEDLLKEFNP
TPAEIQDGLE TIAPWGEIKL DEPRGEPLYS SQ

> RXA02606 (1-1371, translated) 457 residues

MQEIHTIMKH MDALADPSA AAFKATLPFA ELLEKLHNKK ALFDAALAKS AERADAGRII
 GKTSHTIDALA YLLDISKSEA FRRTKRAEEH YGNPSPEPSS ELAEKATPEE KLAREEKEKQ
 DLAEQAEANR IAREHGISAE KQDTIRYELE KLNDNTSLSR ASLRKLAMQE ATSRTPEDLR
 NWTNRKVIRI NPTAKDPLAA VKKRSLSIGR QDHGSGAKAS LYLDAGKGLAL LKSLMSKAKP
 GHLLSDSLAE KRRTKFPQRY DAFADILHRA HSDLLPARSG VGTILVSLSA KDVTNLKAAGS
 PDHRYPTSTG IKLTPLEILR LGAAKYDFVT VLDESGRPL HLARTQRTAS LYQLRALFAS
 ELVCTREGCD SPEDNEIHH IRSWLDGGPT DENTINICP HDHGNNNDQR DGKDNMGHMY
 IDPTTGRGVY QPADRRKPMR FNNTAAAAS GGAGART

> RXA02609 (1-249, translated) 83 residues
 VERSAQAQAF LDALKDEKID ISGVEDQLIA TARNYCSEN KDQNVTVDAV AGQLIVQGR
 SVKEDQAAEI STLLKESADR TYC

> RXA02610 (1-927, translated) 309 residues
 MRKTITVIAV LIVLALIGVG IVQYVNTSDD SDFIGQPGEP TGTETTEPPV QPDWCPAVEV
 IAAPGTWESA ANDDPINPTA NPLSFMLSIT QPLQERYSD DVKVTPLPYT AQERNINSON
 EMSYDSSRNE GTAKMNEELI NTHNECPATE FIIVGFSQGA VIAGDVAAQI GSEQGVIPAD
 SVRGVALIAD GRREPGVGQF PGTFVDGIGA EVTLQPLNLV VQPIVPGATM RGRAGGFGV
 LNDRVQDICA PNDAICDAPV NVGNALDRAL AMVSANGVHA LYATNPDPVF GTTTNAWVVD
 WATNLIDNG

> RXA02617 (1-507, translated) 169 residues
 MSIKHALLVL MLDPTSASQ LQTKFEETMG IWQLNIGQVT QTIQRLQRDG LAETAGTTVS
 SNGRTVDTFQ PTDLGRLEVA QWFESPVTVT LSRDELVTK IATAESRGLN LIPLLDIQRN
 TVMALRLALN KSSRDLAETR NTQRLLEVRK IFELEAQAQRW LDRIEALEQ

> RXA02619 (1-900, translated) 300 residues
 MRSVLELLEL NWKESLVLHP SLTELADAAAP LAQDFATVRG VLKESLDLLG NALNHGEEPA
 ELAGWLSQVI TDVLSHSGLD AHVVLGTGPGV RGDALPTSPV RWLAVVDSQD DPNEKISALL
 TEVGFAIAPR GAATREWEQ RARAGEDPEV YLDAGTWAAI IAEVDDKALL QDLSSRRPPA
 VETYEGLSPL DMVWNIRENL MIPTVKIARW AAHKAGSLAP TTAQRVLVAD QVLTNDEVDA
 LTQVWTSALS LQSKRWMDHI HDQETTAWEL PALQRATFGA SARLLSEVL RVEAREIDTK

> RXA02620 (1-654, translated) 218 residues
 VGRFRRSAPR RAGKNPREEI LDASAEFLTR QGFATTSTHQ IADAVGIRQA SLYYHFPSKT
 EIFLTLKST VEPSTVLAED LSTLDAGPEM RLWAIIVASEV RLLSLTKMNV GRLYQLPIVG
 SEEFAYEHSQ REALTNVFRD LATEIVGDDP RAELEPHITM SVIEMRRNDG KIPSPLSADS
 LPETAIMLAD ASLAVLGAPL PADREVEKTE LKQADAK

> RXA02624 (1-714, translated) 238 residues
 QGYDSDASVV ALIVLSILYL PNMMIFAMGN LIGSPLYFGD ASISVFSVHS VPLPPLPILA
 ALPSEALSWA VALLVIPAIW ATWVCVRNPM RLAVNTTAIV ISALCVFLVIA VFAGGTLGVY
 NYVGNLLIAS VGLVFVYFAL VGLLIAGIDK LRNPVEVKSV KAVAVVEPEP EEVEEDEEEH
 VEEVEDEEEE EEVEGVVEVE EDDAEDPEEN PEEESDEEI ETETAEETN DGSEAEEDR

> RXA02639 (1-834, translated) 278 residues
 MIALGSAFPL VASDVGTLI NSSERVQRL RDVITRMTNQ GVTALSTGR PPRWIHYVLD
 QLSVVKPICV ANGAVLYDSA ADEILAAQTL SPEVMASAVM AARAALEEHH GVSIAVERAG
 KSAYDPADEL FLVTPEYSHA WPSNDHGTFE EAEVLSEPAT KLLMRSDYLD SKQLFDIVRA
 SVPEQDVHVT FMSGGLIEI AAPGVTKALG VSMALERLKI AQKDVIITFGD MPNDIEMLQW
 AGRGVAMGNA RPEVKAVSDH ITRTNDGAGV ADVLEWFF

> RXA02647 (1-462, translated) 154 residues
 VALSVFTPVA QAQSSDALTO LSDNITSSQI LDDDGNPVDG NETWPGSSSEG SSMLSNGDIP
 AAPSLSSSGK VTSDDDDIEI EEQALIDRL SEMPVIGSIV SPPEWLAIPIF AVLQGLLAI
 TLASTAASF DTVDSEFKQT LRDMLTQFGI NVDA

> RXA02649 (1-1002, translated) 334 residues
 VKLRFSSHSS PQVLSRKVVA SALALTALA LAACSSSAEP DSPEVEQAVG LAVDTPRVVV
 VDPGTGDLQR LQYKDIAPDA TQEQTNIAE GFAQSVVNAD SVDPQAPAGG DVTFTHLVPK
 ATTEAEAEFS QEMVSATRDI SLLFGKPTYT DLSQVEDVNS TEGFTLGIRA TDSGQHTTSL

FAAPVDSTET GRMLMEQYLL TFTSLPIVFP SDDIGVGAKW TVDSRVGTGES TLLQTVTYITI
TGIDGDKVNL DVEVSRQPSM GALEITDEES DETTGQLTVL NSNTSTSVGTL EVDLTQPLPT
SGQVSMTRVR IYGGSENEQVR VQDQSTSSVS FGDQ

> RXA02652 (1-579, translated) 193 residues
MDGVDPKGRRI VALLAILALV VVVAILSFSD RTAKPMQLNG DMLGDQNTET SPEYRQRASE
SLENAVGEAE AYSLSVTFTQP LSPSEANLL KGVGRVNAVY MLSAPAMDLP EPIAGETRED
VFNRQIKLVD AQLSGIGNVR APGELNGVVV WDIPOQKVRVL SESSLVYSVE TLPDDAANGS
FGIRPVDTSQ TNF

> RXA02655 (1-984, translated) 328 residues
MSPEAKEAQD SRRNEMPEKK RAVLRKAIKL EWATIAWVLF SIVLVGVVAG QSQAMRSAMI
EDMLSLVPPPI AFLASRISK AVATRKHYPY KHRSAIGHQ AAALALLIMG SLLIYEAVSA
LIKGERPPIG LAILFGHDVW SGWLMIGVMI SVSIPMVIWG RVKINLAKDL HDKLLYADAD
MAKADWGTAV ASTVGVLGIG LGFWWADAVA ALVISASILR DGVINMKAAI SLDGGRAMT
YDNSAPHPLN DDVEKAALEM HWVKHARARI RDQGRCFHTE LFVEPVEGYT PAPEEITSLV
KRIQNLNDWKL QDVVASVVEK IDRFQAPS

> RXA02662 (1-264, translated) 88 residues
MRRLKLTITLE NKPGRARLGGF RALAPTSKIA LVFLLLIFFL AIFAPLIAKY DPLASGTPEVQ
PPSGEHWFGT DAIGRDIFFR VATAPPEP

> RXA02665 (1-480, translated) 160 residues
VTNPIIPRVG IATDAHQIEA GKPCWIAACL FEGVDGCEGH SDGDVVAHAI VDALLSASGL
FDLGSFVGLG RPEYDGSQT QLLKEVRELL SAHVYVIGNV AAQLVQQTFF FGRPRREEAQQ
VISEIIGAPC SLSATTDDHM GFTGRSEGRA SVATAVVMKA

> RXA02670 (1-582, translated) 194 residues
MEDESVKSLN LAARRGALVT VAAASALALA SCSAQGITQT SSQVAADVGN QAGSANDPVL
VRDVTVHLTT DGEAGVKFTA INQDTSHTSH TLESVTVDGE EVELDDAEPI ERNCSLVADI
QSELDLIEEP EVGCIQH VAT SLENPGFAYG GVVPVEFVFD TGAITTDATV SAPVLESQVE
NREVGDDTAEE ASHH

> RXA02672 (1-1098, translated) 366 residues
MTPTTTTPVSN PDALSTGTQD VHTLKGTLQR LAPGTPLRDG LDRIVRGHTG ALIVIGDDEN
VSSICDGGFE FDSVFAATRL RELCKMDGAV ILSSDLERIK RANVQLLPSP TWPTQESGTR
HRSARTALH TGVPIAVSE SQNTITLYVE GKSHMLEQPA ALLNANQAL TMERYRDLR
DQVNNRLHLA ELHSYVTVID VVSVIQR EEM LRRVGEIIGD DVLELKGDAK EIIQIQLSEL
GDNDRERESI IADYLVTDGI PADEEIIHAAL EAIHSLDDKA LLNPANIARV LGLPPTTEAL
DEPVTFRGYR TLNRIPRVQK FLMDKLIVEF GNLALLNAS VEDLSAVDGV GSWARHITD
GLGRIS

> RXA02673 (1-633, translated) 211 residues
MAALLVLLVV IALIIVAVVA LRGGSSEPEE EQPNNAVTS SMESATSSS SKESTTEAT
TEETSSAEP TATSSVAADA KKTCELSDLV ISASTNQPTF SGSAQPELFM AVHNPTAVDC
EIDLEENKLR FEVYNLATNA RIWSDVDCNP AVEDGTSVFP AGEDRYFQAT WSRTTAPNQP
CNNRTDVPAG GYLLHTVVGN NPSPAVTFNL T

> RXA02678 (1-918, translated) 306 residues
MRMAKTKKKK EQLPEGMSRR QAKLAARAAE RAALEREPRP FEGLAMESQL VALQEFIPSA
TAPITVAGTD RKITILTCLVLP GAAAALVREE AFGGEAFVAM QQAIRSNNSP KDALFALNWV
INAKAGESLA TATADGTQPE LKSLNDADT LEITTHQDFN WFLAENDNLS PEVAQHMQA
NDSILPSHEV EADVPGAVVW VNPGGKAHRI WVRTENETAL FNALARIAAR GELNLGEETK
FAGAFRTHGI VVPVWDLDEP RPSGDYADVL VALNEKIVAE LDNDLAQLNAD ERQLENIKS
RQVTTIR

> RXA02679 (1-426, translated) 142 residues
VAPSSGDDTV DVGTCRTLLV SELNVLDWAT DLEVDAVAGG GVVVLGGAGV DVGVIQGFAD
GIEFSGGFL IGEANPVCDD IDEQFFLLIG EVRAFAQAG VVVARAARCA HHGIQLFTLV
ELCLLLFGEA VVEGEGGVH VA

> RXA02680 (1-1284, translated) 428 residues
 MRLNKRLLPAA LSGLLLSAAL LAGCSTSGTA ETTTTVSSA AASTTTSTSS ASSSSSSSSSS
 SSSSSDSTTA ETISNTAEAA QAFSLTLSTE EQDAVLYDYD AEEKSTGWSN FPVTFVQRSG
 VNLTDLTLEEQ QAAALNVLKN LLNDDAYQMI EDIMASDQYL NDESNTTDS LGQYYIAFFG
 DPSSDSWSI QFGGHHIGIN TTFSGDAITF APTHLGTQPS EWTNEDGETS AALSNMYETA
 FAFYDSLAEQ QQAQLYQGEQ LDSMVCAPGS TCDYPTCTGL KGSDDLDEQK ELLIDIVIANW
 VGLADEETTE TELDAIRETL DDTYINWSGA TEYDTSTGDG IYFQISGPKV YIEFANQQGS
 AGADIDGVIT AGWGHINTIY RDPTNDYANS VTQEAASGMM GGGPGGNGGE MPSSGDMPTGE
 MPSSGAPSN

> RXA02681 (1-444, translated) 148 residues
 VGVGEGDGTG VEGGVADADV SAELDGPVGV AAWIAEECDV VLAEGILGGV AFVVEVLIAS
 HDVFDHLVGV VVEQVLQHVE GSCLLFLSEV GEVHAGTLHE GDWEVRPAGG LFFGVVVVEY
 GVLFFGGQGG QESLGSFRGV GDGFGGGA

> RXA02683 (1-678, translated) 226 residues
 MTLLENSGGD PGSDSGGARY SLNSLKVSEQ AAANAVLKAV LNDVSYQEFA DSSYLEITGT
 PSADGTWGIS FGCPSESASV EFSGGSISFS PVDMTVPATR LPQMGAFYET LTEEQGLMLE
 TGLAVSTWIS SQQEMLLDLV SNSIGLADTE TTATAISKIR ATLSEYTLFG TPDGLTLALS
 GPHVDFEVSH QGSTAKITYR DPSTDTLTAE DRVDATASVAA APPEVV

> RXA02685 (1-657, translated) 219 residues
 MSGLRSLRLR IDDLLAPVAL NDQQVALNAS MANSALDLDT LQLCSAGVLF SWGALAIYLL
 GERGFQWKPK DWAWAGLAA LIGIPGLIFY ASAVHLGLSK QVPTTLETW WEIPVLLIWS
 AANAFGEIIV VVMWFFTRLR QLKWSVPAVI VTSSVLRGSY HLQGGISAGL GNIIMGVAFA
 YFYHRTGKIW PLVIAHFLID AVAFVGYSAI GGNLSWLGL

> RXA02688 (1-669, translated) 223 residues
 MAGRIILLRL QGHTNNVKHL LDRTPPGAEI TDLGRKQALE VGHELATYSG ERLAHVYSSI
 VLRAQQTAVL ATSTFEKARD MQSGAIPLDV VEGIQEINVG DFEMRGDEEA HMNYSRALNG
 WLHGDPAAAG LGGCTYKDLV NRYQPTLDRI MDSHDLDDDR DVAVVSHGAV IRIVATHATG
 VDPNFAPTYR LGNCRFPVLE PGNKKFSQWD VVRWTDSPIL WQE

> RXA02689 (1-342, translated) 114 residues
 MIEVSDERFE ELVELAFDQV PQQFLDHMRN VVLLIEDFNP DSPYILGLYH GVALTERTFN
 HGGLPDSITI YKGLALQNYCN SEEQLVQEVR VTVLHEIGHY FGLGEEDLHR LGYA

> RXA02690 (1-1098, translated) 366 residues
 MSTNFDTSTT PEGETKKNSS FRTAASVQTM LVAALAATAA VGVYSYNTDN SANGGESPTG
 PEQSTVSTTA TIASFTTADV QCATQWDVNN EGLVSGFEQT SCQDEHRFEI SARENLATYP
 SSEGFVDAAP PNLTRQAQLR EELCQSPTLA YLNNRFDPSG RYTIAPILPP AEAWAAGDRT
 MCLGQATDA SGTPTLTVEP IAAANDQARV ETGACVKVES SAEFRQVDOCT EDHHSLESLT
 VNLGVFPFQG APSTDEQNNF LGNTCTQASI DYLGSEENVY QSTLQTFWPT ITNSNWLGGG
 HSNVNCFLMSP STEGAATFNT LNSGATGTFT INGEVPPPQP ERDPLRDTAG TTASAEVGVF
 VEENAP

> RXA02693 (1-1647, translated) 549 residues
 MYSLPRLASL LTTRLATLKP ALKPATHLAS LGAQVIAELV PGIRMSPNRR RILPANMGAG
 FIGAELAMWW ALSPSLLPKP WWTAAANLAV LQAVGHAAAT GIHSILPRTN RRVSRKIYNA
 THIAATGAILT TTVVGLIRH RTQIRLIGQK NFGFKETIAG ISVGTGLGYA LLITGLTQH
 SINEVKILLI RFLPPWISFI AAVSVITLTT LTLADRVLRL RILHNSAIQA AHLNRMVFPFQ
 TEQWEPERS GSPWSYKQW AVGSQGRAVL SGGRPKDDII TVTRLSDDTE HEPIRIFIGM
 VPGRSLSDQV DLVIHEMRRT GALRRDHIVI NNSTGTGWIT DWSAHTFEEL TGGNCVTISM
 QYSYLPALS WYKNDGPIIN AARMLIDAVL HELDQLPTGS RPKLFLAGES LGAYGLAEVW
 GDEKVLGTA DGVLLSGAPR FSDAMNALRT RRDASSSERL PVIDSGRHIR PAGEPEHLDL
 PATWQFFPMI VAQHASDPIV WNAELFIRR FEWLKTPKQD HQDVFNRLRW MPFVAGVQVA
 LDLTSTSTV

> RXA02696 (1-456, translated) 152 residues
 MSMLKKTKKF FGLPAEAEH EDAYYADEPR YEGTAAYAE YRERDYGYP EAAPAVAPSP
 APRSYQSTIV PVELHSFEDA QVIGGAFRDG DAVVDMSSL SREEARIVPD FAAGLCFFALR

GKMQKIDSVT FAVVPELSNI STSELERAAAR IR

> RXA02697 (1-699, translated) 233 residues

PFVWVWIMHH FAGFLATKKG KDSPTLKQV PAFATGGAAG VAVTGVVVA ITWASGASWG
 WISEISGNSK VINPLAFPSL VASVITMVAE VFVDDFDYNA VVNVVRSISM LIMLGLLVVC
 WWLFRQNER AVTGTAAAYA VAFVFNSTVL PWYYASLISL LGTFKPPMWL IFAAGASGVF
 IALMTGSGSN HQLYNIVTVI IAAIIAWLAT VVIFDDTDPD TTATEKPSPH TVS

> RXA02700 (1-1236, translated) 412 residues

VVPSLQQWRK PALILAILTV LGVLLTHWFA WPLTWPLGLR LPVDVEVYVQ GAREFWLADD
 LYDIRYDTHF DNLPTPTYPF GALVFTPLWW IHDLFGLLV TERVFALITLL TTYAVAVFLD
 RLAGVRDVRV EVFAFAALLV SAPVYFTLNI QQINVMMLAL TLFDDVALPRS TRHSGVLKYV
 PLGLVLTGIAA AIKLTPLVFG LYFLILWVVT KSPRGLFGMI GGFGLGASGLA IIFRPSISIQ
 YFTDVLFTAE RIGDLHFARN VSIRAVLERL PELGSAASIM WLVAVALVVI AVAVAAAYRIL
 RTDLSAHNRL LAVSLVSLVA LLCSPVSWYH HWVWLGPLIV ALWLTQHRWL ALWGAFAVTF
 GSFHNFPLSE NMMLTWPWW MHVLAAYHIL FSAVVTAVFS CGKMPQKTEL SH

> RXA02701 (1-1308, translated) 436 residues

LTNPQTAAHA ASDSASQKEA PNPSLSITVG IKDLLGLLSV LGIAAGLIAN KILIERYNWR
 IDAAVYREGA IALVNGESLY AQPFDMGDIS LPFIYPPIGA ILFAPWGYFD FITVELAGNL
 VVIGSSLLLL LCLYLVTNAV LSGRDKLLAF TIAAISWPIA LFAEPVFLNA DLQCNILIM
 ALVVMDDLFI KRRIPRGVLI GLAAAIKITP LAMLLYFLVK KDRGWINAV ISLLATIG
 AVLAWENTKE FFSSTLLNLS AEGDSGVDTT FQSNSSIQAM LYRWWTSKAD ABASSLPTIL
 WIVLSLIAVA AVAYLMHQLF SRGLHVEAVM VNAMLMLLIS PISWSHHWV LPLWAVFEV
 RYRQHRSHPK FLLWSGVILS VMMLMLPPKW WFGRDGVNVF ELNFWKEILLI SDWTWLSIGL
 MITLGLGLKA FPKISK

> RXA02712 (1-795, translated) 265 residues

MTMNGSRTE SGKTRDRRAV DADPRYGRV SVSRDFSTAE ASRGASIST QPRRDMAPER
 RHTTRALVNP GVQPTKRRLM QHKLGSQVVM SVRGRVREAK RADPKVIQLS VLVVLLLCVG
 VGATMGLSGT STQTFQLQE LQATETDLSN RIESLNDRVE DASARTALAA NATEMGLVSP
 VEPGVLAQVE NGDVVEEREA NPETRPVIDI NGQQTRFNRA SSNPDETNAV TENLQAIQPE
 AAAPPYQNT VPYAAATGQA GGAQG

> RXA02714 (1-429, translated) 143 residues

MFLGTYTPKL DDKGRLLTLP KFPREDLAGL MVTKGQDHSV AVYPKEEFAA RARKAAAVSR
 TNPEARAFIR NLAASADEQR PDGQGRITLS AARHTYAGLT KECVVIGSVD FLEIWDQAQW
 AAYQEETEA FSAEDDDVLG GLL

> RXA02715 (1-390, translated) 130 residues

VSLSEQEQR LREIEQALMA DDPKFGKAVA SNNGLAGGGF TLRGIALFVL GLVLLVAGVA
 LSQQTLMFVA LGIIGFLVMF GSGVWMLRGG GSNKISVTSR TSNAKNRQQG NSTIGDKMEE
 NFRRRFEQGN

> RXA02719 (1-648, translated) 216 residues

MTLFQRLTN VVLGGLAGVL LLLGSFGGA IRYRGGVLD LGLNLFAPGH AQGISNTVLW
 VGQLLLIAGV VHLGRRLFKV KVADDTADAA DLGLVKRTILY AMVVPILFAA PMMSRDVSY
 LMQGAMLRDG FDPYTEAAV NPGPMLLEVS HDWRNTTTFY GPLHLWIGDM ITTVGVDNVT
 LCVVAYKILS IIGLAVTGWG IVRIAQHGA NPAIAL

> RXA02720 (1-627, translated) 209 residues

LERREELQVR LQQVQARIDA TLNEHNRPGE SVRLLPVTFK HPVEDIKILQ EFGVTAVGEN
 REQEARKAL ELPMDDFHMI GQIQSKKANS IARWAAVHS VDSEKIAEAL GRGVALALDR
 GDRTSDELPC FIQLSLDGDG SRGGTPLSQV TQLADCISDT THLRFEGLMC VPPLGWGPEK
 AFSQARDVLS GLEEHFDRSL EFSAGMSGD

> RXA02721 (1-738, translated) 246 residues

MSDLDPNRNP VRKVFTTRAG GVSQSPYASF NLGDHVGDDP QAVASNRNRL ADIIGLSPDK
 VVYMEQHISN TVTVIDEAPA DGQAVEATDA LVTTQRLGAL AVLWADCVVP LLSDDTDAVGI
 AAVHAGRMGA RNVIAKTTA KMEELGAKPS RIHALMGAAA SGANYEVPEA MARDVEAKLP
 GSIARTTKGT TGLDIRAGLL RQMLSLGVQM IDSDPRCTIE DEDLFSYRRE GTTGRQAGVV

WLPKEA

> RXA02725 (1-612, translated) 204 residues
 MNDFEHSNAS IRLQAALAAG TAEDTTAIDI LLYRSGVEED FFVRDMITWA LTRMPVDDVF
 TSLVADLDSE VPDREFGASQ ALHTLSKLRV AQSQWQLQAR FWLLHREDTA QTAWRTFVGL
 VPDDQTAWLA HQLLQELDKG TPEIQRSLSR AMAELEGREA SISVLLGALT SAHAVATAKL
 IADPDSDFMA DLEEARVDN MGAC

> RXA02727 (1-912, translated) 304 residues
 VVLLPLLVPQ LQVQQLQLP SLLTRQRCAR KSKRSCAPNT ASKDDASKA AQAQNDKAS
 AQDQQLRQAQ DAKAARDEAE KAKAEAKSAA SSSTTKAAAV GAVGAGTGAA VATGAANVDT
 HMQAQVLGL AQEMADRLTS EARSSEKSM DEAREAAEQI IEEANSGNN LTRDARANAE
 KQIAEAQNRA DTLVNEADAK AKNLVSEAEK KSAATLAAST SRAEAQIRQA EDKANALQAD
 AERKHTETMA AVKEQQNALE TRIAELQTFE REYRTRKLKSL LEQOLEELHA RGSSAPTNNK
 PSGE

> RXA02734 (1-384, translated) 128 residues
 MRIAIVGATG SLGGHVVDLS LNKGVASDI VAIVRNEEKA ADLKARGIAL GVATFEDETA
 LTAALGVDR LVFISGSEVG QRVAQHTNVI NAAKATGVTF IAYTSLNLG PQSLHLQST
 LQPEKLLA

> RXA02735 (1-705, translated) 235 residues
 MVDVVRARDT EDLVAQAASK FIEVVEAATA NNGTAQVVLV GGGAGIKLE KLSVDAADLA
 WDRIHVFFGD ERNVFVSDSE SNEGQAREAL LSKVSIPEAN IHGYGIGDVD LAFAARAYEA
 VDEFAFNPGL DLHLLMGGE GHINSLFPHT DAVKESSAKV IAVFDSPKFP SERATLLTLP
 VHSAKRVWLL VSGAEKAEAA AAVINGEPAV EWPAAGATGS EETVFLADD AAGNL

> RXA02736 (1-957, translated) 319 residues
 MIFELPDTIT QQISKTLTRL RESGTQVTTG RVLTILIVVD SESDVAAVTE STNEASREHP
 SRVILLVVDG KTAENKVDAA VRIGGDAGAS EMIIMHLNG VADKLQYVVT PLLLPDTPIV
 ANWPGESEPK PQSDPIGRIA QRRITDALYD RDDALEDRVE NYHPGDTMT WARTLQWRGL
 VASSLDHPFH SEITFSVRLTG ASGSTSVDLA AGWLARLLKV PVIREVTADP TVPTDEFTGP
 LLAIQRLIEV RTTGSIIITI YDAHTLQVEM PESGNAPSIV AIGRRSESDC LSEELRHMDP
 DLGYQHLSG LSSVKLETV

> RXA02744 (1-804, translated) 268 residues
 MSKPFENSAL RGSSRFPAQT FTPAPKRATP AKMLAAQGMK ESSLFLRHGE QQLLSIIIFL
 VALIALANFD FIPGENSLDK TFPFALATAP MSAGFTGQAI SLAFDRRYGA LKRTGASGVP
 AWTIIFGKVI AVIAVTIVQI IFLGVTALLL GWSAPVGGVL FGIVITLVGVV SSFTALGLML
 GGTLSSSELV ALANLIVIVL SGLAAWAVES PSVNAEGVLS IIPSVALSQG MVDAPENGELP
 WLQLGLIVLG LIITGVAANK LFNFSASR

> RXA02751 (1-474, translated) 158 residues
 VLPIASGNDD RNLIRYVDGG RFDEIMLTGD LTGLSSFLTN AGPNARDDFD LTVLMRAAEA
 GNLMVMVARL DLGANPRLTN PRGVTALHIA AIAGDDGIVE CLIDAGAEVD AVDDQGRTPFL
 WNAAAHHLPD SAVDVLLRA GANVNLRCDN GVSPEMDL

> RXA02753 (1-2493, translated) 831 residues
 MLDLSKNRET KAKSGHVGGE GAVSGDAVAK PLRKEERLAS VIQETEPGAA VEVMRNDADF
 ALFGETGWVV MLLPTHDSQF GGLNAKEKNR EDKGTIINLV VNDIDIHSVVT PELLDSOVLG
 VIPDASDFDL MDEFDLRLNK ARWYHGVAAI EPDTELGVVF KVPKANSASA RGDIFSEVGD
 VLSGAADLEL VDFVEVIAFV LEVLNETSEV DIDDEDGDVP YGLEGVNAAG VITDOLIREK
 LDVDSYPSSA EIIDNIVHVF TKLGQKHHA V PQPVLHSADV VDVAQESHD TVVIESPDV
 ALAEQVDPD FSDGEIDDA EVTEPEDEEV VEATADAPDF GDVAEDDPFG SDDEPDFGAS
 DVVAAPAPVA GMSDEQIQAL IRGVSESVQA KTGSELNALR EELAQALAYN PVQDSQAALA
 QVHAADARSF DADQVGDVAT KRYVNDDLGL YVDEANFNNA LTRAPFOVMN PQQFETTPWL
 GQDLRTLVAV FNGQLLDQHQ RDEVEVRAM IALNDRSNLE IARDLGLDNK DSFEVYVRA
 IERORDLVAG DOQRVESERR QQLQCEYAN REEYVMAKIA EQRVEYDRRH MPRHTASLEA
 VGREITSLRD RTIEDYTARM NTLRRARAGE RANAASRII DELRPIVERQ AELQRAAFDG
 FIVDLDFKFA DHREDDRLA SVNEQKLAAD NRVAQLTKEA EERIEGIRVE TDKMTIASQRK
 ALERGEAEFA AELKRRDITV AASERAEERE ITTARLDAEA ALKRMEEQIR VNNEAHEAEI

VIERDRATQA EANSMTFVES VKQQDRSNNI ILIAVLIVGL IAGMVAGAAF F

> RXA02756 (1-891, translated) 297 residues
 MTSPLYGSQPY GDDNNNNWSQ FGNPSGEGNY GQPYGAPYQG PYGQPFDDQGF NAYSSPIPPE
 VPQPSMDQEA WRSFDLGTVE GQAWKGFAT QQAWVLSALI YFAVLLVLMF AWILPMVSVL
 AATSSGSDSA AIAATGTSF FGFMLMIVLA FIFSVYSLNC YRNAARVVRG EQITIQSFEK
 MKGLGKALGI YILINIVIFI GMILLIIPGI IAAVVLIFAV PVAFQLRSDAS IGDFAFSASWK
 AVSKNVQQVI LLELAIFALS FLGSAVIIGM LVTTPLTFL L YAYAFQTASG GPIMQROQ

> RXA02757 (1-546, translated) 182 residues
 VVKLCLDERV STDPDFRAAL ERWVGLIRK VSRARNAAW DRVQDLPGVT VEDDAAKVRA
 FLPSAVDVDP ADIKKLQISG TELPLDEPNP INDEYPIYI DESLKMILGK AAAQVGHASM
 LLAAHQPFWE VEQWEAADFA LHVREIFSEE FLRLIESPGA VVPRDGGFTE VAPNTVTVVA
 IP

> RXA02765 (1-759, translated) 253 residues
 MSNQLPDHVR DAFQVGAGPA EQLQAWDFG FRVGNVTFAK VTAPEVSGWS SKTRETCLKPE
 GVRVVRPIRS TDGRFVVAGW RASVFSTGTI SKRVDETVVA GLRLADALVD THAEPFVDNV
 FNRADVQAVE EQPGRIGELL EPINRVNQVG HADMLATLTY AGTQPPAVTD LVPVLRPHGF
 TAAVLIVDGL LLGAVDEGIL RRFSHLPEIE QLVLAFLFR RNLQEFSENN DPNVISNLNR
 VESTLVSYSV DK I

> RXA02766 (1-393, translated) 131 residues
 MTTSENFYDS VGGEEFSLI VHRFYEQVPN DDILGPMYPP DDFEGAEQRL KMFLSQYWGG
 PKDYQEQRGH PRLRMRHVNY PIGVTAAERW LQLMSNALDG VDLTAEQREA IWEHVMRAAD
 MLINSNPDPH A

> RXA02770 (1-1320, translated) 440 residues
 GINRQLYITI NEDATYSDDG PVVCDDFLLS ATAGQMPFLF QSHVPLTSQI ERVDCVSGSK
 VATVVFKEFL GERWRYLFEQ GDLLPAHAVA SKAGMTLEEL NQALKDKDPE ALTEPARVWS
 EGFQSFQFDP ELQTAFCPYK VDSVGEFGEV KLVNREFYSG DQAVEAEITM WPKGSDLIAI
 ADNGNLQIAH VVAWESEPPW NRDDPLNPYD IKEEVGVLTE QLTASAGVF YAAEARQAPA
 ACVQDEQVAH ASSSISGIDV PAVGVHVSVRH QNPVVHQIGD LPAQHMVADI NAASALAGQS
 IRIQYDGPDE KKAAMVEAIR QSCEPAGITV IDASQEAVAL NDLRSITEVE WGYEQYFEGT
 LDAVLRVTDP HREYENANTI GTDAESTRRT EEQLWAEVPS IPLAAQPRVF VIDRTVGNVNV
 VNTDLAGIGW NMDRWSRSEE

> RXA02774 (1-471, translated) 157 residues
 PCPPTQKLLY AQMREIAAEL TACDATRGLH AEVAAEWLSD AITGEPTSIE IDPHRNLFYA
 LNVHEPRLHE LFAGYATRLD ELDRAPQQCE SRQYFLDYVC ADNPFSGDKP EGIIVLLADH
 VLAADPVTNK PALKSEAFPT VTDYCRTHSA KPTDILI

> RXA02775 (1-258, translated) 75 residues
 MTTVQVSTRT VREHRTFVPV DYAVGATISE IYACAMAEK KANNLGLNTT KDDWARVTVT
 DNADVFEVEN VIGNT

> RXA02776 (1-342, translated) 114 residues
 VLYPVAGTV SLVDVKKAAAS RAFEQWEKHN ESAGDVGGDL SLQSIVDLIE RDTFPTDDEQ
 ELNNVALLIG ELLVREAGGE WTSYISKKND EDESLEIFGV FTGGTGEGLS VVGN

> RXA02777 (1-1107, translated) 369 residues
 MNRPLQSQNF SITSEWANAT FNDIEDSLEG SFDIEPGQYI GRGEYFVATS GTGSKKFIKV
 VLGDGIDSEL NRRIEGEILA SSLHLPTDIT ISPVVIQYVK ESSNFPGDYF IVSGDKDOTE
 TLELSKASLP LTDLAKIGAF LFRLESVTVP PQNPARRAMD VLDGLSLLAN KGNIEGTGAQL
 TKGTIQALEI INQEA TN IEN ALEKVTKVGS RKFFSHGDLK FSQFLINGET GKIFLCDWEE
 CGSAHFANDL CFLAGDLFYS TIRELVDTNI KNKIGSSIIQ EAYDNATLEA VSKVNAILTG
 YSSERGSYSL SDEKRIISIR IGLAGLFRLY TVSAKSNELR PRELALASIG MQITLGQAPFN
 LVFTDSKVV

> RXA02778 (1-225, translated) 75 residues
 MQVIETLDPD QRAAVLAAAI PREAKILGRK VTLRPGWGNM RVHVVIIVAF IKFLQPDLRQ

ALLTTGDAVL VEDDT

> RXA02779 (1-279, translated) 93 residues
MGEYFQVQVN IAMTLGAGES VDLVVREYN DVEGNPTIYH GMLPRTYEYRA FIDLHDCDPS
AGEPEPRLLG VTPYWHPSVM EKALRLCFKR CWC

> RXA02780 (1-327, translated) 109 residues
MSKFHTRHRD VISRITALLP QLRAQELQGG WSDVIMKNGE DFYLIDMALM CESALSELLT
VTDEYATVEP SVINDFANQL VIDYDEHDMG FDRDFPAGVY NTRQASAIN

> RXA02781 (1-1191, translated) 397 residues
VVAALVFGFL LPTWERGLSD AALKFVFEGG PDAAREVLGT IAASTISVTG LIFSITLVVL
QLVSSQSFSPR MLNGFLNRRI VQATLAMFLG TFVFSLTVIR YVWSEDEDIT GFVPRASVS
AFLLVLGCLG LFLAFIRLIT FSMRVANAIS EIGEETMALA ARIYPVQSDD AGPVQGPCWS
PRPGDPREEI RVGNHGLSVW IDYRKLVSW S TEHQAVITVD RVPQGFVLEG QPLLRLVWWDG
ELSDRRRRLV HSAIEVRTER ELHQDVAFLG RLQVLDIADRA LSPGINDPAT AQQCQVEIHR
IFRYLVTVIE PSPYIADDDG RVRVHVHPQR IADMLYEVIR EIHLYGADSA MIPRLRLTMV
EDLVTAADH SLPFAVERARG ILDDETDEDR DSDTANV

> RXA02782 (1-672, translated) 224 residues
VAPALNDLAT THPKLAEQIA DPQPSGVSA AIIPTISRGS HTQLTWQCSK NHDHQWVATV
KDRVRGTDCP TCANTGTSRK EAEELIEVIRA LFPNTDVQQG ALINGRTGNQ GASPSSTDVLI
PSKNLATEFN GLYMHSELFIT KDKHYHANKS ALAEQAGVQL IHVWEDDWNL RRDIVIRMA
HKLHATHNLS AVLPTETTDS RVATTFAFVH SHCRWSLVHA LLHS

> RXA02783 (1-549, translated) 183 residues
VVGSGRAAAV LMSNHIQGA V SATKHFA LDC NDDIRALLS VRSPKNARM YRKKGTWEIQ
RYATLGNVPG GETRLLKFAE HTLNEHSTVL KQWISFSAAD VSDGSLYRTA GFTAEQQ LAP
DYRVVGGATG WRRTPKESFQ RKRFRDDPAL LWNESWTEHE AALNNELYRI YDAGKTRWVK
NVA

> RXA02784 (1-186, translated) 62 residues
VAFAEQYYQE MAEVVCEARE EGITHEDTLH MLNDMMAMKR SGEVLNTLAD VLYANECPEY
RI

> RXA02786 (1-807, translated) 269 residues
ILRNLGQSLG SLHAATADRE EDFNILLNRM LAKYPATAEM QKNRDRLLPA AIEVGKKILV
DAGVTVPVAV EEFARVARR LISGRHRAFT PFDLSPDNII VAERTHFLDY EVAGFRDATF
DVACVIAGFP QVFVSRPISD DEVDELIESW VQEVIRGIWPN VNNEERLQAR IVTALIGWAL
SSVAFMKLGS ISGMLNLLHV TEDGNTTLDV SNLDELLIPR SAEDDELVQQ DLHDTFSLAQ
RFAARGLDSR FFEVARFADD VVRLFLKND

> RXA02789 (1-546, translated) 182 residues
MKVSADTPGH DDPGPGRRRLG LDVGTVRIGV AASDRDAKLA MPVETVPRET GFKGPD LADI
DRLVAIVEEY NAVEVIVGLP TDLQNGSAS VKHAKIEAFR VRRRLTNAGK NIPVRLGDER
LTTVVATQAL RASGVSEKAG RKVIDQAAAV EILQTLWLDAR TRALEPQSTD TQDFDEKGNF
PG

> RXA02793 (1-702, translated) 234 residues
MKSAAVFTLD ALGVLDREVVT KAGAFFPAGY DADLSERVTD IPTLSNKIDA SGHVLISKEV
VVAANPDIVF GETDTINRAS MASSNIPVVE EPAFCGSDIG DVSFDDVWSQ ISTYGTIFDR
STEADAYIAT LKERVSEVSS RVTDSGKTVA VLYPTIGGGV TYAYGRGMSA NPLVAEAGLT
NVFADQSERV FEVTAELIS ETPTHHRFTQ RRFPRHRHR GGQSPRVQRT HCSE

> RXA02796 (1-549, translated) 183 residues
MRLFASTTPP IEVTEHLINA LRPYKDDLRLW SDDPNWHITL AFYGELPDGA VEDLIEHLTS
AARINEFTTI RIKGAGSFNR KNLWMGVGGD TKDLRLMAD CLIDPEERRR QRAHLTVAKP
TQRQSRDWD PVIPDLVHAL SIYEGPEWPV DEIELVSSEF GKGRSGGPLY TTVATIALSS
ALV

> RXA02798 (1-1425, translated) 475 residues

MRSVLVDWIM TLAPSTNAVS QQTRRNPSQA PRLHLRLHFF AGIICAPLIF IAALTGLVYA
 FSPTIESISN QEMLTVSKSA SDTALPVREQ VSLAQELHPD LDLSGVRLGD DSSTTRVLFA
 DETLAEASTVR AVFVDPYTGE ITGDTTQYGS SAALPFRQWV SQGHRLMLWG EPGRIYSELA
 ASWLGVLAVG GFALLWLRNK KPGRLRMVVR TGGRGVVKTY RRHAALGTVA GLGFVFLTFE
 GLTWSTYAGS NITDLRQLN WTQPSVNASL TAAFPQVDMH EHAHHHME SATSGSGSID
 LVAATAISEL RTPLTITPPA QDGLAWTATE NRDAYRFTTD TIAVDGDTGM LTNRLNSTDW
 PLAAQASAWL IQLHMGTLFG LPNQVVLGLL AASIIVMIGL GYWMLWQHPR REGWPSAFKR
 AGFEKPTW9I IALGVVVIAY GLLAPLFAVS LLVFIGLSLG VRFISRMGR ADTSN

> RXA02799 (1-273, translated) 91 residues
 VARNIEDIQR DIETRRLQLA STLDELADRS KPSNLVDDAK NQATAKLQES NVQKVLGLVA
 AVVVGAVVFS VVRGRKKAND LKEIQRLLSE R

> RXA02812 (1-567, translated) 189 residues
 ASGTDASTIT LDQVALPVAT NSGASAAVAL ALAETPEAAA AALNRDADVT ATGAADSPAF
 ATVEGAELPE GYTFEAVDSA EVPVWAVAIN AGNGISEDQA RAASDFSSFS FDTGNADNSA
 LESVLTQASS ESAAETEAQ PSETFVEPAA ASPSDTIINL DTSSNMDRVV DGSQETYHTV
 TSRTLANLA

> RXA02815 (1-552, translated) 184 residues
 WLRSSTKEFD QFVPAFEVI ATVASEFAGD DGNYSNEFPV EDLVGVYDAI TEAGGYAVLD
 LQPGRANFLD QAKMYEELLK RPNVGLALDP EWKIGPDEQP MTRVGSADAA EINEVSQWLA
 DLTAENLDLP KAFVLHQFQL EMLTNRDQIN TDHLELAVVL HADHGNGAGD KYATWNMLRE
 GLSP

> RXA02817 (1-399, translated) 133 residues
 MILGVPTQYL LYSWNNWIVD TGFDVAILLV LAFILPRIGR LAMRIKRRV ESAADADTTK
 NQLAFAGVG VYIAQIVAFM LAVSAMQAFG FSLAGAAIPA TIASAAIGL AQSIVADFLA
 GFFILTEKQF GVG

> RXA02818 (1-606, translated) 202 residues
 SYSRKFLTQV WIRDNVGDYK GLTDATFRKK LQRDLAYLR VGVPIEQFTV TSGIAEQQA
 YRLAQDSYKL YEVEFTPDEA AVLGMAGEMG HNQELGAFAR SGWTKLAAGG AQRDLSSTA
 LTNAGDLGSL SAKLTDAIK ARQLGKQISF EYRRAPKPAD SLRHMMPWGL VPERIRIYLV
 GFDDLDRQEAR FRTRTRVRNI KL

> RXA02823 (1-270, translated) 90 residues
 MIVRNPDREA IRHGKITTEA LRERPAPYTW AMKLTMAITG LMFGEFVLVH MIGNLKIFMP
 DYAADSAHPG EAQVDVYGEF LREIGSPILP

> RXA02824 (1-528, translated) 176 residues
 FYETGEALDP TGDSLTISST TTAPOSTSTS TSASTSGGTA DCSSGALGVV TTGTNDGMLG
 TIQEVNNTFA IWNNLIVNTE RMFCNIDTLK ARFDTDDSD SATSATSGET ASTGTTAATT
 AGTTGTGTGA TSASGTSGETS GTSGTAATVA GTTPTDNGVC TASGSLGVQ ASAQWG

> RXA02825 (1-384, translated) 128 residues
 NVSATEASGS ASVSLSQSGS QAFADFYTPG TQLDPISFSA TLGGDASCAT GSTSTTGAAA
 TANTDNTGCV AGEESTTPAN QNSQFQIRQA AADSTGLDPT TMLLLILAAF VVAGGSMTRF
 TVGNPTGK

> RXA02827 (1-423, translated) 141 residues
 MYEQQKILNE VSEKRLQAIK DFTELGSQFK IAMRDLISRG AGNLLGAQQH GFIDAVGFDM
 YSQLSEAVX RKQGNKSQVE KXXVEIDXGV DAYLPETYVA DXRQKIEIYK RIRELDSQEM
 LDELEDDLDD RFGEEXPEEVA H

> RXA02838 (1-462, translated) 154 residues
 TVPLGDGQGR YIAKIPSTAF GCVSENKFN LALAEAIOME VPARELVGRA QFEGVPPEFE
 AMTDGLVLLV RRFDRAGDGV RVHMEFAQY FGLYPARKYD GAASHDIAAV LGSAVSIAAG
 LEFVRRLLALS VVMGNGDMHL KNWSLIYHGR GDVP

> RXA02840 (1-150, translated) 50 residues

MTVISGALNV LLPDATDQWV YEAGSVFNVP GHSEFHLQVA EPTSYLCRYL

> RXA02841 (1-279, translated) 93 residues
MFAAFKSNLP TIKKLVEVI NGVDAAINEL ERHVTNESVR ARELPNVQYK ATAGRNFAS
KLVLQNLRRIN KAQNPRGVP THATVILLKG DGS

> RXA02842 (1-342, translated) 114 residues
DAGFVYFGEI DDAGHIFGLA GDEYRGGIRR VOTHVKKVLS EVSRRSDELG EDWLVIITTD
HGHLEDEGGH GTTDRERESW IITWSPHREL PQWPEEIAFX ELAELMLVER RTLR

> RXA02845 (1-615, translated) 205 residues
EDHTSMILTHF SAAVGMHHRD PARFPGQGDG SYPDLFWLYK NALNLVISSV LFTREQMDNM
LDQMDHEFTR AGIPRIAINI ERRDALLMNG SLERALELQE LIDASQHDDP FDDCPTCQIA
GKAALAMAAD DYDELTQNLVS QIISYGSIGC VMEPETTLAA FMLRLVLSGD ADYARYLQDV
SAKANPEFQS LDSVGRHLEF LGITG

> RXA02846 (1-573, translated) 191 residues
VNGLSIINAV NNAWSVRKRT DWAKFRILAG ALVLGSPVAV AVVYFLNGPW LLIFVGAMVL
LALGVSLEFPT EKFGALKQEAQ LPMVIFGMIG GFMSTVAGIA GPSLTVYARL SRWDYRDFVA
TLHPVLLVAN TVSFLLKVIL IGGLDGFGAP AWLWIGAVAM IFVGAWLGEI VNAKVSTPMA
KRIATLLAAA G

> RXA02847 (1-594, translated) 198 residues
MAVQQQFYLF AILLSMAILL IRRYRPEYSA VRLATPVLAV LTVSFFSAI LWHFIDQSVN
YYSTPTFRFE LGLGALLVLH APRILISAKT KSLAAVGLF MVLSTGFMD SRWTFPGFA
LYPILGACLV ILGDGKISVF LSRKMWMLWG DIAYPLYLWH WPLLIIFTAL FNQEEPSIWL
GAIVIMLSLG LAQLTNKY

> RXA02848 (1-399, translated) 133 residues
MQIVLASQSP SRRRIINSAG VEPLIHPADV DEDALLHSIN GSAPEEIVRQ LALAKAQVVA
PSYPGDVVIG GDSMLLIDAT LQGGKPHTRA TIERWKQQRG NKATLITGHA IIFGDEVIVE
SSSTNIHFEE ASD

> RXA02849 (1-282, translated) 94 residues
SPYPMVISTS ADASNVTVRI MGVDTTSVES INNGRWSTTQ PNTVRVSGSD CVPSTGAPGF
TTSDDRIISD LSGNEITREP VTTYVDPSN VVCS

> RXA02856 (1-249, translated) 83 residues
LPHAKELAHE LCLLPTPAVP ALPTDSGAQF DIHQALSASL ATYARNLTLL SHTAENLNGR
ALTGLAIED TDQQLAHAE RLT

> RXA02858 (1-1026, translated) 342 residues
PEWKKFNSGD AARVVPDANA ELDIIGAPAL LADRPSTYANV KTLSRIFAVM RSLGHVTAAS
PVTVFFSSHS VLSNVDRGSE HYSGPNGLGE WTSVGRVAVT NNWGVVDALD EAITVKEVNS
LFTEDAATRI QEAQAAVQAA REAEEQIAKE EAEKVDPYDN SPWAAAGIDP IKVSDGRTI
YTLRTYLGQG PVFLGKFGEI FTFNSQKSL LRLVEHDDHD LARASTWSDL MLGINAGETE
LLVHSDNVYS FNGVLKNDIT SVDADVDTQM ARAYELMADT ADWADDDSMN SYPLANPRMQ
DIYSYMLGGS DTSGYVPHAP FNDHSESWE LEEMLIKRES KF

> RXA02862 (1-636, translated) 212 residues
MNTNLPLNYL AFDLDRSESS EALGVLSLAR DLRLEQMGA QDDPRRAQTV QAFVADLPA
KRATYDAQLE AGVPLTWAQI QHLGNFGLP STPTAQPFPA PQPEPSPEPQ QWNNSGQNYA
YGNPTMDYQT QQSYPNMQDQ TQASMYAQPF ANTPAFMYS NQVENRPTAG TRLWMAILDS
IFAGIAGGIV SIGIFGGESEF LTVSIMLVIL IV

> RXA02867 (1-606, translated) 202 residues
MSATNPDALD VQHVVPKTK KTPLAVIFNI ISGGLIGMAE LVPVIGSGTV ALVLGIYERA
LHNGDLLIDL IKVLIKDRSK VKEAAKIDW WFLGAIGVM VVMVFSMSSI LHTVVDYPE
ITRGLFLGMV AVSLILVPLGM MDMRDACKRL AIVIPLEIC AMLGFFGTST TSAPRTDPSL
IVFFICAAIA VCALVLPGVQ DH

> RXA02874 (1-480, translated) 160 residues
TELNNDTHHL WVVLTTSDDD FDADSFTEV IRTIGYSRHE VNNGLNMAAA MTNPLHLRAI
QERYYFSLIR YLASIMIAVA KADPTLWEL DLRTIDALTPT VTAGEVMQIS STLKXHXRP
GSKNSTPNPH QSPHRKRTMF TSTPLMRPM SASKSAAPTA

> RXA02876 (1-663, translated) 221 residues
MTSKDKTEQL EAAGETILMF RRRFAQQRSR ERFNRILTAA RSVLVDLGFE SFTFDEVAKR
AEVPIGTLYQ FFANKYVLIC ELDRVDATAE VAEKKKFSQD VPALQWPIL DEFIEHLARL
WRDDPSRRAR WHAQSTPAT RATAATEKE MELIIAEVMR PLARGAGYEE RMSLAGLLVH
TVSSLLNAY RDVNSSEEDF DSIVEEIKRM LISYLFVSAT G

> RXA02881 (1-666, translated) 222 residues
VKKKMLPLFI VAALGLSACS SEPAAAPLEA EPLNLLIDG SESGLDNATE GNDTSLSGQP
INLTVVNGAL DIDGSCGKAL QAVEDVNLD VASASRALAS GDKQVGIAMY STAEDNDISP
MDLYADIANA CEDPVVDSSD TTYTFGKLD APDGAFTL DIEVTPDNQG STVMMIQELG
NHIIIVAGLE TPEETATVF EAQRTKLEEG LQLQKNWQLG WV

> RXA02884 (1-462, translated) 154 residues
MLLTILWAIG ITAEGMTGAL AAGRQKMDLF GVSVIACVTA IGGGSIRDML LGHYPLVWVE
KPLYLLLIIG AAILTVSISF LMEHFRVLFL VLDAGVLSAF AVIGTQIALE MGYGFIIAVV
ASVLTGVGFG VRDOLLCDRI PLVFQKELYA SIAF

> RXA02885 (1-1536, translated) 512 residues
RGKGHFHTST EFAGSYSLVT NGLNDVAGEY VGVMRGDVNN SAVLFDVDWR SGHVVCADSS
INTSPLLKRP RVVMMWGSKI SQAALLNNRR VVHLVLNGAK LDIMGPKLES MTAHVDMTSG
DLNMFELFGK QEDLSLYST HMDKIVFMT QALGDKTSEL ALLRGKLEI ITAFVVMKMM
WALNAGENRD KLRVGVPH E QIPLLSVFVS YLDQEYERQK YEGTKDPEMF RAISVLRITY
KDLDTLGDH FNQHTADGID SVNSARRVIY DFGSVLRRAA GVAMAQLVNV IGFVAVETLQ
GDVVIHGAD LVQDVVDQYD LANQFAYMAE RGRGVAYLYS SMDAMLGTVG FNOFORAAAT
ILGPMNVDSV DTYQSLNSQ IPMDLARLV TQNSGASYLR RGSTNVVFEET NLALGVNPPM
EQRRKIEAQR QORRSKRDKH YGGGTTMVG TADLVVAIQA KAEHREERFD EKSARKMKEL
DVEAKELAL TRPKGNLDDA LAQVEKKRLA RDL

> RXA02888 (1-429, translated) 143 residues
MYSKLLILLF LSEQDSSYEC CVGLLDGSDG RDYIEKLLKG RKLKNHFLEW EDINKADVAR
EEIYKQLVH LVFWTALSTP GEISFVFPQG SLMSATLEED FAALVLEER TSFREPLSHL
WSLPVGVWAP GLEGFVERNS EAA

> RXA02892 (1-504, translated) 168 residues
MEGPFAFTVA AIAAAAGVSP RTFHNYPSPR EDALVQFVVI RVQELTDQLY EFPTSVPPRD
AIEQLVINQL RDGDDAMDSF SAMFRIGEIL ENLDPIKCVI DKERLIAPLL EFMVERDKDL
DKFDAATLIH LHAAAIATSL HTFFQASEPR DIEDGVALIR RACAWIKK

> RXA02898 (1-1626, translated) 542 residues
LVVDSGGRYN VTIIGLTTE TDSATALNLQ MSEAGYLER Y TDGATVPSVM LSAADGTTPQ
ELVDLAAEL GSNFDVETGE ALVEQATGMI TQALSFVQYF LVAFGLIALL VGTFFIIANTF
SMIVAQRMRE FALLRAGAA PQQITRSVVL EATIVGLFGS ALGVLGGMGL VAIISAVLNN
LGMPMGSSVG LTPSAVTAL VLGTVVTIVS AWAPARRAGE VKPVEAMRNM ETTTMRSMGM
RTITGGIVLA LGIIFAIAGA MMTDSSTATR SILVGIGALF VIVGTFLFSP ALMPVVGGL
GKVIAGPFGS VGSIAATNSK RNPRTATTA FALTGLIALV TAIGMLSATM KDAVSDMMAE
QYTADYILQG PTNGSITMPK ESYVNDVRDAE GVADVLVLSM NSASVNGQAS YVQLQCSQVTF
VADGDLKSVI STESIDGSLD LSNPGVVTNQ TFADENGWAV GDTLQLESNG QTIGDIELIG
FTTGNDAGN MISESLAD TPAADTAVPQ MMLVVGEEGF DKEQLRTNLE DAVADYIVIS
VK

> RXA02899 (1-480, translated) 160 residues
MNSGCTMRRI SLRNIAGHKV RLFLTIVLAV LGTSFVSGAM MFTNALSSTF DEAIASSFDG
VDVVVS PNGA SEVQGVPEV VESLREDSRI NHLNINGSQT VVLADADSKA IQTTGGSSLS
IYYSADDAVA QAPELAEGEA PTGTEEVLAS KAGAEANGLE

> RXA02905 (1-474, translated) 158 residues

MDSVNVLLIG IIVAIAALLP RKGKYGPIAT LLVAGDWLGV FLLSILVMLV FDGLEDLVQG
FLDSWVFGVI LLVTGIVSVF ATLVSKTSDT RKLGDGLAPV KTPSWKTGVA GLILGIVQSA
TSVPFYAGLG YLSVGNFSPE TRYGLVYVA TLALSLEI

>RXN00022 TRANSLATE of: rxn00022.seq check: 7277 from: 1 to: 1701
MSAPTIVPGTKTSIDPTIMDDARIIFFDIESLHNIPTVATYDSLHHVDFVFLDLHTTSP
QITVLPHSMYDQTRSDAVMAAII EQNPAFAEIKGSPITADVALHNLGDTNANRRWQS
NVLLARLLGISVRGEVPEHQSHNLAKQFAEATLVTRDFVNYDPTSAHPFTAGFNSIN
YDITLLSLYFAMLTSGNIGSTPTYPVPIAQLRAHNDKLFSEFIKNMPKYLWDRDSSGAG
LRAASGFRNAMLKSGRHIDIRLNEKQLFVGLKRLLGLLGHQILESRLSGDDAHVDTNE
DVLDLIAYNVSDVVGTRLLAEDPVYSGSFDMLRAGLLSTYETVFDHGTFRQPSQMRKO
RLTINTSSAQFAARILAPYRPLRDVDAIGDMPVVSYLYPDAVAEATGQKQVNVLDSEK
KFFYDNITDPEARAADFVFAFYADIEGRNFSHNEAIDTQINQLRAYLNQVVAEDAAGY
ALYDVRTRFEQIFPKDRSYINDATDMT PRAVSSFDLLVALCDDIRGVLDRLGEISSPNHH
EMVDAMRKLHYIQAFYRAWDPTPLQ

>RXN00027 TRANSLATE of: rxn00027.seq check: 3923 from: 1 to: 366
VDERSRPARSVFFDGEEPRFTLANERTFLAWTRTSLAFLAGGIAFEAFQISGLSDTVR
TTIAVFIIVAGMIIAAGAAVRWMNVERAMRKQKPLVPVPAIIFFLSIAALVASAVALVLI
VQ

>RXN00028 TRANSLATE of: rxn00028.seq check: 5847 from: 1 to: 1947
MTLTASSLEAGKMSFSGGYIVGETMIFLVDPEVEIRRSFNSLHVLRNGSDILRRNEHC
WYFENFNKPIIDPPVRLGPROIICPSALAWVLQHQHSRSLSLHHHADKITAGEIAGRTW
ILREPTSGGGQDPSRLVSLIDQEHGVILAVETGQERLEATEISFPDTLPNPSWDGAWEP
FHYDPTPTHTAPDVAEIPGYIQSLPPQSEDPRRLRVFNEIALEGDFPDYRQGQSVRLTL
GISSPVPLEGMTTRRRGRVRNLGEEASPGDGMQPWILLTGDGWTALAYTPIPKRGA
EQQWFFYYSAGIVDVPDRLRVERIFAGIGTSGTNERLWQEI DNTSSAYHSEDWIRDDV
LDVTLGAVFPPLLRDVTAVDPIVAGDKLWLCOVHFFVARCWETTGRYLQGLTLPVPAI
RDRSVVLEHSDQQLGAVAAAGSKSGWILTPGQAVATKAPDWTPTTRATDLQPVSPFWE
AVRGGQGLFELQVETSRRTALGRVNATGGVDIGELPPNGYTISVVQIGDEIYVGRWVEEY
RLNSKLEVISTKELDISAGWKSQGTVAYLSEDTHTICFFDQVSGAELPSLGAIEGHQGEV
MSATSSESI VLIYRRNPNNSMSIVPTSVATYDNGTWTMTPLQEAPELS

>RXN00033 TRANSLATE of: rxn00033.seq check: 3319 from: 1 to: 1335
MSVQQSGLLERLIGRPLIFGFIGLTFIMIGDGVETNILEPFLSSEHGFSVSLAGTLVTV
YGVAVAI AFAAALSDLWGPRKVMILGASIWIVFELIFLTVALTIDHTWLIFLAYLGR
FGYPFFAYFGLVMI TATASPKQLGTGVGWYFVAFSAGLPTLGALVATISMQYVNLTFYET
LWVSLVLVVIGSLIALLVKERRGRHPLVANPDDVKQTLGQGFLLRNDRRARFVDTYIRT
INSIPTYAMAVFFPSFFTDLLKQWLSWFLITTVIYAVNLFPNFFPGSFGDRHWARTVFD
WGGSIGAVTLALVYFIPMGVQAGMSNGVFGITIAAGALFGVSLAGFVLSATVSLD
PKHPGAAMATYNLGVGGA VAVGPLLVAVFHLIGTGLILVMIALYLLSGWMTLQLRGTO
PGFDGVPALEADAHIEDLADVNANA

>RXN00056 TRANSLATE of: rxn00056.seq check: 471 from: 1 to: 750
LLNRVRSIAGASAITLCIGLTTILSPSTAQSLEQITPLPESAIIDLNAEIHVNTSDISAE
QILGAQDEITMYDSDHPYEYDITLTOIEQRSITAAALKRDPSSLQQRQETRLAAQSDPYK
IYISGLEMLSCINLVDVSGCIANQAATKANNEAVARYPGDSLNGKGDFAFRHCSWNAWL
TRIGSNGAERIATNHETIGDGPADENAMDLFNNAQGRQIGAGFINSKDETSALAIICALW
TNLGRLLKTLK

>RXN00067 TRANSLATE of: rxn00067.seq check: 5053 from: 1 to: 486
MYDAQRPKAGIFGSHTEETWVWLGNELFDESSEVIADVRSDVLYVDRERLLIESTPGTMR
FRCAIRLSGGEVYTHMQNSFTVGDLTAVCGRRITSYLRKVS PWRKERLITNNGVEVARLRP
MTSGKVEFIVGTAGSEALFPVDVAVLSWACVLVDSAVRRPKI

>RXN00077 TRANSLATE of: rxn00077.seq check: 3953 from: 1 to: 1362
MNDENIQSSNYQPPFSFDDWKQIEVSLLDVIESSRHFSDLKSDTSRSDALDAALERAKRAA
AVDTNAIEGIFQDRGFTHTVATQVGAWEQMMKMGKHVKPAFDDTLEGEFVLSATVAGTR
PTISQQWIRNLHVALRQSQESHVFTAVGVQNALQKGYKTKPNSQRSDDGVS HAYAPV

EDTPAEMARFISELESKEFLAAEKVIAQAAHYAFVCIHPFADGNRVARALASVFLYKD
PGVPLVYQQQRDYIHALEAADKNNPLLLIRFFAERVTDITINSIIVDLTTPIAGKSGSA
KLSDALRPTRVLPDLHDAHRLQESLFTIERSLDEEGKRNGLEFLLRQIFITGSPFNLE
GYNAPFDSYCLTLAFNSNSPKQIFHPLSIVIAARDGKRASSDLVAATSIGYNFHYAGREV
EPVVTESFRERVKIYADGIVDHLTELAKKFKQN

>RXN00080 TRANSLATE of: rxn00080.seq check: 4040 from: 1 to: 1530
MDILSLLMEGFAGALTPMNLLWVIVGCLLGTAVGVMPGLGSSMAVALLPMTFALDPTAA
FIMFSGVYVGGFLPGDSTMAILMNTPGQASATISTFEHGRMALNGRAPQALATAAIGAFIG
GIVSSFIUVFLAPT LAELSTAFGPAEYFALALFAFVATSSVVSDFKGLASLI FGLGIA
TIGDSDVTGIERFTLGAPQLFDGISLVTVTVAI LALGEVFIYAARARRDKANLETSRAGR
PWLTTGEFKEAAPAWARGTIIIGLPFGVIVPGVSGEVPITFLAYSTERALDKRRKDPQFGDKG
AIRGLAAPEAGNATMGAMGALLALGLPVSATAAIMLAAFRQYQIGPQPLLFDRNPELV
WALLASFFIAMIVLFLINLPFAQLWAKLLLI PNHYLSYGIALFCGLGIYATSGAVFDLML
LLGIGVVALIMRRYGYPLAPLMIGMVLPLAETSLRDALLSSVGDFSILVSSPITWSLYA
VLAI FIAVSVITAIRGRKHLTSQLETIDA

>RXN00087 TRANSLATE of: rxn00087.seq check: 6949 from: 1 to: 528
MIGGIIGLISLVII MAEKLAILEDGPHITSCDFNAVLACGDVMSRQQAFAFGINPLIGI
AGFAVAIIGAGILAGGGFRGWFWFQAAGLT FAMMFCHWLAAYQSMVSIRALCPYCMGVW
TVSII MFVLTAWNVKT FSGSDSTFVNALYKXKWVIAVWLLTAAAVVPSFRYFM

>RXN00096 TRANSLATE of: rxn00096.seq check: 1688 from: 1 to: 303
MTNAGDNFEIRMPSGTDDPLSDAEIQKYREEINRLDREILDVAKRRTKISQITIGKTRMSS
GTRLVHTREVAIINQFREEIGEEGPAAGILLAMGRGKLG

>RXN00097 TRANSLATE of: rxn00097.seq check: 3726 from: 1 to: 1176
MEVPSLTFNFFAVNPNPSPPARQKTKLRELEHFRFWQEHLPDGDHSTAISLSAIVTGLT
KAQVSRISIAFATLADLPKALQKQLYHLDLSRLITISNELAGINPDNLGADAIITEY
LTATSPQIILPSPASIGRIKKEIRDLDDARATSGRGTDQDSFSGVTFSFGDTAEIGASV
DAVDGHIINDAVTQHAKKNDLTYGEAFSDILRNNIQVQVVLNLYTAKDLANAPVWASGIG
WLDAKTGFWSEKANKEQMDAAAKISTDKHDPFPALRDALIGRDGTCREPGCSVPALKT
QADHRI PYEGEGTECLGGIGCLCQHNNHNMKTDRGVTYLLDPFSGIIVWLMGDGTWAVSEP
NGPLNPKNARWAGTVAQHRARHHKRWVKEDAK

>RXN00114 TRANSLATE of: rxn00114.seq check: 4118 from: 1 to: 489
MKLLKFAAAGTALALAGCTQTESLVATIESATSAQAAGNVOGEDGTSAFELSVGECFN
DTYEEIESEVIVDCAEPHDNEIYYLYDIEGDDFPTDITTTGEGCLPTFEGFVGAPYET
SIYEVYPMPTFGSWTNGDREVCSVYLATGEQMTGTAAGTAQ

>RXN00120 TRANSLATE of: rxn00120.seq check: 1348 from: 1 to: 840
MLIGMSNQTYNQAVSSGVKASPHRFNRFEIKYLITEQDVPALEQLATRMSTDDPLSPGG
YKESLDFDSADRLCYTEKIEGLKFRKRLRITRYDGVLTPESTVSVEIKQRNVKVTQKR
RLDLPTFYALALGDSTGAAGVGEQVDVEKLLI SPENQHALLIHEMASFAKNYRLRPIATTK
YHREAFVGADEAESSRVTIDHGVSGRDRDFFLLGDQDLED RPTVAQGLAVVEIKCDERVPFW
LTDMTAQLEMSVIRMSKYCETIEAFHNRFASAFGAVDPF

>RXN00128 TRANSLATE of: rxn00128.seq check: 1749 from: 1 to: 1704
VSKISTKLKALTAVLSVTTLVAGCSTLPQNTDPQVLRFSGQSQTQEIAGPTPNQDPPLL
IRGFSAGAYPTQCYEAAKAYLTEGRSTWNPAASTRI LDRIDLNTLPGSTNAERTIAIR
GTQVGTLLSGGVYQENAEFEAEITMRREDGEWRIDALPDGILLERNLDNRNHYTHPDVYF
FDPSSQVILVGDRLWLFNESQSMSTVLMALLVNGPSPAISPGVNVQLSTDASVFGPNDEGY
QFTGLGNLDDARLRFARAAQAVWTLAHADVAGPYTLVADGAPLLSEFTLTDDLAENPE
AYTNTVTSTLFAQDGLSRVSSGNVSP LQGIWSSGDDIDSAI SSANVVAAVRHENNEAV
LTVGSMEGVTSDALRSETITRPTFEYASSGLWAVVDGETPVRVARSAATTGELVQTEAEIV
LPRDVTGFI SEFQLSRTGVRAAMIIEGKYVGVVTRPGPGERRVNTITEVAPSLGEAALS
INWRPDGILLVGTSIPETFLWRVEQDGSIAISSMPSGNLSAPVAVASSATTVYVTD SHAM
LQLPTADNDIWRVEPGLLGTAAAPVAVY

>RXN00154 TRANSLATE of: rxn00154.seq check: 3981 from: 1 to: 843
MSFSDPYAGNI FGGHSRKNQCEYPDPVPKPLGVVVRGDDGFGVAGTGFERTYDGGFVRLE

DRRGRDALYKLRKGAFMIDGQIVNLTRFVEKQAPRKSNSGSRVVENAQAKVAAPSRIWVE
GTHDAAIYVEKVGHDRLRVGVVVEYLEGLDNLEERLAEFPQPGRRIGVLADHVLVEGSK
TRMTKSLPADVAVTGHPYIIDIWAAVKPERLGLKAWPEVYPGEDWKTGICKRVGWSDPKEG
WHRVYNAVNSFRDLDYTLIGAVERLVDFVTNLDSLKEDVLA

>RXN00162 TRANSLATE of: rxn00162.seq check: 4822 from: 1 to: 354
STTTTFHFERKKRVQRALTMFISIAAWVTGVLALVAEMIMKYIIGMDLPEWARFVPIA
HGWVYIVFLMTLLNLGLKARWNPTRWVTTAIGVVPLLSFFVEHNRREKVTQTQFLNS

>RXN00167 TRANSLATE of: rxn00167.seq check: 5803 from: 1 to: 498
MYLLNPPVTEPEILTVNEIPTVVAVFDNHPMNDMPAAFDQTYQVLFPTLGAIGIPIGPG
FALYTSEPTDTSFEVGIQVPSQPLEGDVSAASGIVLKNVVPAGKIARISHIGSFDDLQSG
AWGSEFVALESAGHEIDMPCWEVYVTEPSPMDBPATLQTDLYVLLK

>RXN00171 TRANSLATE of: rxn00171.seq check: 2615 from: 1 to: 258
KQKQKQIHNLADEVKRLRERDDARDQQLGVLNEAMFSLLDGLDRFRESGDEASFNALN
YQAVVAPMEFKTVYGVDPSTGEPIPT

>RXN00194 TRANSLATE of: rxn00194.seq check: 2468 from: 1 to: 441
VAGSSHTIEPIYRGVSTLDEPSAAGWHGLKRNTIQLAGWISVLEMLGYNFGNHKGHVE
TIWLLVITALLVIGLLIHLFEPKLFQVRTITSRNKPVGHVPEPDWTYDQATLTGTWGNLTD
SQLRSVNIIEPSRVAHLRAADSARELDN

>RXN00197 TRANSLATE of: rxn00197.seq check: 7429 from: 1 to: 1212
VAAVLLGVVLFELGIAVTIALHEWGHFITARIFGMKVRFFIFGFGPTVFAKRRGETVYGL
KAIIPVGGFCIDAGMTAQDELDPEDLPRMYLKPWWQRIIVLSSGGVIMNLIVGFLVLYVGA
VSSGIPNPVDVTTATVDTVQCVPTQISATELSSCVGSGPAGDAGIEHGDKNILAVNGQEM
ASFTAIRDAILELPGETATLTIEREGTLFVDVLDQVAVSTRLASDGEITVGVAVGMSLPP
TDVYKKGPIEGVGATARTFGDMISATWDGLKAFPAKIPGVVASIFGAERDVESEPMVVG
AVRIGEFVSRMMDMMMLASLNFLLALFNLVPLPLDGGHIAVVIYEKIRDFFRKLRL
GKPPAGGADYTKLMPVTVAVALMTVGGVLIVADVNNIRPLFG

>RXN00216 TRANSLATE of: rxn00216.seq check: 8301 from: 1 to: 990
LGAYGLGELPGKSAEAAADIIQGETGDLHLHIPQLPARGLGADLIGRTVGLLDMINVRDGA
RSWVMSTRPSRLTHLTGDFLMDLDACEETWGTGVDKLKIQVAGPWTLGARIELANGHRV
LSDRGAMRDLTQALIGADAHARKVAGRFRAEVQVQIDPELKLSDGLSPLGTSTFDIIP
AVNVADASERLQGVFSSIEGPTYNLNTGQIPTWVARGAGADTVQISMDQVRGNEHLDDGF
GETITSGIRLGLGITGKDVVDLELLERPRQKAVEVARFDRDLGVGRNYLVDAVDIHPGED
LVQGTITEAAQYRMARVMSEMSKSDSCDL

>RXN00222 TRANSLATE of: rxn00222.seq check: 4411 from: 1 to: 1146
MTPTADWFKDTLAAHFTRDGQTTFSYATYAGPPATSLPINSEPVITRSGAIPFFFA
GLLPEGRRLSSLRNIIKASADDELSLLAVGADPVGAVAIFPHGENTQAPAPPTVDFDDEL
DPSAALTESGIADPVALAGVQDKASARTIAPVPASDAILKLSPPEYPLYVENEAAACYQLL
TKNKLRIELSKVEVLHDKHGRSGLLVHREFDRTPKGKIPVEDAGQVLGIWPAKGLVSVYED
IAQALTQVCASPIAMRNLAFAQIYAVAWLSGNGDLHAKNISIIINKGRGEFISPIYDIPATA
VYGDTTMALEIQGSKKDLQKFLKFCSTIGLPEKTAMSVANAALLATENAAETILASGN
FDTRMNRDLARVLKRRSAWGA

>RXN00232 TRANSLATE of: rxn00232.seq check: 1106 from: 1 to: 510
MNDRAHQRIQDIERSQALDRLSYFADGYLDIDEFDTRTGAAAIARTAGIEDVLVLTDLPE
QOASTAVTPVQDDTEKELDLVLQRGKKLQKIDSIAWAVVMVSFFLGLGFVFNVPYFVVVFI
LGGASAGARFLKLVDDEKLFEEHLSKEQSEREARLIRAAQRRRELEQ

>RXN00236 TRANSLATE of: rxn00236.seq check: 116 from: 1 to: 726
MVISFVGWALSFMDDGTAPIRQLQIPEVPPARGVEVPQIDTEADGRTSNHLRFWAEP
QDTGVSQAATAAYGNAELIASTAWPGCNLGWNTLAGIGQVETRHGTYNGKMFEGGSLDNG
GVATPEPIIGVPLDGS PGFAEIPDTDGGELDGDTEYDRAVGMQCFIPETWRLMGLDANDGG
VADENQIDDAALSAANLLCSNDRDLSTPEGWTAHVSHYNSMSQYLMQVDRDAASAYALRQP
AI

>RXN00242 TRANSLATE of: rxn00242.seq check: 7148 from: 1 to: 1278
VNEWRTVSLVDSTALTVIIISVAVFTSALLGVVKKRSRWRVGLALISSAVITSGAWVVI
EKLWKPFPDPNPWTIYLSAGLAVFPLLSILFRTGRTRILMATLTIVALTAAVINVIYQ
PYPTLGSFNPVPTAVMSYADFESQTTAPTMTDDREVGAIVQVPLAGTTDDSTSGFDARDA
YAYIPPAYWDPNSLQLPVLVLMPCNPQGQPDQWFSSGNADQTADNFQATHDGIPIVISVD
GTGFSFGNPAFVDSDAQSVMTYLSHDVPMILIKQKFRVNDQDRTWTIGGLSYGGTCALQIM
TNHPFAYGSLFDGSGQEEPTLGRQQTVDQLFGGDEDAFKAVNPEDLLNQATSSGAHTYS
GISGRFIAGSNDKSAVSALSHLDNLSNQAGMSTFTFTVAGGHSFQVWRVALANTFDVWAK
RGGLQV

>RXN00247 TRANSLATE of: rxn00247.seq check: 2491 from: 1 to: 927
MQTLIFIAIAGVAAQLVDGGLGMGFGVTSTTILIMLAGLPAQASAVVHTAEVGTTLVSG
LSHWKFGNVWDKVVVRLGIPGAIGAFAGATFLSNISTEAAAPITSLILALIGMNLVWRF
KGRIRRDYSDRPHSRGFLGGLGIVGGFVDASGGGGWGPVTTSTLLSLGRTEPRKVVGTVN
TAEFLVLSAATLGFVVGLWDDL VANLSAVLALLIGGAIAAPIGAWMISRVNATVLGGFVG
TLIVTLNLKPVNLNVGLDFIPTGLIQTVTLVLIPLTLGFRRYRKNLLNETISSEVVSE
PKGQKIKST

>RXN00256 TRANSLATE of: rxn00256.seq check: 519 from: 1 to: 771
MFMSLKTRIFGALAVLSISFSAIATPAASAQQLVSTSAVNEFGVVTSDITAEQILQA
QDLIAEMKQSEDIYEFGALSVDVEQRISIIAAVKENPYLIENESPRMRVQSETPDEETPDK
KPKSKTYKLYMSILEMMSCINLVDVPSCAQALKAANIAEREAKARYPDSVTNGKGDALRH
CAWSALMTIRIGKDAERIGNAHETVVRGEPEEREMDLINNALGRDIGERFIINGDETGA
LSTCVSMANIGLLHTLL

>RXN00264 TRANSLATE of: rxn00264.seq check: 1681 from: 1 to: 378
LLVDSGDVQLEGVTVETPQLAYTGINETQLIRINIGTTPARTVLLGGEPTEDIVMWNF
IGRSHEEIAEYRKQWQAEADRFGITHGYISHHKDGTLRLPAPELPNAAIKARKNPAPTAR
PETRID

>RXN00267 TRANSLATE of: rxn00267.seq check: 9930 from: 1 to: 318
MRNSKSLFASAAALFCVAVITRIASSPSFIAIVAIIVAAATLFFVGLNSRVGTFLVDQP
VVFTQEIQIDQLKELKSRDQEAARQAQLWSRSGSSEAAVEAVRKL

>RXN00271 TRANSLATE of: rxn00271.seq check: 7582 from: 1 to: 990
MFSSRSKVLASIFTVGALALASCSSDSSDSTSTDAAGGDSYRVGINQLVQHPALDAATT
GFKEAFEEAGVDVTFDEQNANGEQGTALTISQQFASDNLDLVLAVATPAAQATAQNTIDI
PVLFTAVTDVAESAELVDSNEAPGGNVGTGTSIAPIEQQLLEQLQLVDPDAKSIGIVYASGE
VNSQVQVDEVTAKAEPLGLSVNTQTVTTVNEIQQAVALGDVDVIVYPTDNMVVSGISSL
VQVAEQKQIPVIGAESGTVEGGALATLGIDYTELGRQGTGEMALRILQDGEDPATMPVETA
TEFTYVINEDAARQGVLEIQEILDKAERV

>RXN00272 TRANSLATE of: rxn00272.seq check: 8098 from: 1 to: 372
MPEPETSTMGSIQKSGEWLPAYSAYKLNAGDLFLDIRHATAAAPVITFDVNMTMGSMTL
IVPPGVYVEVQMASKNWSDFKVQTTNPLPGAPRVFITGVARASGLKVFTKHPHEPFPGFWQ
KMFE

>RXN00283 TRANSLATE of: rxn00283.seq check: 5995 from: 1 to: 1032
VASATASDSHLSTCCSSGRSASPSPGLAPSWLTGELFAQFTSTDCNAAITAASGGGA
IGFQALFDASVRTFLISAPALLVAVVAVFAYRRRDPEPIIPALIGSVVFQIITYSLG
STFGLLRFFLTALPLTIILLFQIIPPRHRFPRLRPGACVDRVTKGVYKTIITGLVLAI
FGGTGITLYGMSSANWAPQEIYAIQELVFMGSPQDAVHTLNTFTSTEMDVADFVDSLNLG
DGEVLLSTTYGFAVLTAASNQKQFIIPSDDEFITTLNEPAEHGVKYILALPREGRGATDP
INLRYPMYETGSHIATMEIEFINQGGQGNWRILYRVLTTPQGS

>RXN00334 TRANSLATE of: rxn00334.seq check: 4035 from: 1 to: 336
MAKLLDDNVQIETVNVSFEGAGRTNWHTHPVGQNIIVLSGLGIYEAGEPARLLEPGDVFV
AAAGVRWHGAVSGAFMHVVVNLKIDGETVDWEEPVDEEYHRSVSAELQR

>RXN00338 TRANSLATE of: rxn00338.seq check: 9343 from: 1 to: 1140
VSDVTVDGDIRRILDEAYPPALAESWDKVGILICDPTESVKRVGLALDCTQAVADKAVDMG

LDMLIIHHPHLLLRGVTSVAADPEPKGVHTLIRGGVALFSAHTNADSARPGVNDKLAELV
GITAGRPIATRLGLGMDKGVHVLPKDAAYLKKMLFDAGAGAIGDYRECAFEIETGQFR
PVEGANPAEGDVKLFKSLERIEFVAPRNLRLRSLVREAHPEEPAFIDIVEMHSAES
LENATGLGRVGLPEPMRLADFVQQVANNLPTVEGWVRATGDEPQMVSRAVSSGSDSF
LNDVILKLGVDVYVTSDLRHHFVDEYLRGGPAVIDTAHWASEFPWTSQAQEIQLDKAPQV
EVDVISIRTPDWTMSARVN

>RXN00342 TRANSLATE of: rxn00342.seq check: 3222 from: 1 to: 429
VADAPGAVKQCAQDYAQLLGIQSGHIVQEIGWDESDTLISESIEDAIGEELLDEETDEL
CDVLLNWRREDGDVLDGLVDSIRLSAENGRIWVLPFGIGKEGALAPGVISESAQLAGLV
QTKAERLGNWQGSCLVQRGNKKP

>RXN00344 TRANSLATE of: rxn00344.seq check: 1354 from: 1 to: 879
VDLSLWLSDTQYILISVDFVQHAIASALLGLLSGVIAPIVVRQQSFVHGTAEALALMGA
AAALLFGLNVGGGAVIGSVVAAILLALLGMKQQDSAVGAVMSFGLGLSVLFTHLYPGRSS
TAFSLTLGVIVGVSSSSWLILVAVTVIVVSAVFIWRPLLFASADPIMAAQASGVNRFIA
VAFVGLVQITTSQSQVIGALLVMALLITPGAAAVAVTANPVKAVVLAVIFAEVSAVGLL
LLSLAPGLPVSVFVTTISFVIYLVCRLLIGWLGRGQAQRDEDAYRRRQHDHHPH

>RXN00353 TRANSLATE of: rxn00353.seq check: 5475 from: 1 to: 693
VGRSFTNRITFDPLPFMVVYPDGVDQHWNDARLGLDENTRHLGIDVGFVFKLATHLNGTY
GKKRIFIVGYNSGGQMVLRMLHEVPKMLSGAATIASNMPVAENTLPQVTKFTKTHEVPYLA
MAGTADTFSPYEGGDAGIGREHRRGVGMSAFDASAAYIAARNGLTTEHRHDVIDDVVSIDTW
DGENPVEFWTLNIGHGLVPSGKTYPEFLGPSTTSVIAAEEIGKFFDGVRRR

>RXN00354 TRANSLATE of: rxn00354.seq check: 80 from: 1 to: 813
MGKLLFVDIGGTLDDYSNEVRSAYDAIRKARAKHVRVYLLSSGRSSAEVTSQWLQWIDVG
LIGANGGVYESAQESVTHRLSGEETHRIVEWLYNRGLEFYLENNGLYASRGFREASKP
VLSRLSEKTDVTVDSMYPDMFWGASLDORDDVNKISYIFNSQEDLDAAREAFPNEHTTWG
GQTGALFGTIGVSNVKKIGVDRLLKYLNADRANTIAFGSDSDSLFEASAQGVAMGEAT
ESLKAADLVTDVAVGQDGLRNAFLKLELIDA

>RXN00362 TRANSLATE of: rxn00362.seq check: 1707 from: 1 to: 1347
MGIITALLVFIAVILNVFLKRDISEALLVGLVGTALVGGVNAPTLIDAVVDAQQSEVT
FAGMAFVFMGIIVQSTGLIDRLIAILNSIFGRLRGGAGYVSTLGSALIGLIAGSTAGNSA
TVGSGTIPWMKKTGWTAERSATLVAGNSGLGVALPPNSTMTFIIALPAAAASSASQVYIA
LACCGAYAVLYRLAVVYVTRKDKIPATPDQQRVSFGEAMKTGWRSPLIFGLILIPVILT
IGFLESEWLKTHGVGESGVKMSIIVVVPILITAIALIEGRKKRIANNMAHFRVQISKDLPO
FATVGISLFSALAAANIMEELGVGPQLSNWLDSDMLPKSVMVIIVCIMCIVVATPLSSTA
TAAAI GAFVAALAAAGIDPTVAIVVILCTSTEGASPEVGPAPIYLSAIAIDANPTKMFV
PLITYFVVPMILLANLWGMGFLPVIVPTG

>RXN00373 TRANSLATE of: rxn00373.seq check: 1756 from: 1 to: 339
MDIQLQDAETTAWKDSLRLAAQEAHGFEPKLPFEDFETMVEQYKQAAASDPIDVTDIQ
QMWGIVVGEYLRKMGMEWVITDDYGTDLAILATAPNGDHVYSCPIIVVGRK

>RXN00390 TRANSLATE of: rxn00390.seq check: 7582 from: 1 to: 405
MSTTREAFILARIILLGVILIAHGWKDFAITGLEVTGFDFSLGPAAGIAAIAAAVVEL
LGGILIIILGVFTRIVAAVFAIDMLFAALFAHVSSGIFVTNNGWELTGAIGAGALLLIAGV
ASAWSIDGVLAKRKA

>RXN00399 TRANSLATE of: rxn00399.seq check: 2271 from: 1 to: 315
MSHNDSPNFARRALNWLKQGYPTGPRHDTFALFYVLERLEETEDLNELAELLIAEGENN
GLHNDNPIITREKIKGLITHVHSQPFEDIDRIQKKLQAEFGPTRN

>RXN00416 TRANSLATE of: rxn00416.seq check: 8529 from: 1 to: 1650
LASLYSPALVVAVLAIPLSATRLYLDGISVDQGFRTQFLTRMADDIGLSDMNYIDMPTF
YPAGFWMGLGRLANLGLPGWEAFQPAWIVSMAVAASVLPVWQRITGSLPVATGIALVT
TCIILAMNSEEPYAAIVAMGIPAMLVASRIAKGDKFALAGGIIYLVGSATFYTLTGAI
ALSAVAVCIVVAAIVQRSIKPLLLWAVLVLGGGSIVIALISWGPLYLASINGAERSGDSATH
YLFLEGTFQFVVPFLASSVVGLLCLVGLIYLVVRHNNVNRAMVWGIADVYAMMGMSMAIT

LLGNTLLGFRDLTVLVLIFATAGVLGIADFRLASVYQLYPTQITERTATHLTNLIVLVL
 LGGLTYAQDLPGKNARAIDLAYTDGTYGERADLYPAGARYYKDINDHLLDQGFEPSET
 VVLTDELDFMSYYPYRGYQAFTHSYANPLGEFGNRNFIEDLAIRSWDELADPQQFSAL
 NTSPTWITPEVFI FRGSIDDPDAGWKYDVAEDLYPNNPNVRFRGVYFNPFESFDQMWTQKV
 GPFFVVVTHNE

>RXN00422 TRANSLATE of: rxn00422.seq check: 3762 from: 1 to: 894
 MPTNYARDNVI SLASAREQRSKGKPEPKPELT LIVRATNYQADGEVHRQIGLSAMSDEL
 HNVLNI VFGVGGEQSPWRFEQDQHPSAPDNLGELLPEPGDFLYFWGLWQFNQCVM
 YPRDNGTPRALCIGSGGLGDDPQATINAE LTGTDTIRDVLSGVRPEVIDLVDRGTGVD
 FLPLQALDLKREPLIDATRYHTCRTL PVENSASDAFWSCVLALSCLEDLIEVIE
 STMSTL GWVADDGSP LRAPEITSACEASLKILAE LGGYGPERLAPVDRLDIYRELLCF

>RXN00447 TRANSLATE of: rxn00447.seq check: 3535 from: 1 to: 420
 MLGSLWRFAVRTAAGAVALLVWIKLIDGISLSFPTTPLYQDGHDLNLTLFLAVAAIIVL
 NATVKPVLKLLGLPLTITLGLFSLVINAVIMLLAEVSDILGFLRIETFGAAFWGAIV
 LALVNWVLGPITGLLGAKKD

>RXN00455 TRANSLATE of: rxn00455.seq check: 9756 from: 1 to: 750
 MYVDVQNSHTPETQPQPGGAAKKTPVASGNSFTIHIQPSLYPILLALFVAVFLISNIT
 ATKGEIGPLVTDGAFFLFPISYVLGDVLAECYGFKSTRALLTGFGITMLAAFLSYIS
 WLPGASWEGQEAFATLGLVPQII VASLAGYIVQLLNAKVLVAKKRTGEKSLWARLI
 GSTVVGFEVDTLFCAIAAPVIGIATAPDFINYVVVGFWKTLLEVLIMPITYAVIRWVK
 RREGYETFDA

>RXN00473 TRANSLATE of: rxn00473.seq check: 5144 from: 1 to: 789
 MSGTGVRKLWGDGTPVSLPDL SGLSRAERIDALRSRMSTMGAAVFKFEPSEESAEQKD
 SLAEKQD I VAVPSAFSDLPFGDGLPRRAVTQLVEQPLVVVDFLAHITAQGGHAAVIGWKD
 LAYAGVIDSGGCVCENIIAIPNPGTEPLNVAALCEGLDVVYKGPETISLSPTRARPLLGK
 LRQGTALVMVGTQVSSPALSVDAEITDVGIGAGSGRIRGVEMQVRAVSKTHGVRSGKV
 LISRPQDAALLEPEQPTTLRAVP

>RXN00485 TRANSLATE of: rxn00485.seq check: 6436 from: 1 to: 2295
 VSSVNDLFAKPYENADLVVTVSAKNEDSFAAEQQLATT PGVEALAFDQNFASAVKQSDG
 IYASTSVQSI SEGPLQWRPFILEGRLPQGPGEIATVTAPGAPEVGEHVSIRLSQNTEDTEV
 LVVGVEPAAQETLGGAPFVVASPDALMEWNSSGVRGEFRVATSDPASLEAASFSDATVV
 VASAEHGVDKLADSYLQQRDRYFLLLAAFFVAVAAVAVLVVFSAYSVLTERVREFGLIR
 SVGASTPQILGSVIFEAGILGVVAAAGFGAPAGLMAARLLADNAAFRGIRVPIDVDLPSS
 TMWLITAGGVVMSVIAALPAVFSVCRKS AVESLSTPAISRTSPFWGALWLLLAGIVGAGG
 MWAYEATSDYRGMRSVALS IAGSGALVCALLIATAVLVPWLLHVFVSIRVGGTVPTLQLGL
 AFAAKQKRSAAI IAVILAGSALSSAVLHGQAHIGHLVAVAKMGMTMMVTALDGEI P
 AGMLEEISSIDGVKTAIAPATTAVELEDSGNFSVLM LAEEDGASVMRAGDTGAPAGGLV
 GRNSPDQDAYPAGQAAANIIVADTPTQAEIFHSDNYFSMIDPALATGPSTTRNVLLLDGD
 SNQAPDNATAQAVRKTISLFDGRYSITEGFSARQNTFELVSRTTMTSTLLAIALIAAV
 GLINTVALTISERARDRYLLRTIGLSTGQILVMMAIEMIALLSLPAIVGAVSGGFLGRFV
 ASSANTNTAATPLQVDILGGTVLAMVAGSVLCALIVLANKRRRVV

>RXN00496 TRANSLATE of: rxn00496.seq check: 7171 from: 1 to: 1026
 MTRRLHGGEGDQGHVKQLQGLFDDDAFLTDL SRGVDPSGDDDALAGLLDLKEAQEP
 PATMPDWSTLLPGILDQDQLPVESTSDTTVMQASNPATQEFAPVISIDTPNTATNSADA
 DESATVVP LAARREKRAKSGSSGVHSLDASATQRKSHFLLSGLVGAAAATLVIAGGGA
 VYNADENSPLYGMNQQLFGNQDPSVVELASTLEEVDRTASGDVEGARALLEQARAMLDG
 MAPPKAPSEARTVSEFPGTQTITATVTESASPEPPVTETQVTSTEVQTVTTTAVAPP
 VWTNPNEPTTTAAPTSTPSTGGEGTGNDGDSGLVPPQTPGN

>RXN00503 TRANSLATE of: rxn00503.seq check: 5802 from: 1 to: 1722
 MKPVFSVDQIRRAENTL FELQADPDELMISAASAVADVAMVDPGAPAVSSEESILLVL
 GPGGNGDGLYAGAF LAEEGHVDALLLNGKVVHQSALAYYESLGGQIISDFPPHYLYRL
 VIDGLFTGIGRGGTLPELASLVSEFSASGIPILADVP SGVHADSGELPGPVMTVEGFD
 NDAPMARQKI PAHIDADVTITFGGLRRAHAVSPACGEVLCADIN IAGGGKSSLAELSQV
 QEDATPQMFASKAYQRKDSL FERANLKATAPHIHRGQHFVTNLNMEPGPDHDKYSGGIV

GIVAGSGTYPGAAVLSVKAARVATSAMVRYVGPALNFVQSLPEVVATQSLATAGRVQAW
VHGPGRGLEAEQSAELAEALLSRPEVLIDADSLLQLSAELRQALRERKAPTTLVTPHKG
EFERTAAELRSEGEVLPQADKDPIGAQAALAKEFDCCVLLKGKYTVIAAHDVPHAINAGH
SWLATPGSGDVLGSLVGAHLAQSYAELNRLPEFFPDVTLSDSAIYTIQIAPAATHIHAVAAG
LAAARTEFGFAPTASLIADAI PAATAKVDLKRIV

>RXN00504 TRANSLATE of: rxn00504.seq check: 4338 from: 1 to: 420
MTYGFVLNRLTHRAIDFDLENAAKFLGGADDGRVAVAFQEDGTLYAALYSASAKDEGAA
ANPVASLGRNAATGDGSSFFSDPTTAICGPVIFVGAEGEDITLDEIERIKDGIARAARNYR
DDYPEEFNLWRNAVYNLRTA

>RXN00505 TRANSLATE of: rxn00505.seq check: 7863 from: 1 to: 495
MKSEFPVSGTRRFEHAADQNFGEELGRHLEAGDVVLDGFLGAGKTTFTTQGIARGLQVK
GRVTSPTFEVIARHRSIEGGPDLIHMDAYRLLEDSEADADPICALDSDLDTDLDAVAVV
AEWGGGLVEQIADSYLLITIDRETAVEDPESEARIFHWEWREGR

>RXN00507 TRANSLATE of: rxn00507.seq check: 8687 from: 1 to: 855
VAENLNKHLKSLKRGPHRVLVGDMNYAGIPGKIYTFPAGDGPVAVFGHDMWKSIKYH
QTLRLHLSWGIAVAAPDTENGFMPDHKGFPASDLESSIQLGGVKLGSGNVTVNPACLGVG
GHMGAGAAVLSAANRDLVRAVGAIYPKATSPSAIDAAFAVKAPGLVIGSSSLGLFESGE
PKLAAANWAGDVYRESEKGNQGGFSEDTMFKLVAGISGSPQTGAQETVRGLLTGFLHLQL
AGEKKYKAFSEPDAAEAKKVSYPGQELQEHAFPKDTSPPAFNLNEK

>RXN00510 TRANSLATE of: rxn00510.seq check: 4920 from: 1 to: 1509
VNDPLAGYGAVISALQAGSGMYRGPAKSEGLREMYQTIEGLDTSLSRLAAEAAGVGTN
EARIQGVWVPLLKFPGTVGGGMIAIEIAERAVDWFKNRNDVEEVESEADAKADAIDSTVT
ESDQMMHIIQLQLDIVSTLTQILGSMDBRGKFPQEFRRDCVQTGADLIDQAGDMLBGLCAD
RDDAISQCFSAITDHGKQVCETEPKPLCSAASGSSGGATSSAASGSSSSSTASSGSS
GSSSAADSSTSTNAESSVEKEKTTAAPEVKPDEKPEKPEKPEKPEKPEKPEKPEKPEK
KPDPDPEKCKTEPEVECEPTPKPETEPEKPTPTPTPGTPTPIPELETEDCEPGKETGTD
ESESECAPELNDVPEESDLIGLQIKGAIIGIVVVGVLVNLVEQCVPIEVEVPPVPEP
EPIPEPAPQPEPTSVKPESELDKVAEPAPKPIQANYTAAATNYSAPAHAPVVPITPA
APEVPAAPFVPAFVNLHAKGW

>RXN00515 TRANSLATE of: rxn00515.seq check: 5675 from: 1 to: 702
MRESRVLPALLITAVSIPTASATLTADTKELCIASNTDDSAVVTFWNSIEDSVREQR
LDELQADDPGIGKAAIESYIAQDDNAPTAELQVRLDAIESGEGVGLMALLPDDPTLADPNAE
ESFKTEYTYDEAKDIISGSSDPASDVLSQLQAAATGTTRTAIRAEVFAADRTDDYNESQ
TALKEDFQNCIDAIIDARPIPLQYILIGGAIALAVIVLGIRAWTNSRKQSKHSQ

>RXN00527 TRANSLATE of: rxn00527.seq check: 7113 from: 1 to: 1764
VIATSDVREISSSEGIARVSVNGNIEAARTTTIYTSITVPANLFPVAGDVRVAAQDVLA
LDASALQRQLEDTDANNARAAMANNRSIAQSQYAYEQSRELLDSGLSPFINSARSSSLRAS
SQAYQDAIRSFEEKQRDVGGLDSTMTVAQS DALKAAREQADAAEIERLRADFGLNNDRS
NLNDVIGLLDERESLASAESELAQARAAGDLEAVAAAEAKVAGLEQSIASKTSTWPSQDQ
TYLQSYTALEEAERRVASTTEALEIAERIYIDSLGKVDSELAQAQRAVAEHAQAQDAAAL
GLETAQLSTOHLQEAQSSAIDALGLASVDNEAARTSTSQLRMDINNTTVRSYSGSIVSS
VQAAGQQAAGALLSVADDSELKITANVKEAIESNVTIGSRVTFPTTSDQTEKFEAGRVK
VSPFIAAASAPATGEGAAAGATTNTDVTFPFIEISVTDGREGNLGGSARVRVIEHIAFH
VLTVPLEAVYKNDGDKDAVLIISDDNKVEEVEVKTAESDDFDIAVSGAGISSEDARVLTQP
GNRYRLIGITEVKLHADTVEQAAAPFSPAAPFDPAAPAVSAKQTVGVQVI

>RXN00547 TRANSLATE of: rxn00547.seq check: 6032 from: 1 to: 1398
VARDPINAIIGRFRGFAQVGTQRFWTPLRVLITTSVLFLAMGFLTKANCQGSRGTDGVV
SLNWGSGRQYTSACYNDIVPLYGGRGIDAPGFPYAFWSQEGDLTRYMEYVPLVLLGIGFIQWIC
GIITRFLYPVVDVIPFHTLPESGLYPIVTALALAFFVVLVIRMMVELTGNRVNDTVLVAA
SPLVAVHAFETNWDTPAIAAVIGAMLAVKRGNPLVAGVLIGAGTAFKLWFLYLLGAYLVLA
VKNKMLKFFTITMAAAAVTWLVNVNVPVMIAYPKAWNEFLRLNREGAETWTTIYQVIDRNL
PINLNDPVLNLVLSFGLFGASCVAILILGLKVQRTPRVAELAFVLVAAFLFNKWSVSPQ
SLWLVPFLAVLAFQPKWLVFPMMVTDAMVPMILMHMLGTDNKGLPHEMLDLIVSRDAFI
VVMIVGVIRQMLGRADPVMDAHAGRDLLAGFPFAGERRKALKEVS

>RXN00552 TRANSLATE of: rxn00552.seq check: 471 from: 1 to: 936
VATSKILLYYAFTPLSDPKAVQLWQRELCESLNLGRILISTHGINGTGGIDDDCKAYI
KKTREYPGFNRMQFKWSEGGAEDEFKLSVKVRDEIVAFGAPDELKVVDENGWVGGGVHLKP
QQVNELVEARGDEVVFFDGRNAMEAQICKFKDAVVPDVEITTHDFIAIESGKYDDLKDKP
VVTYCTGGIRCEILSSLMINRGFEVYQIDGGIVRYGEQFGNKGWEGSLYVFDKRMHME
FGEDYKEVGHGICHCDTPTNKFEHCLNEDDCRELVLMLPCPCFANVETRHCKRRCACAAIAD
FAEQGIDPLVTS

>RXN00555 TRANSLATE of: rxn00555.seq check: 6336 from: 1 to: 939
MKQPLRVLISCRPEENSGGKRSEQNDVFEFAAWLARTSDINVRGITTFRPWPSSISK
LGGYHKWYKNLDSYYRSRTIKGLKEAGVEKSWDDVSVFVDGPGSESTLLTHAAEEFEA
DLILLGSDATAPKGRFLASSTADALLHSSPVPLGLVPRGVKLSKGVTRVNYAFNTESND
FEQGLRSSAELATNWNVPLRILAFSPTGITSAPTSRLDISTELSSREWRELT/LAMLDRAR
DGLVTDHPNLSVSSSTGSGWGWGAIDALRWKGGDLLCMGSHRTDTLSRVFVGSSETMEII
RNSPVPTIYPGL

>RXN00560 TRANSLATE of: rxn00560.seq check: 5757 from: 1 to: 375
MRIDPLETRQAVLAVKDWIEGEGDVKKPGRAALAAATRLSVRLLAHQAPGNSVEVRVPPF
VAVQCIEGPKHTRGTFFNVVETDAKTWLRAPGQTTFDAEFESGKISASGTRAKEIADWL
PVVKL

>RXN00574 TRANSLATE of: rxn00574.seq check: 6894 from: 1 to: 879
MSFVISTGFPQAIQFDRGRFGFASAGVGTSGSFDRLSAARANHALGNDPNATVVEIILGG
FEVHALHTTSIVFTGTEAEVMVRTAGGQSKNATNTI IDVAGGERIRVEPATYGMRAYFA
ARGGFVAVKKTLSASTDLISHMGPCPIEPGDVIDVATDIADSQWPKLRQLPTLWKRPMT
ETLTVIRGPRDKWFTQESLNNFTQVFTVSNDSNRIGLRMHSSSEPIQHRVEGELKSEGMV
RGSIQIPPGGNVVFPGDPHVPVTGGYFVIAVLTSRSCDRSAQLLPGDKVRFKLL

>RXN00589 TRANSLATE of: rxn00589.seq check: 4154 from: 1 to: 450
MTTLRSKFFVSATTALAAVALVACSPNEIDSELKVPTATGVSLSKNSVSTATTTDEDA
PGYIDCVAAPTQQPAEISLNCAMDIDRLTDISWEWDTDSATGTGTRIVTAANGQETETE
DIEVKLSFPTESSQGLVFTQVTVDGQVLF

>RXN00616 TRANSLATE of: rxn00616.seq check: 2419 from: 1 to: 345
MKSLEPRFAPLITILALLVLVAIGGSALANNRATPNVESEPATVNRQSTPTTSAYEPPATE
SFEEPTTQIQESFVQPPVPAQAIQPAQVPLNYQYDDDDDDDDDDDDDDDDDDDD

>RXN00647 TRANSLATE of: rxn00647.seq check: 2211 from: 1 to: 633
MGIFEARAARAKTKAEIKAAEAKVKTEAKNKAKLLDKREKLLVQOEKNLLKVEEKLKK
RNKHELKMAKNILQCKRQGRNLKDKVKRWAGTARVLTPLLLPIYRLSTEARDQVVKGRA
RRAGVTAEQLSQFAGHAAALKARIQGVRETAKNSSLFAGFVRDVEERLNELEAANNSEF
MSPQQRNRHAQHSISRDNLQVSDQIQDRLLDK

>RXN00653 TRANSLATE of: rxn00653.seq check: 8269 from: 1 to: 765
VSVSQVVGIEILLTVGILALLFAYEAYWYNVESGKLQESAGQKLEDWNEARVNPQRKLT
PELGEAFARMYVPAFGSDFNFAVIEGTDEEDLLAGPRYVDVDSQMFGEAGNFVAVAGRVGK
GAPFNDLGNLEVCDAIVVETYNWDVYRVMPMSTNGADRAEAACDFCNEQVSRMAEGDY
VNVSGRSITTPDRIDATYPTPGVFDTAVERGEALTLTTCHPQFSNAERMIVHAMLVVE
IDKSSGERPAALEEN

>RXN00662 TRANSLATE of: rxn00662.seq check: 7679 from: 1 to: 1269
VSTIPLNRLAVIAAIIIGVGTGLFVAALNWSAIGVERLVYGADHLHNYNPFVANVSPRLLSI
TVIVLSVVASWAWFVHRTGPKESIVGAIRGKMPILETIAASFQVTTVAAGAPVGA
NAPRIAGALVGERFSRWQLDIDAKRILVASAAGAGLGASFHPLPLAGVLFALEVLVVAS
TRTVYIAIIITTTAAVATTGFFVQTPDVFTVPLTESPWMLLAAMVTGVVAGMCGHLVFS
AHKMAQASPGVKWILWQMLPGFVVIAAVIYFFPETLANPRWLADSMGLGDLILLSTILVL
VLRTAMFLLAFRVMVGGNLIAPAFALGSMVGGVGVAVLEPITNVPIAFAFALLGAAAFIST
TMAAPLFLGLIAAEVFTDMEAQGYLPFLAVASAVLAVRVWSVIAKHELRAIPITYASWTG
ELK

>RXN00666 TRANSLATE of: rxn00666.seq check: 5076 from: 1 to: 915
MTEAGEATHSVRAAQIAEEHNYARFVVAEHHNSEGLASSATTLLMGHIAGHTSRIRVSGG
GIMMPNHSALHVAEELGTLEAIYPGRIEAGLRAGPDTDPMTARELGRASSLVDDVLTSTIV
SLQNYLDTPEERPNIIIAHFGINSRVLPLFMLGSSNLGAAMAALDLPPAFASHAFPFQMGV
ATASYRELAANFYVMAAANVLVCDTEEEAEFQISTLHQMFAGIVTNSRGKLAPPVVRNLKD
KLDPMIWKHIEDSLEMTFIGTAESVVLQLEFADRYKLEIITVTYSYDPEVFRFSIAAL
GTAWN

>RXN00704 TRANSLATE of: rxn00704.seq check: 5954 from: 1 to: 627
LTITFSRVALTTLAVTATTLSTLAANAQSSLLDKTLARQCIDANVWVSYDYGDSEK
EPEGACATEFTDGVVALESAGFKLTFDESEMCKYMTINGVVPDWVETGTWYSYSGEVA
DDYSVDYTYEYVGSNSPEGGTVEAWVVGTGEETPALETLPETPAATGSSDEGGWIAVI
AGLLALIGGGVAALYQGLITIPGLVLPKF

>RXN00712 TRANSLATE of: rxn00712.seq check: 8070 from: 1 to: 696
MSLRKNLALGSSVTLTAVLSGCVSLDERSTDSTENVTTVATLTSTAAEPTTRTTVQ
SATEASTAFVQCNLDPRSTDGFPYLAQSRTPVGLAGSADSVVQVPDWYFHFQMGDNGY
DSCSKLSYVVLNGSNGDAERSTGTGAIAADVVLFDGDMVARPAPFEMKTVESVSTRVSD
SEIQVYVGHAGRSTAEGVTDYFTNFVFDNGVLSGRGDLPEHIDTHMRLYLL

>RXN00720 TRANSLATE of: rxn00720.seq check: 5001 from: 1 to: 666
MASPRRPQVAAPRIKELRLTGLDNADPDQDIESNEQIESCRFNEALSERDLGGAGFIECE
FLGLEAHETELRRQFVETRIERANAPSFKAARSIWNRNATISDSRFCAVEMYEATVQALK
ISDSKLSFVNLRGASLRDVLFEENCVIDELDLGQARAERIAFKDCTVHSLTFDHAIVLSND
LRGLDIERISGVESMSGTVISSLQAADLSGAFARHLGITVD

>RXN00722 TRANSLATE of: rxn00722.seq check: 460 from: 1 to: 1065
AVLREAGVVDAGGQGLVILLESALAEINGNPPHPSHHSEPAEEPSFHGKTGDLEVMFYI
ACDSAQTLDALHNELETLDGSLIARETNTRGTVHIHSRRAGEVIQKAFAGDVSELRLR
ILPDTSGSFTEEPRRVLMVAPDGLVAELYSAGVKVVARNIAGSKSDDDVAKIVSLARK
SGADEVILLPGLLTKRELVSIERSSHAFEQSVILPTATLVAGLAASVHEPAQPLAVD
SYAMAEAAAGSMRTATIRAATSALTOAGACSKGDLSTFTGPEIALVSEELNDALSRALTALR
LLDGSSEQITLLIAQDRQSAFDEDFVRRLGLTHTDVEITVYPATGMENLVEIGVE

>RXN00729 TRANSLATE of: rxn00729.seq check: 9733 from: 1 to: 978
MSATNPDLVDQHVYPIKTKTFLAVIFNIISSGLIGMAELVPGISGGTVALVLGIYERA
LHNGDLLIDLKVLKIDRSKVKEAAAKIDWWFLGAIGVGMVVMVMSSSLHTVVEDYPE
ITRGLFLGMVAVSILVPLGMMMDRDAKKRLAIVPLFIICAMLGFFGTSTFSAPRTDPFL
IFVFICAIAVACALVPLGVSGSFLLAVGMYAPIMESLSNRDLISVIGVFLGALGTGVILF
VKVLSYVLEHRTITLTIMAGLMLGSLRALWFPQDGDANLAPGDNAVMI FSIITLGGAI
VAALMFAERVSSKNIDSETVAEEHPR

>RXN00730 TRANSLATE of: rxn00730.seq check: 2858 from: 1 to: 807
MSSQQTIFILLFAVILISIVMITAAFKTRKKRFAARAEGBMANPTIPATYVFWQRFAGA
LAALYARPEWHKTRGAKRVYSAEQTYFGVVSAMPLGMVQNMQLQTDWGVKKSEHAVDQLSK
GVEVIVGVAAGNWRKNGVSPAQVEEGQRLAAEGLAHPHFVVFQKQLQADDPNAGYEDLDV
LAFDIARVANLLRWAAITDLLLPAEARWFQDQLGIAAASFGSWEYGERYVRGQKNFK
GNGKPYIEGERWLNTAESPKWTQKWISA

>RXN00731 TRANSLATE of: rxn00731.seq check: 8578 from: 1 to: 2496
MKDASQSYLLFGLRWLGRSLRFAPLSLLMIVVMRGLREVFGAEDPANSSSLVDNLGLTLPW
SLNDPHFLTAGFSASTTTAALMSTLWII VFAVPSEIRILGSLKFAITAAALHITSPLIGI
IAHLTEADLNRRWGNMNLADVLLTPDFWVFGVAAAFASASMPLLWRRRTFLFETITLTL
LYTGTFLADVMTLTATII GTVAGELNRRHRTPGGRWLPGSLTVREARIMTALITVAAVAGP
VLAALNPLTHGFPFSATKLIWQPLVTEEHMHHLCTDSTSDACQALDQLQKHGCVGPSVA
NLIPLILTVVLAMGLSRGRRLAWILAVLAQLISIAVIMFQLTKLSADSTDLLWSVNAFSV
IVPWLVALAVLVFSRRARFQVKIDTTRISKSLGALVMTWLATAALWILATILFLPHAFHFP
TLGLAFLEFPRLYLPPTIETVLSHQLFPRSPAGWAVEFWGTFLFWLVAAATYLHLLMGVP
SNKAHEQDENAAATLLRSGSGDHLSSMTIWGGNTWWAPENAGYVAVRVKRGIAITLGEPI
LGPDSVYSKAEALAAQFEFASNQGWIVAWYSVCEFSKERINAGHHTLRVAEEAVALSSAN
ADFKGKHQNVTRARNRAAKEGVSSITWTWADLSAEMQHKIITLSEEWVSDKALPEMGFT

LGTVNELSDPDYTYLLAIDEEEHLHVTSWLPVYKGRIVGYTLDMRRDPQGFKSVIEF
LISEAVVIAARDHLEWMSMSGAPLSTPPGVADDDGTQILELLGRAMEPPYGFSLAASK
NKFHPEHHGWLYCYRDELSLPSIGLAVAACYLNEFFLPNWLKKTATSAPSHS

>RXN00738 TRANSLATE of: rxn00738.seq check: 6764 from: 1 to: 363
CQEEETDGFDFGDRMPGERRSYGTLLNDATTQVSHILGNAFTRSGLNAEYANLYGQALV
GMVSMTAQWWLDERTPPKKEEVAAHIVNLCWNGLTGMEADPKLTPISSAEGAIFGQKESE
A

>RXN00750 TRANSLATE of: rxn00750.seq check: 8593 from: 1 to: 438
MDWSIIINVLAIVATVILTLIIAAALYRGFTRNKIKKLEAIRAQQHERDNPTIRIADLR
GIMDTHHVIYTDVMVTRAHELMITAPAFDDVTLPEAVLYEDTKRAAHDALNGYKDTTAVS
AEKIMLVDAVTAATWLYSTKANTGST

>RXN00762 TRANSLATE of: rxn00762.seq check: 9427 from: 1 to: 876
MNTSDRIKSTQIALDRDLREQALLLLKEVRAVDGVDALSEQFVRGLAEPGLVHSHLIVTL
NSELVGLAAADEETTELAVHPAHRRGIGIGKALIDAAFTSSIIWAHNGTAGAQALASTLRMK
KTRELLVMEISDRALDDSAAYKDPDGTTHSSLANAPVEKSVAEAKWLQSNNEAFDWHPEF
GGWTHRLAQAKADWYKDSVLFWDGEEIVGFHWVKQHSPELQEIYVVGSLSSAYRGRG
LGDFLVRGLHMHRAHGARKVILYVEAGNTPAVAAEYKLGFTVAESHVVYK

>RXN00768 TRANSLATE of: rxn00768.seq check: 4486 from: 1 to: 1119
VGTIEDVANEQIEVANNTDQIPAGYKSPLLSRSGAAEAQGAAGTEGVAWHYGSPLVE
QRIFETGTGLVDRSNRKVIVKEGPDAPFTLNNILSQKQVDSVENGFTAGALDLDAQGRIGH
TMQVTVVDGVFYFLDTSAAEFDTLIGFTKMIWFSEVTVQEADLAIITLLQGEIALPDPAV
ARRVDWNGPSRIDVAIRRENLEEGVDKLEAGAKLTGLMAYTAERVKALEPPAGVDLDDK
TIPHEIPIHWTGRGEHLGAHLTKGCGYRQGETVARVDNLGRSPVLLVLLHLDGSAFLDPFT
GAETKAGARTVGRGLTVVHDADYGPIALGVKRSALDKELHIDVSVNVDRDLLPAESEE
QRGRAAINKLKGL

>RXN00769 TRANSLATE of: rxn00769.seq check: 3734 from: 1 to: 213
MGRGRAKAKQTKVARQLKYSSPDMDDLQRELANSPPRRSYSDTPDDEQYAEYADWDE
DDTDNRAYGTN

>RXN00771 TRANSLATE of: rxn00771.seq check: 865 from: 1 to: 819
MTNPYEAFIPLKHRTGIEPEHTFEWENKRVHIARRRREAPVRVIVVHGLGTHSGALWPL
VAAIEGADLAAIDLKPTPLYDDWLRLLSFISSEDDGRPLILIGAGTGGLLCAEAHRTG
LVAVHIATCLLNPSDQPTRRALFRFSPLTRLIQGRLENREIPIVTRVLNFKISRSPLSK
LCAADEFGSAGKITWGFSLASYVQHAKLGAVPVTLMPHDHLLTPVELSLRFLSRKAPT
DVVMLKDCGHFPIIEPGFTTMTLETVTSVIARNS

>RXN00785 TRANSLATE of: rxn00785.seq check: 7074 from: 1 to: 657
IIATLGVTLLVEARGFLTVASIPILFGIFTPLTSWFVSQQGVAANVSPGVSVTEILTAV
YPLAQLFPTLIMVTLVAALIAVVRILLRNQESRQVSGELTRRAQREAEANQAARRA
RAQSTRVQSKTRNRRAQPTGDTGSQVTVDELIRRSQERRQTVAAQRQTERGVFTPTTGP
VVAKPFRPSAPEAPAPTQVGERRQAAPKRRSLDDLLYS

>RXN00795 TRANSLATE of: rxn00795.seq check: 1530 from: 1 to: 528
MIIISLVSAIIMLVAVGFTGMCSEFNTGSPENGQVPEVDASTFMSMEARANTHATRLPET
PEGWTTNSARRMTVDDTPASVVGYYTADGEGYIQLTQTGETVEDAVAGYDTRWRDLSESYD
LDGHDVGIYTSQESDVRDLRVMDLGDARVMVMSGATDEEFNDLLRAVANSEPLPTN

>RXN00831 TRANSLATE of: rxn00831.seq check: 2669 from: 1 to: 702
MSALETQLQWQDSSVLIIVAHPPDDPEYGLSAAVKEWTDAGVEVSYLLTHGEAGIQGLDP
KETGSLRAAEQRAACDVVGVRNLTILNHPDSMLVYNLVRKDIAREIRIRKPNVAVVSNF
DVEAYGGLNQADHRVAGLAAIDATRDANPWAQPELLQEDLPQWGAEVII IAGHPENQTH
MDLAKDSVDAGVASLQAHKEYLAALPDPKPEEPIPAFLEVEGGYAAAFRVFGR

>RXN00835 TRANSLATE of: rxn00835.seq check: 6529 from: 1 to: 954
MAGGLAALLDDVAAITRAAAASLDDVTAMAGKTSVKAAGVVVDVTAVTPQYVQGVKPAARE
LPMIWIARIKSGSLVNKIIIIILPIALLLSAFAPWALTPILMLGGSYLCFGEAKIWHSLHRR

IKGEQHSSTEPKSQESPKSEDQLVKSAITTDLILSAEIMVISLNQIADQTIWMQAAVLFFV
GIGITALVYGVGVGLVKMDVDGLTLSKRDSAQIKQFGRGLVKAMPVLQVSVGVFVFM
WVGGHIMVVGTEELGWELPHYHLVHGLESWANGIGGSALGWGNTFGSLVFLGIWGAITTV
VVSIVKKFIPQRAQNSSH

>RXN00836 TRANSLATE of: rxn00836.seq check: 6589 from: 1 to: 1716
MYTHSTGTPLQDFDGDIIYPLHLFFSAQTAQHFALEVRVNNVHLRAIVKPEGEGELIVEALLA
PIESATKIGVWVQDEFLGVIAESQFLNLSQLSRI PASGHLSISQQLLTPSKSGSLASVLLP
NLKFGILSNPDPRADSHLLPLGRMWRVEPTVHALFEDFSLGSTILFGLRLDLEALIVSYN
GIECGILNDDASALSSAVKFSNANGLTPTVLGHVVRENGETSFEIDVLELELWSSKKQHR
LEVLTKITPRLIPKEADSQNYVKATALLSDEILRPQTLSKKALSLSDTAVKYSHPHVACGVGM
FSLFAVIFPDKLSDSHSAMLLAVISLMLFVLALVILFKRIQSTNTQRNWLASSVGLLATLP
ITILFVADTLIFQGSLENHAQPDVQVTTLANRNPSSPTSLDSLGAALNPSPPSPSSSSML
QNSEMFASPPIASGQSPVSTFRSWLDRSILPLTRENSASESAVLTALGPSIVQPASESITIT
PAQTSQSRHAI DDGDDSKTSY TGRPAFTNPSPIALPPTNIIGPEDPESTDPTAPTEPTEP
SEPVADEPSETSEQTSPLLRDTPELNRKQL

>RXN00840 TRANSLATE of: rxn00840.seq check: 2272 from: 1 to: 714
VTKTLPRLLTVFAAALAIAPATPVASAVTPVEQAFNASSNLSSGLPVDQWGRFNPQEFQQ
IEQAVNQVPPVQEIKNIVSQAMGFIITGDGSEGGDIEIPDNAPRIAQFVTRSENCING
SAAVGSFAFVFGPADLPFGAGVGQTSFVFTALGTGLAEQQOSTAMTVQKANLSNFTHGT
TTLSTNTGINPDGPSTISGVADTGRGIIVASMSGGLTTSTENGSA NCNFIPTAVVFDVR

>RXN00841 TRANSLATE of: rxn00841.seq check: 5409 from: 1 to: 537
MTDLHPVKQEI FNTAESINTDPKGFLREVDTFKVTDFGLMARGANHPKFGYLESWLLPE
GLLRANLIFHRKGVDERQDYIDVAEIRVEDNIINTRDLYVDLISVCGEPTVVMIDELA
AATSSAGLITADDAERAIDATINAVEGITRHGDPMQWLSRKGIELTWADASVGLVPEAE

>RXN00846 TRANSLATE of: rxn00846.seq check: 1812 from: 1 to: 870
MLKNDLSGARVVVAHHPDDEAITTGGVLADLAARGADVTMITGLGEQGEVIGETFAQL
VNGDADQLGCFRIHLYASLEILGVRGILHGGAGCWDRSGMVGDFPANEHPRATFHSQDRA
VEQLKELLAELKPHLLITYGPDGGYGHDPDHIARAHEITHAAAEQRIWLAVWSDRLEEDGL
KAITGLPEGWGRGELSASVDSVLSVELNDEVYATKVESMRAHATQLWIADGQSVSRNTNVA
AHAVTQQDNVKNVWALSNLIAQPIMRHEHYQLGAGTLPLEGATGVLDGLEF

>RXN00850 TRANSLATE of: rxn00850.seq check: 9820 from: 1 to: 828
MANPFSKAWKYLMALFDSKIEENADPKVQIQQAIEDAQRQHQSQQAAAVICGNORQLEM
QLNRRRLAEIEKLQGNTRQAIQLADKARADGDVKKATEYENAAEFAAQLVTAEQSVEDTK
QLHQDQALQQADQAKKAVERNSMALQOKVAERTKLLSQLEQAKMQEKVSELSKMSDSLTS
STPNLDQVREKTIERRYANALGOAELASNSVEGRMAEVEQAGVQMAGHSRLQEIARAEMAGG
SLTAGNKQESIEAPAAGNVNTDDAVAQRMRELGEA

>RXN00854 TRANSLATE of: rxn00854.seq check: 1696 from: 1 to: 213
MRLSEFRQLIEDEFGEAKGEWIAHSHVIGALGVTDADVADTGVLDVDRVWEQLCIDFSVPE
ERRLGKDEPGF

>RXN00855 TRANSLATE of: rxn00855.seq check: 9166 from: 1 to: 285
MPTFAVLYTYNPDSKVAEVRTVHREFIANHAEKGKIVGSGPFVDGDDGALIVIKLEEGS
NLVDAETLMNNDPFHVENVLNDRVIRSWNPVTKDF

>RXN00869 TRANSLATE of: rxn00869.seq check: 9381 from: 1 to: 921
MTPTPIISPEFEALRRMAAEFTMVAREFKQRKRELLGEDGKFLIVAADHPARGALAVG
DNETAMANNYELLERMAIALSRPGVDGVLGTPDIIDDLAALGLLDDKIVVGNRRGLRG
ASFEMDDRYGYNVSSMVDRGVDFAKTLVRINLSDAGTPTLEATAHAVNEAAQALPIM
LEPFMSNWVNGKVNDLSDAVIQSVAIAAGLGNDSSYTMWMLPVVEEMERVVESTTMT
LLLGEGGNDPDATFASWEHALTLPVGRGLTVGRLLYPQDGDVAAAVDTAARLVPTDIQ
QTSQSGI

>RXN00915 TRANSLATE of: rxn00915.seq check: 6638 from: 1 to: 630
MSAAYSQDTLLITVFLGRGLTAEIGRTLEDFAETGLVRNLVWIDADSFHESSEVTHLAT
NQDGLPELQRRPFNELVSRSTTKLHIGVINVDGSEGLMAHEELNPLVGIIIDSVCSHHQ

IHRSNVMIGAVAATLDEELPILRGVYNMLAPEDSHSPGTATVTRYRHGFS DHRLPCTAWL
ISPACTDCGKAHPQSNSSYLKVPFAFW

>RXN00917 TRANSLATE of: rxn00917.seq check: 3769 from: 1 to: 2679
MYNTLNKSTVNVPRFARGVVAATATLFFGALVSLAPSALAEPPAVEAGASGSLNLGAC
IADKDTLDVLIIMIDETESLIEHARDGVVNAEPGADAQHHRVPAQSFVDELLAQKSDGD
LNTRIRVAGFGQTYKSGATDPDNYGAWTQLDASTVGGVQDEISRFADRTQEYQYTNYSASAI
EGAYQDFTNRSGSEDACRLMVTFTDGALTAQEGADVAAALCAPGGVTDRLRSAGITHIGI
GLSAPTNFSDPSLLRGTTAGGGTCGEVPANGAFFPADNVGGLFAAFREALAIGGETIGET
RAGDPFSTLTDNSVNSVRFRTAIAKDDLGNPAHLVLTAPNGETVELKDSGSSVANSTDVSW
EAESSPVKMDGSLNLQGGGDWGVWQIQFGQIDPAADVGRVFNVSVEIQPDLQLVFSGGD
STSGALNLDQDQQLNMQLVGRDQGPRILEGSAVDLGFTRADTGEFAPLAQGIDISGGEL
FSLDITISQLPAIGTVEARTTITTAGVDDLPGTTLSPIILNTRITITQORDMQLPASVRF
TADEDVVTVDIPITGPGKVWIAPGTQLSGVLPDGVGDIAASSTFSDPDNALVLGLDEQGT
IPVELTVSDLRDLGVNGSIPQLISNAEGANETSVDLPTEGTLVSFINASTALAFIALV
LSLLIPLLLIYIVRFLSAKVSSAMSGVRIPEVFSGEALRYAGSTMPDLASQTATTKQVV
VHGDTFNVVGHKLKVRQFLNPIASPAVIVQTDPSISFDGKQKGTQAKLPLAVQGSWFLT
AGSDPSKMEILIALTNLPLEQGQIDRMIAIGTISKAPDRARELQKLLDDAATSQPAKVPPR
APAAQGHVEKQAPSPGTGSGGGFGSSNGGGFGSGSGSNDTNGFGSGGGFGGAR

>RXN00921 TRANSLATE of: rxn00921.seq check: 1572 from: 1 to: 513
PAAILLDHIVPNFSRDRSLPDIEDWTSDEAQIFAGIAGASVQTGRSHFWMWLLRAYF
GVALLGDEDTYRAFTTLTVDSVLSFVQLTLQEGRTEDIRRFKEKYGEQIAREDLPSILTNA
RAVQYLYGIDQDIINKKVSRSRDVNQIFTEMARAIIRASIRNNIGKDMRS

>RXN00943 TRANSLATE of: rxn00943.seq check: 2288 from: 1 to: 912
MIRKLARPLMASVYVADGAETVNLNTSAHVEGTQVVLDRIRYVLPKRYAKRISRDPELVTR
VIGGTGVKAGSLLAIGRAPRTSAATLAILTIPNILARNAFWETQDADEKRNRRNGFLTNI
ALLGGLFITSVDTGKPGVKWRATNATKRKKQLQALPTKSETEKFGKASDWNFDNTSD
KVTEYAYTAQDFVGENKDDWIKSATETAHKVADTVSDYAHKATSYLEENSGDWLEAAQAN
AKTARKSAVKAAGKAQEKANFALQVAETSGRANKKATKSYDKLQKQADKAIDRAQKKLK
GIEL

>RXN00945 TRANSLATE of: rxn00945.seq check: 2895 from: 1 to: 972
MLERLKRDLPLIVLIVLAVIAIIPVRGVAADWFDVAVKIAIALLLFFLYGARLSTQEAL
NGLKHWRLHLTILATIFGIFPLIGILEPMTAFVSEDIYRGILLFTLVPSVQSSVAFTS
IAKGNVAGAIVSASLSNLGAVLFTPLVLMIMSAGGGVHVDSQVFLDIAIQLLLPFLIGQ
VCRRWVKNFAANKATKIVDRGSIAMVVYSAFSAGMVAGIWSVSVLEIYIYLIVFAILLVM
AMLWFTLFMATRLGFNRADSIAIQCFTGKSLATGLPMAAVIFGGANIGLLILPLMI FHQ
VQLMTCAWLAARYGRDAQEQAANA

>RXN00946 TRANSLATE of: rxn00946.seq check: 9850 from: 1 to: 774
MTHTLQATNPLDQTAWHAWHFSRNKEAISRTGATSLSATSEWISATTLKDAHTFPSPGRW
YKRGGVVGAHLPPAFATGTQVLRPGELLIAEDFTLVIERLGFALQVDFDARNPKRFE
FHSIAAFPSEEWRIEARFEPEDTVNTAAADGVIVATPTAGWVHFLKGRDLRYLRVTVO
KNNLRALESNSSTLGVQYHRFVDIPRPDAEGNTIIDFNRAYLPKALNRKFLCPSPSLN
NHLNLTVAGEAKNVVAGG

>RXN00953 TRANSLATE of: rxn00953.seq check: 8687 from: 1 to: 753
MAPPTVGNVIMQSFTQGLQFGVAVAVILFGVRTILGELVPAFGQIAAKVVPGAIPALDAP
IVFPYQAQVAILGLFSSFVGLVGLTVLASWLNPAFGVALILFLVPHFTGGGAAGVYGN
ATGRRGAVFGAFANGLLITFLPAFLGLVLGSFSGSENTTFGDADFGWFGIVVGSAAKVEG
AGGLILLIILAVALLGAMVFQKRVVNGHWDPAFNRRERVEKAEDATPTAGARTYPKIAP
PAGAPTTPARS

>RXN00959 TRANSLATE of: rxn00959.seq check: 3462 from: 1 to: 456
MTVIGIILGSLFGVLAVLLIVVGALGWAALKPGNPVVGIRVPEVRKSSQELWMAHVRAGP
LWLVSQVSVFIASLVAFVAGSMWMLVVALGVEAAIAFIGMGAGMAAHTVAMVDKRIRET
PQAPVSABIEEAGGVTTISADYQQDSDAECFQD

>RXN00963 TRANSLATE of: rxn00963.seq check: 4671 from: 1 to: 837

MRLATIRNTGTTIAARVESENTATTIEGFANVGELLQESNWRLEAENAAAGEAVTFENKEL
DAVVPAPKKIVCVGLNYANHAKEMGRDLPDPTFLVKFPDALIGFPDDVVPVPEWANKALD
WEGEMAVIIGKRARRVKQADAAEYIAGYAVMNDYTRDFQYAAPAKTPQWHQGSLEKSA
GFGPMWTPDSFEFGGELATYLEGEKVQSTPTNDLVFSPEKLEIYITHIPLDAGDVIIVT
GTPGGVGHARNPQRYIGDGETVKVEIAGLGFIENKTVFE

>RXN00971 TRANSLATE of: rxn00971.seq check: 9758 from: 1 to: 318
KALSIGTQWQAVMGINHAAEELDEALSPLINRLREMGDPTEETEEANSALHSCFPFVVN
DKRPSAFVCAIHAGFIQESLGENNRIQLELKPLNAPGTCVKHVFESE

>RXN00991 TRANSLATE of: rxn00991.seq check: 2362 from: 1 to: 1380
MDILISILSLGFLVLLTASTGLFVAIEFALTGLEKSTVETHVKQKGDSSARAVQRDQHNL
SFVLSGAQLGITITTLATGFLAEFVLAKEFTTFALELVGLNESASSAVALLIALLVATLTS
MVFGELVPMKNWAIITNPLGVARFVVHPVNWFMVLPKPFINGMKNKSANFIVKLGIGEPAEEL
ASARSSQELTALVRSSAESGGDLQNTAAVINRSLQFGDATADEFTMRSTIESLRATDTV
NDLIELALELTGHRSRFPVTEGDLDETIGMVHIKDAFSVVQAEATMTVRDLARKIPVVPAS
LDGDSVLNLAVERSAQSQVILVADEYGGTAGMVTIEDVVEEILGEIHDEHDDSDAERDFQOF
GASVSVGLVRIDELEKRVGVSPDGPVETLGGIMYTVGAIPRVGDVALLPLTDPTMTD
EFESGFSGRWIRAVTVMEDRRIKAVLTPITHEEAKEYEK

>RXN01004 TRANSLATE of: rxn01004.seq check: 9066 from: 1 to: 1062
VSIWATVLLIIIVLLSANAFFVAAEFALISSRRDLDSLVSQKKGAEKVLYATEHLSIML
AGAQGITVCSLILGKVAEPAIAHFIEVFTSWGVPNDLIHFISFVIALAIITWLHLIFG
EMVFNKIIAIGPETLGMWLPVLIADFVKITRPLIEFMNWIARLTLRAFGEQKNELDSTV
DPEQLASMISSRSRSEGLDAAEHARLSKALRSEQSIKELVKDEVRTLAFGKSGPTLH
QLEEAHVRETDGFSRFPVTGRDGSYLGIIHIKIDILPRILADPEMPDSEITPRSALRPLSNVDA
DGLMDLVLDGFMHYRSAHMAQVRLKGELLGVITLEDLIEEYVGTVMNDWTHESSDD

>RXN01016 TRANSLATE of: rxn01016.seq check: 586 from: 1 to: 648
LRPYAIVGLVILLPSSWLPNRAWAVLGEVSLVPAVVFGGGFLILSPMELFSGALVRYGVV
DRAENAPRAMGVFFAVASAAIAPTLIIQARDITSSGFSIVSTVAGLALGVGVISILVRLAL
HTPIRGALAAVFAPLGRMALNTYIGATILMLIGGLIIVDLPHSTSWTATVLLAAGILIIQE
LLSALWLRYHTQGPLGYLWRVWTWGSRSRPFILTRAS

>RXN01023 TRANSLATE of: rxn01023.seq check: 9173 from: 1 to: 978
MSAVNSAGRPANGINKTPMIIALVLSIVLVAVLFGARVLLGPAGQQIAMSGLPAPDA
ESAECALLEDLPGEAFGHTRAEIMDPVPPGAAAWSTSLERVTLRCGVDMFPQYATLAN
TVDVDGTTWLPVSDMTPGSSLETWYSVNRFPVVAITADDISTDSADNPVAFSSAVDKLE
KRDGQGFADPLTGLSAGTTCTSLFDALPRQLEVGDDGTTVERIEEDRMQAAGYSDDAV
AWDTPGLEPVIIRCVGEPSSENYAAGAMLQDIDDIFWFEDTIIASGTTSSTWYALGREIDI
AVSLPQAASSSLITISGFIEDTVPAE

>RXN01028 TRANSLATE of: rxn01028.seq check: 7950 from: 1 to: 2049
VIYPPPLTASEEKFNKITSVAASVSKRPTTLPLYFRADGSPTRGFANFSTGGIHGAENEDR
FDHQDQLHTVATREFFAILDATLAALYAAHQAEPSADYQIAQDALAWAKNVLSQKLI
KSPQLYNPETGVTYEWEFVAQAAMWIRNKPEVILPTGESMTVKHKSVLASASYPLRNDV
AYWRSEPKTQLFPVAKSGGSSLEKKYNTSVGTAIHEDFSSYYPLLTNMAAFNADLG
IDEKTRGRPRDREIYEQKEIYGAQRKDPDSIDEETKQRLGILREGTKLIINSATGAADAG
HDTPLIMNNRVIAMRIIGQLFSWRIGQAQSLAGATIIISTNDGLYSVLDMGTTNQRVLDH
ATAIGVQTEPEELDIVSKDSNRSAEFLNGYINAAGDLACWDGPNRSRNSLDHPAFVDHVL
VKYFQLVNNTVPEIPEPTELEGVPLDALQPMNHRVSKIVATMHKEFEPKLLSFYQNI
LASSRGSNTFLFSVPYIPATEGEETHATDTSITATPTLSFDAYGNKAEVMPQSTVDKR
VPSLLQYYTRTFHVQRDQTQAVFDVIGANFVLIARAAKASISPASADSRKKGLASTNAD
PVAKHVLIEIAGADVESLRHEKDLKVTKHTGQDPLPVVVFNDQTIWNNPDDVILNALLGAI
DQDAYIDMAISSYKSWHNIIPA

>RXN01069 TRANSLATE of: rxn01069.seq check: 984 from: 1 to: 714
VNDLPNLKPLFPNWTWVLATVATTVVLGAGILGYVYPSLPDPMFVHWNGSGEADNWTPKS
VGSFLSLILIGPILILLTSGMQALLTMQSGVITQRGAKSANEAHQWETKYATSMHMG
WYMFVNLALILVMILNEFRPNPLPGGFIIGLIGIIAATIVLVLIKGTSTSLAKKYPMPD
QDGKWTGFIYNDPDDNRILVDTGMGMNYTFNIAHTWGKIFAVLIFAVPVILVLLTVLL

>RXN01071 TRANSLATE of: rxn01071.seq check: 172 from: 1 to: 2064
 LVVDSSGRYNVTITGLTTTETDSATALNLQMSAEGYLERYTDGATVFSVMSAADGTTTPQ
 ELVDALAAELGNSFDVETGEALVEQATGMTQALS FVQYFLVAFGLIALLVGTFTIIANTF
 SMI VAQRMREFALLRALGAAPGQITRSVLEAT IVGLFSGALGVLLGGMGLVAII SAVLNN
 LGMPMGSSVGLTPSAVVTALVLGTVTIVSAWAPARRAGEVVKPEAMRNMEITTMRSMMG
 RTITGGIVLALGII FAIAGAMMTDSSTATRSILVIGIGALFVIVGTFTLFSALMSMPVVGGGL
 KKVIGAPFGSVGLAATNSKRNPRTATTAFALTLGIALVTAIGMLSATMKDAVSDMMAE
 QYTADYILQQPTNGSITMEKESVNDVRDAEGVADVVLVSMNSASVNGQASYSQLGQSSTF
 VADGDLASKVISTESIDGSLDLSNPGVVTNTQTFADENCWAVGDTLQLESMSQOTIGDIELIG
 TTFGNDIAENMI ISESSLADTPAADTAVPQMMLVVEEGFDEKQELRTNLEDAVADYIIVIS
 VKSATEFAGMETVAMIDTMMNLYALLALSIVIAIIGIINTLALNVIERRQEIGMLRAVGV
 KRQGVYRMTITLESVQIAIYGAIVGIAIGLGLGWAFVTVMMSGEGDLAAVSPWGQVGLMLV
 GSAVVGVI AALWPAVKASRTPLPDLAITD

>RXN01075 TRANSLATE of: rxn01075.seq check: 2212 from: 1 to: 411
 MDNPVNILNQEALERLQSVSLGRVVVRSDDEMI FPNVNFIVDKGAIYIRTAEGNKLFSM
 NLNHDLVLEADEVKDKAWSVVVRATAEIVRKLEIATADTLELKPWIPITLKS NFARIVP
 NEITGREFTLGEPEPY

>RXN01085 TRANSLATE of: rxn01085.seq check: 551 from: 1 to: 879
 RRRKGGLDPNSPEAIEQAKKKGERKARNERCRKNFKGGGKDLKQTDRTFDQLRQQRVTD
 KARNRDVHNEQQQLARGEIGEMRSPMWVEVGAAILGVFVLVVMWLAWGGIGLLIQTMMNTG
 SPNDKELFDELGVRYPYVAVEQQIGTSSAHTTCYQPLDEFGNMFGDCTRSVPKPMVWYAD
 YVASVFAEHGFDAPEDINDNSVGSWLLFGHVGI IRVTFVIAVAAGVYAMSRAAMRQLETQ
 NVAVDTTDINQHTNDARLAI PQEIVRDLSLFDPDGAHFTSPALKHDFPCDAVE

>RXN01121 TRANSLATE of: rxn01121.seq check: 3374 from: 1 to: 1086
 MNPEFIHGATEIETNRLGRPHRLSKEIVERYCDPQFSAMERQPSGVRRVCRITTSVTL
 TTYSTRVVYLDSCRPGKIDVLIDGAPTSTPTSGGETTEVNFTGATERRLKDQOVLTV
 DGLSEQEKVVEFWLPHNEEIEVISLKAANAINTVEDTRPVWNYGSSISHGSDVATPATKI
 WPAIIVAGSKNYNLNRNFGGGSAMLDPFMARLIRDTPADLITLIEIGINIVNGDVMRRRGLLE
 AAVDGFINTIRDGHPITPIKIVSPFYCPIHEKTPGPGAFDTSFGSGQIRFIATGEQDEH
 GRLLTEMVREVLEGFVEKQDKPHLTIVDGSQAASDAPLLNHLHPDEASHALIAQPLQL

>RXN01128 TRANSLATE of: rxn01128.seq check: 7667 from: 1 to: 1014
 MSFTFIRTFVFLFGITLLVSCVPEPPDSYTKESTVLRYQVSDFNLFVELAVALGLNNI
 ELQVGVSVQGGVESIESLKKDDIDFAAVPFVILGAVGEIATGAPIKAVAASYGISHDSSA
 LLVLKDSIEIHEVHDLIGKTVGINTLGAALGSAMVERHLFDAGLTETEIVSVTQALPGEYL
 EQLRYQQGVDAIIVWTDASAKHQALETGDFRI LAEDSDLVQELNITGCMVVSQKLI DEHPAVV
 GELVDVQAQALEFERSHSPFEEVRYVFNYLEAHGQSDRISSFRYWEHSIGIATRGVLSDR
 EFSMWSHWIDRQYDVPDINPASIYTNQFNPNYRKVNPS

>RXN01134 TRANSLATE of: rxn01134.seq check: 3892 from: 1 to: 771
 LSLDQVPYTAQIVPLAIVLITLLDAEEMATARSWRNLNQFWSGVLGELYGS PAVIARSGR
 TDQVAAWIREGAGETA VPKTIRDTVFHESRLSATQDTGVNKGIFALLMGRGARDWRT
 GQQFDRWTFDELGCNFHQIFPTKWCKERGIDPVLTESVLNRTPMGRRTVEVIGDTPFSRY
 LSRVQSKLMGDEEFQDMLDTHLLSAEDLHSSNTTHFFASRRTNFIDMVEDAIGKAVIRD
 VNESDLTGGHDGSPSVHG

>RXN01140 TRANSLATE of: rxn01140.seq check: 3026 from: 1 to: 933
 MALDTRGEEMRFRPRALSGAPDTGKDPGLLLLDGQRLTTLYHCFSGDGYVNTVDFRSKK
 VTRKFIYDVAKAVESPVMSDEAIFSVDETGKIISHFGPVIDGGITDLETALAHGLPVS
 LDDNGTDFLFDLADMAGEGAREHAKRFQSQIVKTLVSYDIPMIRLDRETAKGGTGSIFA
 QANSSGLQMDVFDLLTAVFAADESVETESFLRDDWVRVERNLRQHSALDGI GSTEFLTAV
 ALLVSARKGHASGYREDLLNLTLAEYIPAADEMTKGFDEAAEFLLRQRCIFESRPGSIHRA
 DCSTGRDPHPA

>RXN01148 TRANSLATE of: rxn01148.seq check: 3053 from: 1 to: 600
 MTPSPVENVKKKPRPLALSFRAGDYQQCPLLYRFRAIDRLPEPKTVAQVKGLVHAVLEY

MHKLPREEREYYPAMVKQLKPTWQMCEEDAEKELVPEDELYDFLVSRTLLRGYFEMEN
PQGFDATECEMYVDTVLPNGVFPVRGFI DRVDTAPPKSELSTTRLARNSQSRSGASKRSSR
CCSMHWSTGACSMKSQLSFV

>RXN01153 TRANSLATE of: rxn01153.seq check: 8673 from: 1 to: 543
PFLSPITVSTHAVVAYSTARGFGEHRVWDYAQESPLRDTRGFDLRRYHQAPVVDPAHIG
VANVPVNGARFYVDHAHPEYSSPEVTNAWDAMVYDAAGDHILMQAVSDVASFTSQNRSS
LDGHDPCPALKIYKNNVDGKGASYGFHENYLSRETFDVLQAQALIPFFVCQVIGAGR
V

>RXN01154 TRANSLATE of: rxn01154.seq check: 4612 from: 1 to: 639
LSKKISLETTLNRGIIINTRDEPHTDADHWGRLHVIIGDANMSQTANFLKFGMTSLVLDAI
EAGVDFSELKKNNAVSEVAKVSHDLSTLHQLRLADGSELTAIDILRRYLDKQVPPFAETPV
EQRVTLWGEVLGLLLENDLLSTSHLLDWTAKLALIKSFEARGLSINDPKMYLIDLQYSYDI
DPQKSLYHALVSKGRMKTLCQAQDIADAAATSP

>RXN01155 TRANSLATE of: rxn01155.seq check: 3917 from: 1 to: 1470
VESALTRIRMGIEETEYGLTFVDGDSKKLRPDEIARRMFRPIVEKYSSNFIPINGSRLLYL
DVGSHPEYATAECDNLTLQINFEKAGDVIADRMADAEESLAKEDIAGQVYLFKNNDVDS
GNSYGCENHVLVGRSMPLKALGKRLMPFLITRQLICAGRIHHPNPLDKGESFPLGYCIS
QRSDDHWEGVSSATTSRPIINTRDEPHADSHSYRRLHVIIGDANMAEPSIALKVGSTLL
VLEMIEADFGPLSLELANDIASIREISRDATSGSTLLSLKDGTTMTALQIQVVFHASKW
LEQRPEPEFSGTSNTEMARVLDLWGRMLKATESGDFSEVDTEIDWVKKKLDRIQGRN
LGLDDPKLAQVDLTTHDIRPGRGLFSVLQSRGMIKRWTTDEAIIAAVDTAPPTTRAHLRG
RLKKAADTLGVPTVDWMRHKVNRPEPQSVELGDPFSSLNPOQAQETALSILLGGTSY
IAGEIATLTF

>RXN01167 TRANSLATE of: rxn01167.seq check: 6639 from: 1 to: 396
MADRVLGRSGRMGAVSYETDRDHLAPRLVKYKTADGEIYVEVPADDAEIPPEEMCKNGK
LGILMEGEGVESKVPKPRTHWMDLRERRSIEELDVLLEERIEALRKRNRNAAKLLKAQQ
EAEAEKAAEEV

>RXN01169 TRANSLATE of: rxn01169.seq check: 2636 from: 1 to: 996
LKRUVFEAWDRFIPLIYITALIAGALVGLQWPGSTGGFESAINPALMALLYATFLLGIPITR
IGAALKDLRFLIVLMSVNFVAVPLVAFALSRFIAGDEALLIGFLVLAPCIDYVIVFAG
LARAQAQDKLLAATPILMLVQILLIPVFLAVFVGSADALGSISFGPFVEAFFLLILIPLVAA
AGTQQVARKWQVGRTIMAAEAEMVPLMLTLTFAVIASQVEAVSGQFTDIATVVPVLYVAF
LMVMPIPGGGISKLGGGLGFKQRAIVFSGATRNLSVLPLALALPAGLEIAAVVVVTQT
VELIGMVVYRIIPLIFHEKQYTKRLSGIGES

>RXN01173 TRANSLATE of: rxn01173.seq check: 4063 from: 1 to: 615
MHVSTLPNKKLTRIFAGTAVALSLGVASCSNAEDAVSDATDAANSATSAAGSAINDAT
GTSSASTTEPSGTSGSDSGSDSAGGDTTEVESADGSTISIPTAVVTAANAAGFSTPESVE
EGPNGESLVTFFEGYIVNSAEGGAQALVGMIGETWIGEGGLSAAVGLPTGPEEATTNGWT
QQFTSGVSWLDDSGQFAASVEPA

>RXN01174 TRANSLATE of: rxn01174.seq check: 9196 from: 1 to: 750
MSNMQGNDSSKSSGASRAESPLIKFRTLIIIVFVILIVGLASIAVGPPVVQILMGPVGT
EGIQADGAAPASTDMNGTWDVAPGSIPTNTSAGFTFAEILPGEKITSGSTTGVTGEVVI
EDNSLISGLITVNMTHITTDQEKRDINVRTKLFHTDQYPEATFEVTDSDVLSALPDTGSI
AQVVIPEGLTIHGETKAVEPTFDVLTGQVIVASDIEINRLDFGVETPEFIIAAKINETG
EINVRIVLEK

>RXN01206 TRANSLATE of: rxn01206.seq check: 3690 from: 1 to: 300
VSAENTENTDPSFEISFDDHRRPLQALKFGSIALIVFTLISLAIWATRGVPGVSAVV
IGAAGVAGFVLLTALSVLFTTNSNVTTGAVVGLGWLKI

>RXN01210 TRANSLATE of: rxn01210.seq check: 8240 from: 1 to: 831
MTTSTHTARGLQHATPERRKTSFFKTSLFKAEWLQFRNRKTLLEMATVFPVPGIPLLLFLIG
NGGAASEANSFDFYVMYTLLEFQFYTVLSMATTRRDERVLKRLRTGEARDIDIIIGAICFP
GALLTLIFTVVIIPLMLVLAGAPINLVPVIFAVLIGLLCSALALMTSGFTRNEAAQAM

TSPVFMALMGGGLSIRFVFGDSIVADILAYTPFAAISDLVQIGWAGATFADSVGGVEAA
NFAGIFQDMLIFLGLILAAWTAATAAANRYMRWDSYR

>RXN01229 TRANSLATE of: rxn01229.seq check: 2418 from: 1 to: 1278
MIISTNTAGHPLHEPHVPSHHNRNMTLRAGVLGANDGIVSIAALLGVIAATGASDTVVFVGA
GLASTIAGAVSMALGEYVSVSQRDTERVLIKAKEKLAEDPTAEHVLESEILHSYGIXX
XXXXXXXKXGCGDALGAHLQLELGIDNEQLTSLPAAAFSSAVAFLLGALLPMVXVFVXAP
XGWDAGVXFVVTLXLAXTGFISSXXXGTXPMRXCXXXXXGGXLLXALTXPSWXXXXXX
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XXXXXXXXXXXXFXXXXXXXXXPLSGEILLAGLGEIGMGEPRIPVTTGDLERGLCQLCKGL
GQWFPVGGHGMIRHFQRRPGEKGHQQTTLHRHPQCDQGVGLARAHVDQGVPGQQAC
PALRRV

>RXN01231 TRANSLATE of: rxn01231.seq check: 7153 from: 1 to: 243
MLGYTFVIFILAPFLILGTIAMAPAIRSRFPWYVKLFEGGHGARSLEHIAVLMVTGFGVIM
HVGLVFWSMATTWTWSSAI

>RXN01246 TRANSLATE of: rxn01246.seq check: 4104 from: 1 to: 507
MKRTITIAALALSTLVLVSACADNTEGENTDTTIIATTSAPDTTETTGATDPETETGAA
GEVSAEHNADIMFAQMMI PHHQAVEMSEILLAKDDI PAEVIEFTQGVIDAQGEPIDRM
NTMLETWEEDPVTGDMGEMDHGMSGMMSEEDMTALEDAQGTGRCPALP

>RXN01249 TRANSLATE of: rxn01249.seq check: 8446 from: 1 to: 471
SQIVASVSHGLTTIQEIDVKRAIAAALTLTGCSAADPEPTADGTVSQDTFLTTHGL
AAMDAVEI IDHLDRQKVTERPTDIASVRADELLSSDDQEVVVDLPDQTYVSIAPYLN
STHDCFYHSITLCLGDLNEDIHVMITDEATGEVLFD

>RXN01251 TRANSLATE of: rxn01251.seq check: 4314 from: 1 to: 309
MTQPMDSQILAAQQMQAQLQAAQCEILATTVVGNAAGLVTVMAGNGEVSAVTVDPKV
VDPEDVETLQDILLGAFKDAHNKVANVAEEKMPLSQGMGGIF

>RXN01263 TRANSLATE of: rxn01263.seq check: 84 from: 1 to: 912
LTPYDPTAVNKSEKEAAKNLFGAEALTVPDAGEVVDVDRVDFYPTAKAKKRDYPSNYAA
GCHQEVNETSPESCVCYGDKNDSFVALVGDSDHAGHWLPALPEIAEAQGWRLVEYTKSQCP
LISTAKLGSETFYAECYEWNEKLLAKLTGPSAPNHVIVSSQRYASANFLDSDVATGTVSE
GYEMAWNLSLKDAGVSIISVLLDTPRPQIDIPECVASNRDNLSECSVHRSVALGTEAHPQOK
TAAQNDIVPVLDSNWCPEEYCSAIGNVLYRDSHLLTATYARSLSALWNLVNASNG
EPFK

>RXN01266 TRANSLATE of: rxn01266.seq check: 6088 from: 1 to: 1035
MPKVSVVTGFYNRCEHLERTIESILNQYTSDFELIVFDDASTDGTASRLLELKEKYDDPR
FRFIIEENKGFVKGLSEASIGAKQYIAVQSGDVSLEPRLELQVEFLDANPSVGAAGG
ATYNIQEDTGTNRPNQRFKPIATFDDLLTSNPFTHGEVMYRLDLYKSIIGYRSGETFAQD
RDLWLRLMAKKADLGIIPDFLYHRYTLLDGVSFVPDKTIRQRCFSAAVRLALMPPEEGAL
AYSRLAEGPTAVVPIADRAVQKVFVKAIRLCYGAPEGLHMAARDYIQNLRRITRVV
LISYSSRLIKPLQDILYKSIKGVSIKPIKSLVKFTTRIQGK

>RXN01275 TRANSLATE of: rxn01275.seq check: 5209 from: 1 to: 918
MEKIRSPAVQSDALQVFKSALAAVTWWSVNLNSQLPFLAPFWALMTMQFTVYHTFIS
GIQTALASVIGVGLSFVIGTYLDVSVVTFGLAMVIGIIGARVFKLRAEGIGIATTSIFLL
ASGFDQQPLLYDRILEILLGLVAVAIANLIIFFPLRDQEANMMVGNLDRRMGEVLQKMA
DELAEKWNIINADEWLEEINSINNDLEKAWHSVRFRVRESRRVNPRKIRIQEGRPQTETS
YESNLTSIDEGIAHLRLARLRTDPIIDSDGWSGIFATVGPYARCSFARRESGNGRS
YRPRAL

>RXN01276 TRANSLATE of: rxn01276.seq check: 3553 from: 1 to: 444
VSSELSSGTSSESDSDISNRDIIFGIAAAVGGLIASGVHVAQQRMIPNPLPG
IIPNFPALAPQAPAPAPAPAPQAVAPQVAPQVAPAPAPVQTNRTYKNCTEVWNVLG
RSIRQSDFGYGTHLDRDRDGIGCESRPR

>RXN01281 TRANSLATE of: rxn01281.seq check: 193 from: 1 to: 762

VGLSRSHYQLAAENTKSLVRMVPMTVPQGNPAKKLATDLNRNQVVDLSAAVSRGQLTL
EEFEDRSSKAWNARHLDTLVELISDVNDNPYTLGLQQFPGASYAPAAEYETTPAMPNVSD
PNVIVRNRIITGNPGSKMSVSFMGGTVRKGWVHPNVHTSFAMMGQNIDLRDAELES
IQINAYTFMGGIEIIVPEGVFVICDGMGIFGGFEQSVDKAGALNPARLPSNAPT VHIKGL
AFMGVSVVTKNNI

>RXN01296 TRANSLATE of: rxn01296.seq check: 1595 from: 1 to: 1083
MSIEQAITSLSAVRLEKPIIETEEATKTALIIPIFSINVLGYDVTDPREVIEPYTADVG
KKEGVDFAIKTGDDEHFLIECKKVGSPSLDHANQLVRYFNVDTEFAILTNGEIIYQV
GOLDAAANRMDAKPFMTLDLNNIDARQFPHLEMTCKRKHFNQALAAANAEELKYIABLKVV
PQQEQEPDEIVKMLAATVTTKRMTAQNLEFFTRLVNTASSQFLKDEVNRRRLRSQAQFED
ANVTQGDADAETPAEDEAVIEEVSEIVTTEEIIHGSIVRAICCEVSAQETIMRDAKSY
CAILFQDNNRKPIARFYFDRKI PRIGIFNAEGEQEHFDESIEDIYNHADLLHSRVVALN
A

>RXN01301 TRANSLATE of: rxn01301.seq check: 6647 from: 1 to: 525
LIVDTQFEKIPAHDDVVGIRVILSSEDLPELFKRGYAEVKKFLRLLEGIEPKGPARAYVFGD
VSDTVDLIGFVPSPAQAESLRGALSQSGGIDDDVVLHHFRDMKTMHSRHSRSGPFGDVER
VWDEILDEVEDLGLCTLSPSSSIGWEEYIEGPATADTCDQLASEVYVQVCQAPVKSA

>RXN01306 TRANSLATE of: rxn01306.seq check: 7259 from: 1 to: 1008
MTEWVVLVPATILLIALSAFFVIEFALLAARRNRLEETVTSRSSRAALRSLNELMTL
AGAQLGTMVTFALGAIKTPWVHYALMPLFEWARIPLVMADVIAFILSLFIITVFFHLVIG
EMAPKSWAIAHPETALRTIAIPARGFINLFRPLQWINKMANDLVKVGGETPVDRAAAGG
YDPTDLHALIEHSRETGALDQQAQISGIIKLDKTIPTVQTLTASPTFHSASATVAEVQA
AAQSGSLRVLIDAPSHLFPVHVIRDTLGASPOEKAKWSRPILTVAETDTLHQALEYM
REHNEQISAVLSADGKTVLGVITWDHILKYLWPASV

>RXN01324 TRANSLATE of: rxn01324.seq check: 6882 from: 1 to: 300
MSNSECHTHGYIEEKQRYLARLKRIEGQTRGIHRMDEEYQCIDILTQISAVNSALKNVA
FGLLDDHLACHVKEADLGGDELDAKLKEVSDAIAIRFSA

>RXN01326 TRANSLATE of: rxn01326.seq check: 1197 from: 1 to: 366
MAFPVTEDKILAAEETLGRRLPETLRERLLQNNNGGEVIDENNDWILHPVRDSDSRKRLV
RTANDIIRETESAREWDNFPENAIATANDGTGDLIILLPDDDAFYIWSHEDEPLEITELE
DA

>RXN01331 TRANSLATE of: rxn01331.seq check: 1587 from: 1 to: 2397
MLTTWIAVLVFTVPGLVSVWGLKVPWAIAASIPATFGIYGLSAWLLGLWEMRFDLHS
VLTILVFAAVALVWRLFFVGGWLVRRRKARIRRQTLADEERAENAIEVSGAGEPAESSTNE
AAESESETSERGGIWRVIFDYMRDGGILDHRWLLPAAGAITGAWLIIIDRAVLLLLSTEHG
LGDIVQGWVDVHHASTVRFIDETGIASSTMMGQLRNIETQQDLFPYSAWHAGAWLSDVG
NLITVEATNLITGIVLSGLLLPLAVALIAWRMINNRGLTAQIGAGFAGLITIASPVLFWVG
NYVGAWPYVAAIGASGVVLA FMSTPSVPVRIFAAALA FMGQFLHPAPSTIVIMVLLW
WLLKLVVVPSQKVKGWKAGIGIRLKDVGILAITGIGVLFMLPQVIVSGSEQTEDVLSYSA
EEQVTRSESULVSI FMETRHVDFFGNIDIVPVLVFAAIGGVVALVWRGNLWAPVVFYFASV
ALTANSIKPFEFPGWDLNVLVGLHYSTGHRLIMPVAMFTFAAGIGAAAVRLICLGPRI
KFKFTVSGSVSVVMALVAVPLQTKWAKDFVEEGSETTILAPHNDEMRVSNNDLAAWDWLI
QOPGGADMNIMGDPADGNGWMYAYNGLHSVARHYAWPAAGEGATAMLFWWPQLLGVGTD
ENPDQVNDVQAAARDNLVGYFMISPTWTFWDEQIPNERQIDLLWQTPGVTEPVCKKGDVSIF
AVNMDFTDAELDQMRAPGNSPELPELPTLGBELGAETEDVDQTYHRRTPVAGVNSEM
PSAETLYAPDPTPKHTVFN

>RXN01337 TRANSLATE of: rxn01337.seq check: 282 from: 1 to: 1413
VTFRGNGTGAHVAVVSGSGNGLTTAAVLSAKAGQVDVYEAAPT PGGAAARSESVLGEETI
SDLGAAGHPFGVASPAFHYLGLDGHLEWAYS PFAMAHPLDYGRAGLLETSLPETAKKL
PDARRWNKLHQGLTKNIDKHLANLLGPVLKWPAPHPIRMAKEGFPALLPAKRLASAAFEET
EARSFLTGSAMHSVTPPHKPMATASLGLFGALGMSRGWPVAVGSGRIVDALVNVVNIHGG
GTIHCDQSQIDSLSQFRDITDAIINQTPSQVLKKGTDNLNAGLPQRMSTWQKHGSPSYKYVDY
LDEPIFWSNFPQVGQATTVHVGGSSIEIAFAEA EVAAGRMPERPFILCQQVADPSRAR
EGRHVWVWAYAHVPRGVFDKRAALLITAQIERFAPGFRDRIVHSVDTNAEDLEAWNPNVLG

GDITAGSALLRRMPTKIGEKTYMASASNAPGGGVHMGPGWAAQVLADHR

>RXN01351 TRANSLATE of: rxn01351.seq check: 2597 from: 1 to: 585
 MTSLFDAPTLQRVTFTGSGALGSSSYTQAAQTAKTAVDRGIDLTVGGGKVGKLMGIVAD
 ALESGGGEAFGVITESLMKGELGHEKLTLEITVPMHIRKRMAELGDGFIAMPGGAGTL
 EELFEVWTWQQLGIHQKPVALYDVGDFWQPLLEMLEQMTQRGFTRKDFEFECILIVESDPHA
 LLKAMQJTWTPAPKW

>RXN01362 TRANSLATE of: rxn01362.seq check: 8917 from: 1 to: 3654
 KWLGTPAQSLFLIPVPTQHARTGTHLYDSLQLLFTLVVDKGHHPTDAKAVAFDAEAGEEGL
 HFRNLASDLFLPAATELIDRVGLSNEALNKVLENNLLSRVQSGKDRGFISYATLTVGTGELG
 QYIEGLMSYTGFIQAEDLFEVAPHGKADKGSWMLPVSKADEVPADSFIEVDQEAEPGGVTL
 KVRKRHRPRGSFVFRQSSDRDRSASFYTPQVLTSTFTVQAIIEELQASKRITTANDVLSLT
 ICEPAMGSGAFAVEAVRQLAELYELRQEELEQQIPAEADRAKELQKVKAHIALHQVYGVGD
 LNSTAVELAEISLWLDTMNAEMDAPVYGLHLRNGNSLVGATRSLYAPSLNKKAWLTATP
 TRYRLDDIAQAIIDENKAEPFLNHGIHFFLLPSTGWGATADAKDLKDMATEKELKSWRT
 SIRASLQKTIQKQLNNLALRVETLWRFLVMIRIAESQISRSRTLWGQEPAEVSEVVTRE
 QIEQDLFGNIDGAYNRLRLVMDAWCALWFWPLDAVATAEHPERPALPDLEWLATLLEIL
 GIDLPLKSKNENQIVLGPDTNWLAINDEAATDLGFSGALSFEVRSANHPWINVARQVAKQ
 QSFFHWDLDFAHVFAKGGFDLQVGNPPWVRPDVNFEDLLAEHDPWVAVMSKPTQASKKER
 QRNFHNPNKSLHEHVSAGGEPVATSAI LGSVTLYPHLKQRPDLIRYGFMEKWTNSNASPAG
 AISLIHPESHTEKKAAPLRGAYERLRHRHQFINELILFDVHDLVKYGVHVVYQAPGESI
 NFLSAASLYHPQTVLDSFDHDDGSGNLPGLKDDNGNMDRRPHKDRQLVNAADTLTVWKSIL
 EDEQTPYLDTRMVYTVNTEAAAALEKLASAPRIKELGLQFSSGWNETTCKKKGYFDVGTG
 YPASWSAIIQGGPHLG VATPMIQPNPTMKHNQDWEIDFEAIPANFIATAYQPDRTQK
 PTYDADYGTWTFGDKQVPVADTFRIAWREMAATTGFTVYPSVLPFGANHVHTVNSAASR
 SNLKTILVGAQLGAILSDYFARSSGSSHIFNDIVRKIPLPNETSLEKQFARTYLLRLNCLT
 SAYAPLWEETIGEPDWQVQPLRNAEQRRAAQNDIDAMVALSGISADELCMIYRTQFFVM
 RRYDQEDHDFDANGRKVPKEIILKQQLKDGQELSVEKRTVWHPQSEVSYTFEYPPFVRLDR
 EADLRAAYAKFENQLKEP

>RXN01379 TRANSLATE of: rxn01379.seq check: 3028 from: 1 to: 942
 MSAPDSILNVEEWISDHYLTNDADKAGSFSKRVRERKEWKTTEADTQQSGPLTRFSSNR
 LQLQHALSELDATTAAASLVASALGYGVFSARHAQRGSDTISYSSWVGNAGSVEFLAATP
 AESFEENFRSLPLEPVAVNDKPKQDITAAKLVGQIFLSDTPPAFVVITAGKWVVLAEERET
 PLGRHLAIDISLVVERNDTKAQGEMQQTVALARENTERAADGTTWEEITEQSREHAVK
 VSGELRSAVRESIEILGNDVLTTRYEAKELSTAIEDGGELAKQSRLRYLRIELFLFAEASP
 ELEILPTGTPEYDE

>RXN01390 TRANSLATE of: rxn01390.seq check: 97 from: 1 to: 657
 MFRRSLPSNKTSSASSASADTSYSVRLGRPEEPGYQPEPSYSEPYTDSDFAPAGAAAAA
 AAVAFAPAYVIDGGVEEASGTPTSSSESSVAATAAPASSETAAEYRAMLASLVDKGRAPGT
 GYDRELFGPAWTDTVSVEYGHNGCDTRNDILQRDLDDIQLREGTKDCIVTSGLLSDPFSG
 ELIDFVRGERSGDVQIDHLVPLHDAWVKAQQWDEQTRKFNANDEPNLLAVKGLTNLQQKG
 LSEPLMLALILITIVVGLQFTGPGKISLDSGRGQSVHW

>RXN01391 TRANSLATE of: rxn01391.seq check: 3163 from: 1 to: 690
 VAAVAFAPAYVIDGGVEEASGTPTSSSESSVAATAAPASSETAAEYRAMLASLVDKGRAPGT
 GYDRELFGPAWTDTVSVEYGHNGCDTRNDILQRDLDDIQLREGTKDCIVTSGLLSDPFSG
 ELIDFVRGERSGDVQIDHLVPLHDAWVKAQQWDEQTRKFNANDEPNLLAVKGLTNLQQKG
 AGDAATWLPNTAFRCDYAKKIITVKDRYVNVWTEAEASALERQLDTCAA

>RXN01400 TRANSLATE of: rxn01400.seq check: 8655 from: 1 to: 1500
 MAISVSMFKAISREELERAWLEVIERHGTLRTVFTSGMGGVEYQQHRIDVGPQKWDHAVA
 PGESINEALRAVLNQCSPYSRPSHSLCIDAHAPRPTVIIIGDSHSHVMDMSMLVIVRDL
 AALDMELFPVEPPLAFESHTAELLAAPPAPERIHQRWREILEAGGKMPQPLPLGDATSM
 PERVEVRDIFGVNGLAIYSARARAQQVSSALATISVMAVDVTAALADLPLRAVFPVHSRFD
 QRWHDSSGVGFIENSIVIEPDSDPHTAAQAVREAVSLGSPYLAELLEPWGMPETPGMFAI
 SWLDLRLPLVSIIDIGLQAYVSASRLTDGVMLWFLIDRSGAHLRCRYPDLSLVARENVGR
 WIDAIVAQMRAGEAGTVNLQAGGQELTLRHGTRADISEIAPLLARNAADPCELVLDLEHALD
 LLTHESSHFLAVVRNARKIIAAMQTLIVPEFSRGALHLHIEGFFIIPYRTTDLDKKL
 RAWAVEHGRARGVKVEEVVG

>RXN01403 TRANSLATE of: rxn01403.seq check: 3765 from: 1 to: 648
 LVRGRGYFNAVDIYETSTQPDQEFPPDFDTFSADTPEFQLSAVRADTGEVTFWGREDFPD
 LSALMKRRVRASSTMPGFMPIITYIDGHFYPDGVAGVETGGMLQPAIDAGFTRFFVIASRPR
 DYWRKEIGRPGFIKAALRRFPITADLTIAARPALYNSVKQIILDLEKQGSAYVFFADNMNI
 QNTEINLKKLRASFDAGMQQTRKDWPEIMSFLNQTR

>RXN01409 TRANSLATE of: rxn01409.seq check: 6984 from: 1 to: 822
 WVDVDPDVTARLGEYEMQLTPHVDFGPFRRHPKADDDLVAAALKKRAKDAGVTIPALLPVQR
 ISWPEETQORVAARNIKRIIQLAVDLEVDLTINTEFSGRPERSEDEDAFYRSMEELLPIE
 EKEGKIFNIDPHDPDFVENGIEAWRVIRGLNSKQGVFVYVAPHSFHMGDQAEAILPAVGD
 RLGAUYLSDTFDHHKSHGLRYITNPPGNVVRVHQHLKIGDGDVNFEEIFSLRLSTGYLDR
 EDALVSNVFAEDEAADEVSRYQLEKIRSLIENA

>RXN01422 TRANSLATE of: rxn01422.seq check: 4360 from: 1 to: 972
 MAQRKLASVIGAALASAVLVGLMTPATQSSSGSSSTDIITRALTSBGVADSRAPEGGAK
 VVVFSDSHSTSGTNAPFRTDERGCLKGANNWADQLQSGLGAGGLIDVSCSGASINSQD
 HFSDEVRHAAREGAIGPNTTIDFVQLGKNDQWGLSNVNLLQSVQTCITDVFAGCCGDAVA
 AGKMQDPNAVTAENYAERMKPVIDYLKYAPNAEITLVGQYETARSQSQCVRIGGTP
 VKNDAPALVSFMNKLMDAIDGAAGILGVSHVLDLRSAEGHSDSCSNPDVWNGVFDARAIEIV
 GGPWHPSPVKGDSVTAGIILDRVNA

>RXN01434 TRANSLATE of: rxn01434.seq check: 1389 from: 1 to: 2952
 VILGAVLTSLVIPVLTAEKEDADGGSGFFERRLLTSLVTLGGVTILSIIGAPLLTRMMLS
 SEGQVNVVMSTAFAYWLLPQIIFYFGLFALFMAVINTREVFKGAWAPVNVNVTITLVVLGV
 YMVLPARLHPHEQVGIIDFPQIIFLGVGTTLGVVAQCLIMIPYLRAGIDMRPLWGLIDARL
 KQFGGMAAIIVYVAISQFGYITTRIASIADDAAPFIYQQHWMLLQVPYGIIGVITLLTA
 IMPRLSNNAADGGDRRAVSDIQLGSKLTFIALIPIVVFVTFAGFVPIANGLFAYGQFDANA
 ANILGWLTISFSFTLIPYALVLLHLRVFYAREEVMTPTFIIAGITATKVVLISLAPLLSS
 SPERVVVLLGAANGFSFITGAVIGAYLLRNKLGLLGMRSLAKTSLWALGSAAVGAAAAWA
 LGWLIQAVVVDGFLGLTSSVGYLLNLAVLGVFFIFVTGIVLSRSLPEVQNLQALTRIP
 GLSRFIRPNTKISLDVGEVSEQDFSTQLVAPSEFAATPPVPPMPSAGIVRGPRLVPGAPVG
 DGRFRLADHGGGVQGARFQWQAREIATGKEVALIPVDTSGNAPFAPLSSAAAAGIAYEVQR
 RTTKKLASGLSVAAPNIHSEAYRNGCLIVADWVPGSSLSAFAESGADPRAAAAFALAEITE
 TIGEAEHMGPIAGLONKCRIRINTDGHAVLALPAIIPDASELRDAKLSASAEMLIADTL
 APSDVKAMVTEAQGLATEDNPDIASLAMAAMRTCGLTTEEPHLLVVKKEKTPKPATRDFGF
 ASDYTVKGMMAIAAVVIIILVSLVAAGTAFTLSFFGSSSTNEQSLPLASVEATTSATPEPFGP
 PVYLDLQARTWDDGAGTDVTDVTDGNTSTAWTSTGGDGLLVLDLSTPARLDRIIVITGTG
 SDSNVTSTVKIYAFNDASPHSLSEIEIGTVDSGRSLSHSIRDSKSLPQQVESVVIILVD
 EVRSQTSDTNPQMQUIAEVQLVWG

>RXN01448 TRANSLATE of: rxn01448.seq check: 5425 from: 1 to: 1167
 MAKKKLGTVARLSELDKSLNRRLRVRSLPIVHSAIGAVYAIWAEVVIKHGQFFPAP
 MSVAIILGLSGGDRIKRALETGLGALGVGLDGLIMQITGYWQIFVVGGLALIVASFV
 SPAPLVSNQMAIGGIIATMFPPPGDGGSIDRMI DAFIIGGGVGIILVIALPSSPLDAGRHQ
 VANVLGIAASVLEIDVAASLKAKDAKLNNALEALRSLQASVKNLETAASSGKEATVSPF
 LMGDRAVRVSLYRILAPVDNVIRNARVLARRAVLTEDNDTVSDEQIHVIEEADIADLRL
 SDLYEHKKEISEALEIPELVNRLRQLGSEVGEDIAEDRVLSAQVILAQSRSIIVDLQLIC
 GMSRESAVVLVPTSESAPYPELWDDED

>RXN01459 TRANSLATE of: rxn01459.seq check: 4910 from: 1 to: 810
 MNSNGFGFSFGNDDDDDKNNRNDPFLGFGNGFVGQGGGAGGPGGLGDIILNQFGQMLSG
 MGDMSNPEAAGPVNYDLAARIAARQOIGRVAPVKDSEKAEVEESLRALAEWLDNATQLPT
 SGHRVEAWNENWLENTLPVWKRVLSPVAEQMNKAQLENPEEAREMMGPMSSLMNSMSS
 MNFGVQLGNALGDLAKQLTIGSDFGLPISPVGSAVLPGNIAEASKGLNVAPQEMLVYIC
 AREAANAASSSTCRGLSSASFPLRNTPSA

>RXN01460 TRANSLATE of: rxn01460.seq check: 5642 from: 1 to: 294
 VPWLVERLVSSVEEYAVGLEIDTSHIQEAMGNFQMDNPPERLQEMMNEIQQGMDLSPIRG
 SRNANAVRSLETLALVEGWVDIVVTQALSERI PSPTP

>RXN01471 TRANSLATE of: rxn01471.seq check: 6310 from: 1 to: 807
 MQSFKTLSESWPVDNVASVSDGAVHFGVDVDFELMSVTKLLATYGFVLAIEEGVFEL
 DSPMGPEGSTVRHLLSHASGVAFDKPVAEKGVGERRIYSSAGMDILADAVAAEAMPFAE
 YLREAVFEPLGMENSELWGSAGHEARSTVADLTKFGQELTPTLISPETLAEAFQVQPE
 LGTVPGYGMQKPCPWLGLFEIKGQKSPHWTGDLMPENTAGHFGQSGTFFWTVPGSGQVG
 VVLTDRNFGPWAKPLWTAFNDEVWAELENS

>RXN01479 TRANSLATE of: rxn01479.seq check: 8990 from: 1 to: 240
 MQQLVIGAAAGYVLGKAGRKRYHQIKKGYEAAINSPATKSAVNAARKATANKLPDQPRM
 KEVKNLRTADGHEVLEQDQD

>RXN01484 TRANSLATE of: rxn01484.seq check: 1102 from: 1 to: 546
 VLGTQAYDGVPSRQFAARLRHAAKLWRLHEIQHVYTVGGKLPGRDFTAEAVAREYLIKEG
 VDPDLIFVSAGNDTVSSYEALDPEKLGRVLIVTDPNHSYRAVRIARRMGFAKPSPTTY
 SPAKFPSIVYFTLSHEWGGVVQDVSRLLGERVPDKVKHLCAQSKVCCALRGVHAMSNE
 GG

>RXN01485 TRANSLATE of: rxn01485.seq check: 9216 from: 1 to: 2052
 MNFSLVHLRENNRRVSVTVAIGAGALLISGFPTTAHTAEATETVYLAESPEFFQNVNVDY
 TQGISSSDITNIQAAIDDDVKASEQKVI FVVFLSSFDGVDPETWTQQALQANGGNNVLIYA
 LAPEERQYGIQGGTQWTDALDANNAAPQALSQEDWAGSALALAESVSGSSSSSSSGSS
 SSDFSGAWLAAGVGTVAAAGGGIWAYSSRSRKKKTSATLEDARELDPRDNRMLQPMLET
 LEHLAQEELSTDDSIIRGKEELAIATSEFGPRTSRFNAMNHSTGTQLKAFEIQQRNLN
 DSIPESEAEARQSMLEVEISSCGQADDALDAEAQNFADMRNLLINAGSKLDALTQKSDVLR
 TRLPKAQETIAGLRTRYSAEVLESIDDNVDLASASLDEAEVLPQAYEIESMPAGEQGGGL
 IDAIRHEHAITADKLLAGVEHADENISTAKANVADLIQESIDEINEAQGLKQAGADG
 ARADWALLDDAVRAASAALITASADAEDKPLGTYTELVDVDSALDTQLDLTRATAADQAR
 QLRVFDQQLQSARSQIQKAEDELISTRGRIVKSEARTHLANAQKLYAMAQONRTRDTRAGI
 DYGRQAATAVAAQRAKSKAQNDITTYNNRHNSGGGTGAIVTGMVINSILNSGRGGGFCGGG
 GFGGGGGGFCGGGGGGGFCRGRF

>RXN01492 TRANSLATE of: rxn01492.seq check: 9162 from: 1 to: 804
 VTTTLWAVSDLHAAVKANADPIENIQPKDPSDWLIVAGDVAERTELVLEILARLRRRFAK
 VIWVPGNHLEFSRSADRYQGRDKYSELVEGCRKIDVLTPEDPYLTFGGVTVIPLFTLYDY
 SFRRPGFTVEQAVQAARDQVMMTDEFSIAPFVDIRAWCWDRLAYSIKRLSKINGPTILI
 NHWPLVVEPTYQMRWQELALWCGRTRHTRGWAERYNAEAVIYGHLMHPGITNVNGVKHIEV
 SLGYPREWEHWSQHVWVYPVMEVDNAG

>RXN01518 TRANSLATE of: rxn01518.seq check: 9224 from: 1 to: 474
 VAFMOKTSAAGWLIATGGFLAAVSAILTWRFYGSMTSISITVITWLLAVVCGFGAGVKVQ
 GRLEDEGLIGQDKSQMNPVTIAYLAMLGRACAWGGAIFPGVYVIGISYVIPRAGELSAASN
 DLPGVIAICALGGIALSAGLYLRSCEAPPQSGEATS

>RXN01539 TRANSLATE of: rxn01539.seq check: 9014 from: 1 to: 2166
 VVTVAGNEKNKIREERVARRAQAVVEAEISLAAQASEQVREQAEAPDVENQVEEVSVEVS
 VSQSLTQPKTLGLQHDPRKNVMSSSLASIIIGVEQQFVAYGESEEPETLRDVLPRKLHP
 SEITSPSYEVADGEQRSIFGESAPSPDFDLSVDEEFDTSHWVRAGQDDRSDDRLADEAGV
 PRSQAQDVADNEANLSGVDEQLHMRVEHVAQSFDPIDVAKKERKAAEKYAKPKPSDNFYL
 ARDADAAARKRKINAADHNFQAQEMAQAMGLPRKGVNTQVMAACTAAVVMWMSRMT
 GVNVDMMKRFNKDLQAKDTKLSKYVSKDFWKSCLTRDKTEAKESLSDAFMQQKTAIIS
 NREIRIPMSVASAAQTVVRLSDQAYEAMREVDTDGAQIVDAKDVSQAQVAEDIMDVVKQEE
 HGLKSKDITYGAARDIVGRMERDPGYAARFNETAFGTVRLGEQRGRMVISKTFPTWQFPDG
 AGLSKNAGWFSVREPMGNAQNFADNLAAITLATEMRVAGEQYSGDGVDRVAGFMTADV
 ESGLASAKLLPDFDTRGRSASVRQIAMAQRTQAAIKVLQDDGNQMTAMTEPQVEQVQW
 AMDQAEKVMQRDHPAILDKFVRKHGQTFQGDADAFVKSITMEKDTSEYTDAMVRPQENR
 GSGRELAARVQAAQINQAQQLDMNVHDFRESNLPEERPAFNKYEAVRQTEAKNDPQY
 GY

>RXN01549 TRANSLATE of: rxn01549.seq check: 789 from: 1 to: 1659
 VANDFIEPNADAPDAPDNGDSGSGFVDEAKDKTRSAQGLGYGALRVGFGTAAALANGAR
 SMGNLAKNLWTRMMGLAISAGTGISAATGGMITARVGAMLAGTGSVLSVTTIALIVSMI

VVPAGRKDGIIELCPPVTANPFTIDAGDMTENAKLVYGALSYLGMDNQNIAGVLGNFET
ESGIDPTAVEGIFDEPNTIGPRKRAAWDNKFEQPMGIGLQWTAGRTQMLDDFAADRNR
DWHYIDVQLAFATISGDNESDRKVLEMDVNKNSSSSPTAASEYFLREWRPDAVAGNAP
IRAEQASKWYQAQGGWQKNSTLGESVIAMADGAAAKSTARDEQDALNDCEPEDRTSGGNT
SAAEAMVTITSHPYLADSRNGDTIYRIHDEVLTGDPYIASCGRGVATAIRSVSGVDDTF
PAGPTAAQYEVVVTGSGRWEIIGNLATMSENDDLPGLDVLGAPNHVAMVYNSVWDTML
GPGNAEPNAAIGHASLNDRSPGLDTLSLDGWNFKVFRNTQAEITSVFSGVQIPAGKEI
GEMTNPTRTTTPAG

>RXN01557 TRANSLATE of: rxn01557.seq check: 9051 from: 1 to: 816
VRSSNPVFSLSKETQRPQGNPYGGYDNFGGVYQONVAPQKAERPMTVDDVITKTGITLA
VVIIVALTGVLVSPGLGMLTLVGAIGGFTVLVSTFGKKYGSAAVTLIYAVEGFLG
VGGISLLSGFTVGNANAGGLIGQAVLGTIVFIMGFLFVYKTAIKVTPKFNRLITGMV
GVLVLVLGNVVWALFTGGASPLRDGGIIAIIIFSLFCTGLAAFSFLSDFDAADRLVREGAP
SKMAWGVALGLAVTLVWLYTEILRLLSYFQNR

>RXN01574 TRANSLATE of: rxn01574.seq check: 7504 from: 1 to: 1035
MSNKRIGVVIVSYGHEQDVANLVDTFADQLKTGDRVVVDNRKPVVLKDAVGERLEKHGA
EIIINDHNGGFAAGCNVGAHIVDDVLLFFLNPDVTIDDDPTLFNSLRRVDEQWAAAFMYL
LLPDDINSAGNALHISGLSWVTGLDEKPEVGSEVTDISIAGACLAVRVDWVRKLGGM
EELYPMYHEDTDFARLLLAGRIGLLHSAVYTHHYDYAKGQYKWIYIERNRHLVLLSVL
PLPLFLVLIPIQLGVNLGLWIAAAKEKRVGLVKVSLRLLIRDLPAIFKLRRSTQELAEIT
PSQYLAKMEWRLDNPNLGNIGSNKIVATGYKTYKLCMSILKLLA

>RXN01589 TRANSLATE of: rxn01589.seq check: 4956 from: 1 to: 1020
MVEQIKDKLGRPIRDLRLSVTDRCNFRCDYCMKPEVFGDDFVFLPKNELITFDEMAIAR
VYAEGLGVKKIRITGGEPLMRRLDVLIAKLNQIDGIEDIGLTTNGLLKKHGQKLYDAGL
RRINVSLLDAIDDTLFSINNRRNIKATTILEQIDYATISGLNVKVNVIQKIGNDQIITPM
LEYFKDHHIEIRFIEFMDVGNNDGWDGSKVVTKDEMLTMEIQHEIDPVEPKYFGEAKY
YRHKDNQGVQGLTISVSQSFCTCTRARLSDDGKFYGCFLFATVDGDFNVKAFIRSGVTDEE
LKEQFALWQIRDDRYSDERTAQTVANRQRKKINMNIYGG

>RXN01590 TRANSLATE of: rxn01590.seq check: 4837 from: 1 to: 6447
WGQKDHGKAPLGDHDAVRIYRQAEALMKQRAANNKGLDLNDEATYGAIMFASFDDFAAA
DAEAGGCVHRPQFAKVTRRNILNSPQYTAIKSSYDALVQODLVAQQQQAALQAAAYFEQ
QAAIFQARDQATFQAEQTLAQESVRSQEGVGLPVIDPMESYFREYAFYEGVEMFTGWTG
VDAGVYQFSTSDGRAIRALVDEHLATYEPVEQRCSTQAFASVNAAFAEVAPHAAPMFSA
IAREGEGSKGYQALRHRFDMKVGTAGPGLPEGPDLGGRRLPISPYDPRWSDREVVRVH
GTKLLSLSEESVGMIRDLDLATIHQLQNDVYEGTHREDDTKGGVRLPTLQVWNGEAIWRT
ITENDQMRLPNIGQFMATAKEYRAAASWLRAGLIDTADVASKIDPNKVMDSDEIGIAEAI
LTYLSDGEGVDRIEPPREPQGLKVRIEGTRIDIRLTDTRANEQWVGRVYVDSGTIVIKYSAE
QTAERLRAREREMENGDTWTPATDYEPSPTEVVDLVKFAIGREVRQDGGKGLGVFPNAR
HPRALEQAQDAYFTKNRSAFMVRGLSIVQDARDRSAGPGKWFNEAKASEWLGNIALIT
RARVAEELGVVEELIALSAQYADDPDFMPAFAGDELMIAIKQDYWAMLRGEEDTLLNPGVN
RDDYMAAIRDGDHEQIAAMTSAMNAVTVEDRVRQHAALVDDYVGTVEPPVPTGLRNFVN
VTAQHMPASAKLSWNHDDIIAALRATSIITGDELGRDEFYNDVINQQLKFNPTAQKMN
NPDLDPQLAREGTIVIAETISRNADVVDIADVDDNGVVRWTAQRRVQAKDSRAVDSKQVVR
GERTRHVQGEIQGITRGEHGEIVTKFNGENYMFAPGYTASVVPQKPGETKSLERTKL
KGYEQVMSEALVYRVREDLMFTERSRVGATTSINSAYKRLYDNRFPVDFERSAEGLSD
EWRARLELTASLRVYDNRIDGANVMEIDRAQQRGFDARNDRSADALVITGGRNISVLD
VDAGGLGFFPMMTGMAANQGSVRYLLPSAKVGADGMITPGDPADRVVPAHAPESWAMGDF
PHDRQNTMTFSNIMQASAVTGGAATAMIQLGGWNFEDGIVSADFANTHVRITREDEMRPL
VAGDKLSDFHGNKGVTLVVDPMASDADARAAGLESEVAFFRDNPDLGVMSFSAISRF
NGGTARELMNTPDQVVRNNDGSTRVQPGASGDLNFVITHMAVDAKTNVYDEAVREGOG
RKASSQLAWVLQAECEHMEHFGYGNVVSALANFOEYLRVTLGDLVTPYGELEKREGFSESG
QRNIITEMPSTYDENGELNNRVNRAQVREAFVEQISRAGGVMEIPQLQLKQADALQLEESPN
NPDYMLQVLSPHLRSDEDLADGSTRHEVYTRYXAFDTCYKLAEEQNIADALRQBEAQ
HGTLPRAAEKRLSESQKEFVDAQKQVQASFDGIANDIVASRIETKNNVYKDFGFMARSQSH
SATAVWTKDPRLSVDVEMNSSMARELGLVLDNGYAMVWRDPVIRDGGVRYLRVVDNDLH
GVAVNPVSVKSDGDFDGDGSLVGNLPPKAAHEALSRLTVEANMLDLGDKRMEEDGTMTF
YGLTLHDSLDVQVQAQHDHPAMAEKMKVIVSELNRYQREYEAGETSREEELLEVNRAMHDDL

NEHYAQAFANRDLGLVTLRFDGMENHMASVAQCQFETGAKGSPGKLEKEYATYIGADPAQGFK
 DVQQPTPEALRSHYEGSQKATAIKVLTFTGVAGKKEQEMVALCRNLGLTKEMAASAPAQFQ
 SIIQAKHOFIDALYRAETLMGPGVDLYQGRKMRGENEQRYEWEVVRDENHQFPQATKD
 EWVQQYMEYADDKMGVSVGVQVEKIAEEFSDQGYMRVLSHDELPTIEIKPALDQLA
 YGDKNRFDLLCEMAKQQVNIYDGDYDFAPRVVRANMKAMEDAARFGIPDVEIQSISAQ
 QSLASFERVPPQSGFRIERRVPAEVTGTIAAPLPLDAGVQGNVQQVQVQVPPVMPVPTP
 PAQQPVSPAQTDFRGVQPLDQGGKIGNYGHQGPAMGAQQPVVPPQQQNIFFVHNVPQNS
 VPPTPVVPKPGTGNPFTHGANNQFMGRFDTSRYNQQEPPQKQDGGFEL

>RXN01592 TRANSLATE of: rxn01592.seq check: 5848 from: 1 to: 1302
 MADNDFDRSRNDRSSDRTPRGDRGDRGGYRNSRGNDDRGNYRQNRNDRGESRDRGGYLGDRR
 DNRSGEYQRDDRRDRDRNDRSDDRRGGYRSDRNFDDRNSNMRRDRRGGRDSYSDNRSD
 RGYRSDNDRYDRNDRDRDRNDRTRGGDRGDRRYDRRDRDRDRDRDRRGQQGQRPGGDRRR
 ANRAGAGRDQQRDSLHPQQRAGFREERLNRTRNEPDLPGDIDIKDLPLVLQDLKVLKSDN
 ADAVAKHMIAMATWLADDPQLALRHARAADKDRAGRVSVVRETNGIAYAHAGEWKALSEL
 RAARRMSGGGLIAYMADRCERGLGRPEKAI ELAREEDLSSLDQDNLIELAVVAGARHDL
 GQHDSAIVELQKNPSLKSTGFTSHRSLSYAYADALVLVLAGRGDEAREWFQHAATLDEDGYL
 DAEERIEQLDNGNN

>RXN01597 TRANSLATE of: rxn01597.seq check: 4048 from: 1 to: 1182
 MSLFNKRKADLPGLQAGTRICTPQGGKGLKRLSEGLDAIIDAPDLRSTFAQRLLAAKPAAVL
 NVSRFTTGVSVPNFGQMLIDGGIQLVEGFGQELLDDGTGDKGKRLTEDGQLFYGERLISN
 GSVLSGPAENAFADAQSSLDLDRMEAYFGNTIQFIHSEAPLLIDGLGIPDTGNAIEGRKV
 LIASPGDNHRSRLKELRSFIREYDPVLIGVDGAADTLVELGKPAALIVGNPTGIGADALR
 SGANVILPAPDPGHAVGLERIQDLGIGAMTFPSSVNSSTDALLADFNHNPQIMVNVGGP
 VTLDGVFENREDSPPAALLTRAKLGTKLVDGVSIVASLYTVRSSNGLWMMALLAILVVLV
 VVIVVIAGTAGSGSFTDNLDITWNSFALTVOGWFK

>RXN01598 TRANSLATE of: rxn01598.seq check: 5340 from: 1 to: 963
 MAKRRRGGAATFAALGFGAAAGIAFTGYVLAPNLPENIDPNAPTSAELVVAETLAEVNAV
 QADQADSIIHIVEDVVGATLTDRPVLVMTDAEESDADVSVLLQAGAINAGSITILE
 ENFFSQDQAGQLKSIVANTLPAGAQLSETQLDPGTHAGEALGAALLNPNTEGEPILASTAE
 RGLLLNVLDRNGYI SYEDGTILPGQVIVMTGDSGSGSGDGAFAAETQSLFARALDAQSGG
 VVVAGTIIAADTGVIGRLRANPDAAENVSTIDSVNRTWGRKMATVLSVREELAGRSAGFG
 SAASADAAPSLDGTAAAPAQ

>RXN01618 TRANSLATE of: rxn01618.seq check: 189 from: 1 to: 384
 MIIIGAVFAILAVLLHVFIYMESFAWTSEKARGVFGTTEIDAENTKEMAYNQGYNFEL
 AVIAGVGVAFLFAGSTGIGAAALAGTGSMLAAAVALSSPDKRGAAFKQGTFFLLAVV
 FLVIGLLV

>RXN01634 TRANSLATE of: rxn01634.seq check: 2339 from: 1 to: 552
 MAVGQETDLLNAMEITAGVPSDLVVTEILPDTTSYNDFEVEHNTGSAFVPTIGEGEYTF
 AYSFDDSDATSRDKALDLGGEVTVDAGETIVVWIEYSSSTVDTAAFEQDFRDFGYMDDS
 ARIFRATGQAGLANGGDRGIRVLYNGEVSGWSHPSDSAVQKIGIDFALHPKVEQASIAS
 AHQN

>RXN01635 TRANSLATE of: rxn01635.seq check: 47 from: 1 to: 741
 LIPGGLDTPPEPEAPEDSLFEGRTPPRDASTRILITELMVNSTNMGSSDGFEYVEITNTT
 AEPIDFSDYTYLNYLPQDEFTNTNEAVAAEFGDVIIQPGKSLVFWIKNGPNDEATAADF
 NAEYGTINLEAGKDLVEISSGGMANGTARGMQIQTNTGHIVNRGFYNNMAGASDVKNACEHL
 FAVDESLLKQTLVSGCAPTGTGYTSQIPNPLSAVIDASSVPLITDNTATSINPAEFFT
 FAFKYHR

>RXN01638 TRANSLATE of: rxn01638.seq check: 2292 from: 1 to: 900
 MSTQITITIVLETATIFDGPETIYRYDLAAEGILDGWAHSVLDQVQKIGAGENWPTVEIV
 VDGTDNVVNALTSMFASKGVTCGGVGEAPPAVEEPPKIKRPTSGKVQVRFFGYIKPLHLL
 LVSLVGSIGAIWVISGFTGFVDSRPVVKVAEISTQGETISNQGPQQPTVLVLTEDLLIE
 APFGFEMRSEQSRYLEGPDPNLRIHVGVDPDLHGADAALVAEELRRLITEDPSLEEIPAG
 EWGEKTTIVRETPGDGSHVLWVTFWTDTRQLNVGCHSKAAETLVHKAQCRNVIEHLTLK

>RXN01647 TRANSLATE of: rxn01647.seq check: 6883 from: 1 to: 1170
 MGDVRMIHDPLGRRRRALVFGVVACVMLAVGSLALAI FRPAKDPADAPLIRSESGALFEVQ
 LDGSHVHPVANVASARLIVGEPVDPVNASDAI IAGMPRGVPVGPVDPADPLGSSTEEPEQDW
 FVQCQDVGTGLDHLITVPRGGLGPTLIEAGNGWLGASKSETGEVTWNLTITADGRRELPAWGS
 EHGRIMRRHLGISEDTPRVYLTTELLNAIPEHDVAFRFPALPELVDASTRNWLRLDGLALA
 EITPLQRGLLIDAGSGVFPDPTALLGVHEETANTLTLP EQTVSWQDLDGGFACADGEGQI
 GLETLTESGVALSGDSRAKSFSTNAGGAVGVDSGFGYYVVSDFGLMHPVSTGESMVALGI
 TDVQVVPWSVRLRLPQGSELAKETALAPTY

>RXN01658 TRANSLATE of: rxn01658.seq check: 7999 from: 1 to: 1833
 DPQILSPFTTQQQLANFYGFDPQLAMDRFEVDGKLRDFVVAARELDPNALQQNQDWIN
 RHTVYTHNGGFIAAQANQVDEVARVVGSTRGGYPVYTVSDLQSNARAASEDAEELGIKV
 DEPRVYYGPIIASATDGDADYAI VGTGDGPVEYD TDTSSYTYEGAGGVDIGNMVRNMF
 LRYQEMMMLLSDRVGSSEKILFERDPRSRVEKVAPWLTTDSKTYPTVIDGRKMWDCGYT
 TLDLSLPYSTRTSLTEATQDAMPDGTGPQLITDRVGYIRNSKVAVDAYDGTVELYEFDT
 EDPVLKAWRGVFPDTPVKDGEISDELRAHLRYPEDLFKVQRDMLAKYNVDSDSGTFTTND
 FWSVPGDPTAAEGRQELKQPPYYVVAADPETGESSEFQITPFRGLQREYLSAHMSASSDP
 VYGEITTVRVLPTDSVTQGPQKQDAMMSDQVQDQDTLWRGSDNLHNGNLLTLEVGSGGE
 ILYVEPIYSQRKQDASAFKLLRVLVFYKGQVGYAPTIAEALSQVGDIPKEAQDITEEVDG
 TATTPSTDETD TDTDQPATETPTAPVSEAEGLAAINDALS NLEAARDSSFEYGRALDAL
 DRAVDYSQSAQ

>RXN01659 TRANSLATE of: rxn01659.seq check: 8569 from: 1 to: 546
 VAGVAQRFFVDERIHVGLDSMP EAVTAVWMESDWLAEITKGSTPSDWEEILRPLALLTDA
 SFTLPPSTRAQTLDLKHLPE SRLKPEQEKPAFTPNASEEDLSQPLVIRPEEPQLQMPVR
 GVQESRGVVEPRSLGADDDVESIAEGDPERPSDLGYTRVLRLDNLGQSSIFQDSTDADEFPK
 KW

>RXN01663 TRANSLATE of: rxn01663.seq check: 7844 from: 1 to: 858
 MEISVLIIAALILVAGIVLWRADSSKQAAKKAE SPVGSVAPAPVLVEEEDPEPEFELDP
 EPEAQPELEVAAPFPAEPVQDLEPDQAEIYFDDSPELDADVENALAELTEVEDYFEE
 PVQSEQPAPATAEVAADDEEQRGVDKHS FLSSLPQSGRRERRNWAAKHDFIKEDAFIT
 DEWSRGAASTGAVARVDVSGMAEGYETHLVDLAGVPMAMRRGITS DVVIDDARRGEQPAD
 PERGESDLDVEIDTVSGFRLLSTWRGLRSLVSTSAFTSVWIPCQKL

>RXN01669 TRANSLATE of: rxn01669.seq check: 9448 from: 1 to: 915
 LYEIFVPHSHDTADSIDDEAMEANSEGIRALKFSLVLMLLTTVLQAIIVFSFGSVALLADT
 VHNLSDALTAIPLWIAFILSRRAATQKTYGFNRAEDLAGL FIVAMIALSAIVAANQAI
 RMINPRPMENIEWVIAAGVIGELGNEAVAMYIRVGRKIGSAAALVADGVHARTDGFSTLA
 VVAGGVGVFLGFLPADPIIGLIISAMIATLLVGTIRSVGRRIMOGIEPEALVEKATHAIWH
 VKEIESIDRLRLRWVGHRLHGDATVSTSTSSLSSEATAIAEAELSVKQHLFNVDEMTVTI
 TPSKP

>RXN01672 TRANSLATE of: rxn01672.seq check: 2451 from: 1 to: 342
 MASREVSITRISPLATFRVALAMSIIGLVAMI CVTVLYFGLNVAGVWQNFNDVIGGVGA
 EQTITFGLVLISIALLGAIGAITVAVLAPLCAI IYNSIVDLFGGLQLQLQEEVD

>RXN01694 TRANSLATE of: rxn01694.seq check: 8929 from: 1 to: 900
 MOKITPNIWQCGTADAEEFYVNAFSEFFPGAELVTTVKYPEAGLLDFQEPFAGKTLTVE
 LAISGFKIILINAGEEFTPNPISIFMVNFDAVRDENAKEHLDVWWEKLHEGGSTLMPYDT
 YPFSEIYGVWQDKYGVSWQLMLSRPEEKPGPAVITPLLFGAAQNAQCAPQENYVEVEFPN
 SQLGDRAPYQQGTGPATPEALMFSSQFQLDGQWIFAMDSGVEQDFTFSEGVSLMYEAHQGE
 ELDAIWNALS AVPEAEACGWLKDKGFSWQIVPDNMEELMAKPGAYEKLAMKKINIAEF

>RXN01696 TRANSLATE of: rxn01696.seq check: 7405 from: 1 to: 1179
 LSTPIGLGLPPTPPVPLAPRRKTRQLMVGVKGVGSDHPISVSQSMTTTKTHDINGTLQQIA
 QLTATGCDIVRVACPKTVDAEALPIIAKKSPIPIADIHFQPKYIFAADAGCAAVRVNP
 NIKEFGRVKEVAKAAGDAGIPRIGVNGGSLDKRILDKYHGKATPEALVESAMWAEGL
 FEEHGFQDIAISVKHSDPVLMEAYRQLAEQSDYPLHLGVTEAGPKFMGTIKSSVAFGAL
 LSQIGDTRIVSLSDAPVEEIKVGDQILQSLNLRPRKLEIVSCPSCGRAQVDVYSLAEV
 TEALDGMVPLRVAVMGCVVNGPEARDADLGVASGNGKQGIVFVKGVEIKTVFESQIVET

LIEEAMRIAEMDPEVLAAASAGMKAIEVKVTK

>RXN01697 TRANSLATE of: rxn01697.seq check: 2521 from: 1 to: 957
 MFQGLKELTAAGKRTLLITVTVGLIAVLVTLFSLALTAGLGHQSVSALKYLAGDNELILAD
 SGGSTFLASLTSQAVAQLEDEGAQMLWQVDRADVATPTMLNSPDLAPEVSLPAELAD
 SELATAHDVVDSSNDLYLDHLPVVMNMTSDLASLAQVGVTPGAGAFASDVALPSDVTAL
 SGSERWNASAYQGEQMSLNLMIVMLYVISALVLGAFFTVWTIQLRGIAISSALGAARR
 VLIADALGQAIIVLIGITAGTLITIVISAFMGDAMPVVISSTTLFPALILAAAGLIGA
 AISLGPILRVEPRASALMNA

>RXN01701 TRANSLATE of: rxn01701.seq check: 3619 from: 1 to: 372
 MLSHEEIIVAIAEDLLSKRYGGVQTLSDVEQLNGSGTSAVLRARVANSPPFLQQRSVVLKYV
 PSTGDVDDSDALVREIVSYQFTTSLSEDPVRPGPVILAYDIDKRILVISDSGGNDTFADLI
 DQRP

>RXN01703 TRANSLATE of: rxn01703.seq check: 3504 from: 1 to: 1113
 VAWPSNAKEKFLFIHWYHWQAHYLDCLVDAARRRTTKARRDRIRDITIRGISVRNVGKLT
 NRYDDKAWLALALGRAGKVRKVRTPKSLPSLEQNIVDGIDSLTGVLPRWSGETFYNVPS
 NGPAAIMMARTDRLEAMKITDWFIDNLIDGDLVMDGLMRMRMGPELVRSIHPYCGQVIA
 IGACLEIALKLREERAGLTTTVVDHWSADKAEDSLKYFAHIAHVQAVSRKMTNFHGVCD
 WDTGDGGDGLFKGILVRYLADVAIRLPDDSPTNRETKKIAARLVLESAESVWNHRLEVDG
 LEVFATDWTTDARLPQNFGLSSSSLSDLVSVVVRDERDLSVQLSGWMLMEAAAKVAEELE
 NNGNSYTRGR

>RXN01709 TRANSLATE of: rxn01709.seq check: 6991 from: 1 to: 432
 VFEQALGLTTLAQTAGAGAAGGLGFMMALLSAGMSRSGVDMILNETGGEKMLAQADLVIT
 GEGRIDAQTLGSKAPTGIAKRARAIGIPVLAVCGQSLLPAINSELFEDIYSFTDFESDI
 NECIRNPLPLEGIGFNIKKHLS

>RXN01711 TRANSLATE of: rxn01711.seq check: 1589 from: 1 to: 1158
 MLLMAHREFFVLAINGAVTDDFTTVYSALRRFVEGIPVYNEVYHFDVPHYLNPGATLLLA
 PLGYITHFTLARWMFIAVNLATVLAFLGLTRLGSGWALRSMWFIATALAMLTETVQNTL
 IFSNINGILLMLAIFLWCVVHKKWSLGLGLVIGLAILIKPMFLPLPLPLVKKQWGLSLIL
 GLTPTVINAVAWFLVPGASEYVTRTMPYLGETRDFANSSSLPGLAIFYGPMPTWMEITWFL
 IFGAMVGLAVLALLRFRNTEPYFWAATTGVLTLTGVFLLSGQMYYSMMPFMIPTLLG
 SRSEVHNWVAWVAAYFLLSPDTFTSQRLFDVARWMEFFSATVGVGGLLIVTVFSALIWFI
 GDIRAKGTPSSPITTDPTHDLHERTA

>RXN01721 TRANSLATE of: rxn01721.seq check: 7358 from: 1 to: 1023
 VLVDREFGRIARDLRVSLTRCNLRCTYCMPEGLEWLPTEQTLNDAEVLRLIRIAVVKLG
 IRQIRFTGGFELLRNKLEDIAGTAALRTDEGEKVHIALTTNGLGLDKRIAGLKEAGLDR
 VNISLDITDAERYVSLTKRDRLSGVLASIDAAVAAGLHPVKINAVVMPGVNEVDIVPLAE
 YCISKGSQRLRFIEQMFPGPREQWKRGDMVTAEILARLEEKFTLSPAKEPRGAAPALWN
 VDLKSNPDITGQIGIIASVTHPFCGDCDRSLTDTGTIRNCLFSRTETPLRDALRGASD
 VDAQLWAGAMWKKPGHGIDDEGLQPDPRMSAIGASPYQ

>RXN01734 TRANSLATE of: rxn01734.seq check: 3461 from: 1 to: 534
 MTDPIEQAFERIAEAMRRNGSVPLNKNDAFRPPAPKGGVEKKRGRASGLDGRQKRY
 VRGAESLGSVLNKEIQRRGWCKDIAGGWTSNWEELVGAKIAQHTVEMIKDKKLEFITCD
 STAWATNLRRMQRQILQVIAEKVGPNIIITELRIFGQPAPSWRKGLPHVKGGRPRTYQ

>RXN01742 TRANSLATE of: rxn01742.seq check: 7621 from: 1 to: 504
 MQEKPMPAIEVIRSAKRTKTVQARIVDGGQIQVRIAPARMSKAEEEKAVGEIVAKLKRRTQ
 SARVSDADLIERAHLNKTVLEGRARVESIRVSNQKGRWGSCTVATAEIRSDRLKHVP
 DTVLDVAVLVHELTHFTIAGHSAEFFEWADKTPLAERAKGYLEATYQRWG

>RXN01754 TRANSLATE of: rxn01754.seq check: 1605 from: 1 to: 1941
 VIKSVPLSTALSASLLGITPPVLGATINPSLPLSALSSDDIAVNFALKEPLAFADVQ
 AGTVFQSLSGTLQIPAEFSGGVVEFYDGDRLFHTLRLLEVNDRAHIEVPLQSVVPEDEGRA
 TEWLRAMLDPVNNQWCYEEQEVRFLDGNVTLEGATINPAVVADYFPSVLKALTIVYENP
 SEAVQEAITLEVATSLDSVYRRSGLDVNVNLTETGTGAPTRPQDQFERQIVLDEATESNT

QKTELVPNPGQDNFAFLRLNGNADELYDQARLLTDTATPLAVDTEVTASGFGDVPNLSTDVA
 TLQELGITQLTSESVA RTSVTLGIERSRLRTYSQSMDLHITGT YTPLPQNAQGITFSIG
 DTVLSLTLTDDTGIIIDREFNVPGDLVNRYTAIVVEFTSTGDVNCVGTQPVGLNIDSLSLV
 TSQHSDDVPVLNGFRSLPQSFQPRVDVAFADPSVQELSRVSVVLGIQSMSSQRIRPHLVN
 WDEAVASERPTIFIDAAGAKTDQVPSYLAQQQGTLEITSKNQDNADGEQLHIEKCLAEADV
 VVGSIQAVWADAKKRTIVIVASSQDNPPDLDALISWMGEDRERWSLDNGDLIVKVRDREP
 QLTTEADPQGRSATAFIAIGVSLVIALIVA AAVSVSVRRSQKGYK

>RXN01761 TRANSLATE of: rxn01761.seq check: 9482 from: 1 to: 4464
 VTATVLEPQPVLSEQDQDAEIAARMELKHNRHKTWRRRTMAVVMFTLLISVGLSFGAFGNK
 EREANAFAISAI IAVVVGAMGEVAFEAICPSDGDTEMLLKICITENLGEMHIIEKCLAEADV
 LKCFVDIAKNEEQORKEQNLDAKADPYDSMYRMASAMASYFGNCRATACVEEGGPNFLDSED
 AGLKVFYEGILSKAANGGNVLGYADAKHNEDSCWFGNGVANNEKTSYSDSLADHAFQGPY
 HFALFGATLSGLGFDSSKAEDSQDTDAFQRKMGYAMMIAYIISGGIDLVTNTVLNIST
 NPFRLLLGVPVSQNTNKTFTENMAGGQTTGTPFEGMTDFFGLIYNWSVTUGWLIGIPVSI
 GLFMMGALFRMRDCKGSAFKKVVIRVVYGVVGLPLLVGYTGA LDSFLDSGSSSTAGNSA
 TKI VLSTYVDFQSWAENTRMRVPDKVTLAWSLEDQAPTQGSMMVRNSALEINAGSNESF
 TTFKNPGSMDLGYSDWMEKMA DPANSGTDGTSSSSATTIFQGTIALLSRYINDNISISSG
 SFETSIRAMESLTSKEGSGEAVAGGDVMWAVTYGNTASGLNETIAAELADANNLPLEVS
 DSAGLQGRPIDRNAVSVFKSGDATASCNNSTVTYGSRAVVDGYRSDCNMSPLTMYNFLNTSF
 HPADASVFSTSTASSYTRASHAVSLIGSGAMNFVWFVSAMSLMGFSFIVIGIYGAGAMFL
 FNTIRRTLSLIGAVPFAAMGFAGVAKVIVYTIAMLVFVIGITIIYQLIRFLMVAAPL
 EQPLADLSLSESAELVAGAGMGLVGMALATSGNWAIA GMVITVASSMGVIFITIIAMKV
 RGSLSVSGVDETVTSVINRFLDTQVSSAGATSGDGMRRRAATGLGIGATHMVLNRDGGGG
 GSDSSGGSGGGSDSLGEKAAGLAKVVTVAGAGLVGYATDALDNDYADGVINGDDGDA
 FAAGGDATVDG DYADGDAIASADANADVFVGVVDGAGRASFSNAAYSDDGTTLDGEGAS
 VDAQGNPLHADGT PMSAAEAEMKAGLSSSGTMEKSGVKS SGTITAADVMDDQSLASSV
 TESGLSKI PDTYGADVSGAAGTVGTTGADYSATDSSAGLNMSEALQSGT PMGALAGGSV
 SSSDQAMNDALQIAASQGLAPAGSIAGMEQLSAQATEAPAGKAGKQLDGLSGSALNTQL
 ASMGGQVGDVSNYASAYAGGMMGGVDVAGKVTEAAQHLSQVPGGIQNAVYNADAGSSGASFG
 QMAQGIAGVAGVIGAGAAASSAAQAGAGTVQAGAMGNAAAGAMINNAVSSGGAGTSGTA
 AHVNVNASHGVPVAGQAHYQESGHAQAFVQNNQANTANTRAPSSAQIMGANVAGSLAS
 QAVRIGIQPGQMGANVRDAMCGSGRSGRGAGTQCGRQAGRSVSAKNRIARQGRQKPSV
 TQGMANMAAMRSAAVSGRMANMDGNSVGGTEADPQQGSGVTEKDGKGVK

>RXN01765 TRANSLATE of: rxn01765.seq check: 8067 from: 1 to: 942
 MSNNVVYKCAVDADNIIVAVDMHVHLEVDS CGHKSPADIMAASSKYFKTAERTPSADAI
 ADIYREHKMAAVFTIDARTQMGLHPNSIDDLVASCARNNDVLI PFGSVDPRTGEDALVE
 ARROVEELGVGRGFKFHPVQGGFDPSPAPEFYPLWELLESFGLPCVHTGQNGMGAGLPGRG
 GKLFKFSNPLMLDDVAADPNLNTIIMAHPSVPWQDEANSIATHKANVFIDLSGWSPKYFP
 ESLVRQSNVLSKKVLFGTDPLITPEKWLAAAFANLPLKDEVRPGILKDNVAVKVLGLAAS
 TERGSQAEKVQHA

>RXN01767 TRANSLATE of: rxn01767.seq check: 5940 from: 1 to: 465
 MIDHKLFWNTVNTNNA SVREAGKCDPIRPTLNEQLNRRILPEKTVIALARAYDLSFPVDAL
 VRTGHLTEEEAGSREEDAS PDSADDYPTWALNSHLDYGLGAFGDIAEEVNSERNVRDNA
 IEQIRAWLDELPGSLFNNLRSTKTYIELFETYLID

>RXN01769 TRANSLATE of: rxn01769.seq check: 4062 from: 1 to: 441
 VTGLGRAPHSLFFPIGYYTPTMTSITTTDTPLYTALPHTRISDAELLTPTTTVHEILVY
 GPAECPGCTATLDFFARKNMPATKVTVAGDVHAITYITQDLGYLQAPIVTVRISSASNH
 DNEHNTQILHWSGVNRYLMQALSRTHF

>RXN01771 TRANSLATE of: rxn01771.seq check: 4536 from: 1 to: 702
 MHQACQLINDP SQGLWRTSALRSPVARVGHAVLRQRAGEISRMQGREFSRPGDQFRQVDL
 RRLLIQVHPQSIPTADAMAVTITMALTAATIDPVKFVADSQNPDEEYILAQQIALREMI
 AMPLEDLEI GVRIDLEPVLVAAQAAAKNVGVVSSILKDLNLPQYSGYALQESIVAKTQA
 ETDLERARNVEKTTARILASAKVLEQNPLAKIRMI EALPPGSTIEVRGDSKA

>RXN01774 TRANSLATE of: rxn01774.seq check: 7116 from: 1 to: 726
 MSPNFQARGTAPTVALSMRQIAHIREEEKKSPLAASVFITPTTKQMVVRDLESFLQQLY

HTDLPESIKDGLISAIGSSAGNTNNPALALETQMAYHLVLAMHHTDVTATWHKVVTKNI
TESAAQAQDAVEHSKAYDAVYDAAQLMGITVEEGNVGSIATAFSTARADGKSDWCVSIS
RYIEVTEALDAARAVTKNTDALNKTALPDVQFAPVHVHSAQFMNKSADHGVNTAEKDQPT
LF

>RXN01787 TRANSLATE of: rxn01787.seq check: 474 from: 1 to: 693
MSNNALVANEADIGLYLHWNGGRDSIEAFLAYAAQAQLPPINENNNDWLPFITVLKNFF
GNDGSGGVLEPVNQDYLDGIDYDNGVYMLDDYEITERINPPAVEQDSHDLHMDLIKIDKA
QPPVDQLGSLFLHGLETSVADLGVGDRVFLPRFSTFDKLGGRYRIHTVLGFAENDPFPNMT
SSERFKGKPVVDMFNDQNAFNPNSYITTDTVRIVVDPVPEETNPDEKAGR

>RXN01796 TRANSLATE of: rxn01796.seq check: 303 from: 1 to: 774
LLLGGNPAEIDQVLGGDQTQIESGESTGAGDFDHCQTGADANASDDCRLYYTSFVNMW
QTLFLPAQAGIEYTEPTLTLFKNSTQTGCGFASASTGPFYCPSDQDAYFDLTLFFDQMRQFG
AENAPLAQMYYVAHEYGHVQNLEGTGLSNYNPDGADSNVAKIELQADCYAGIWAHNS
EGPDLPLQITSESELDALLAASAVGDDNIQQRSGGDVNPESWTHGSSQQRKDAFLAGYN
TQGMASACDFLGRGVYND

>RXN01803 TRANSLATE of: rxn01803.seq check: 8304 from: 1 to: 960
MRKKKDGQNLPDFRKNPKPLDKKAYEKELKRLQAEVLVQWVVTGARVVVIMEGRDA
GKGSATIKRITQYINPRASRIEALPTPNSREKQWYFQRYIEKLPTAGEIIVFDRSWYNR
GVERVMGFCTSQEYRRFLHQAPIFERLLVDGHIHLRKYVFSVDEEQIERFERDLSDPLR
RWKLSMDLQSSITRWEDYSRAKDEMFHTDIPSAWYVSEEDKKRSRINIVISHLSTIP
YEKIDRPLPEIHRPDSSESIVRPPRDEFRYVDPVAAHLEERIKKEEKAKKAKKPAKAA
GKNSDKQKSSGGGKKKKSKK

>RXN01809 TRANSLATE of: rxn01809.seq check: 4529 from: 1 to: 1176
MNEQREALEDAEAAALADELAALAEAGVQGSVEPYDYAADLDEDEDFEDPFAQDE
PRDAGPLGLQSSDNHVEAUAEDTGTSTEEAQAEGSHEESVONPRDFTGTATAVRSFRP
LPVFNALRPGPPIRTQPAVNTDIDDGGQENTAGATAADVAGVFGTHFLAFAGQVVDVHR
HIRHEQAMRGHQDLSVFGVADGAIMLEELKNRYQRPNENPHDDQVTEMIKTETEKE
NVEMDQDIADVNDVDEQVVVTFAHDADSVAVVAEQVVAEPTPEPVKVEHVMSVDLAG
ETITPIDQAIRSMQNLNGIEHSVVLRLGLMTQVAHNKLEDEVYAKALAEGESHAQQQHE
LEAENERLKEVDALAAELSAALMGEGGDHD

>RXN01811 TRANSLATE of: rxn01811.seq check: 3834 from: 1 to: 681
VFEFDLTKADIQVDRSTSMQVFEASETVKEAIKASIEQGHTRYPVILESKDNVLGYVTL
DLIKQSYKDDQLTVEQLIEEPVTTETIPIKKLLTMRKKGKHAIKLDYGGTSGLVTI
EDILEEIVGEIRDETDLDEALIAEQSDGSYIISGKLTLDQFQRYFHEVIEPEFETNFTTL
AGFASSRYKEIKAGTIIIEIASFRFVLEYQHAHIDYFKVESTERKTE

>RXN01813 TRANSLATE of: rxn01813.seq check: 1579 from: 1 to: 666
MVAIVVVAIVVGVFIVIQGQSKAAKLGDRDYEDTSLAMEVGSDSITLTSANTSADAKSV
QLFEDFSCSHCSELSLATDAMKTQIEDGNLVVEIKFLNFLDRENI DGHSTHALAALAV
ABSDNATLYWNFRFLMEDQSEIYNQWSDDFADGVEALGADSSVVDAIRNGDNIQRAYD
LATANGELTEETGSLSSPRVLQDGKDVEGNISDWITTVLAS

>RXN01815 TRANSLATE of: rxn01815.seq check: 2232 from: 1 to: 792
MNRSTISPVEARQOFRAGLIQPTSGWSAGFAQANLISMPQDLAYDFLLFAQRNPKPCPIL
EVLNAGETFGGIFGSNATEADIRTDAPQYRIYAHGELIDSPASADVYWRDVLVSFIIGCS
FTFEHPMVQAGVPRHLEAGRNVMYETSLACRPAAGSLSGNLVVSRLMIPASQVADAVRI
TSRYPAVHGAPVHIGDPSLIGIDDINNPDFGDAPLSEPSDVVPVWACGVTPQAMVMSKP
PLAITHAPGHMLITDAPDLGQVFP

>RXN01825 TRANSLATE of: rxn01825.seq check: 7373 from: 1 to: 270
MPKARVTKNETAPVSSNPNANRTPVKINSAGTPMWYKVMFMFAFMIVGLAWLIINLVGPQ
IPFMADLGAWNNGYIGFGLMIIGLLMTMGWR

>RXN01831 TRANSLATE of: rxn01831.seq check: 8077 from: 1 to: 462
MDSLVLLGLRIALLVWLWFFVLMALRAMRADLKVTGQASTSSSSVAAPQGLARAFNRSSP
PRLLTIVVEGLAGSSIEVSEDMTMRGSPECTFVVGDDYASGMHARVFKRGESEWFEDLDS

RNGTFVGGTRIDQPEQIAVGTDIRIGRTAVRLVP

>RXN01834 TRANSLATE of: rxn01834.seq check: 6044 from: 1 to: 702
MLGGGGAILAIPLLIYGFSSATQATAASLIIGLIGLIGLSQYAAGHVRLKEGLSFG
LGLVGSFVGSGLASNIIPDLSLLSGFAILTLVVALTMIKSLRSTREYITRRPSILAI
TGVGLTFGFGVGGGFAIIPALIFALGFMSRQASATSLVVIANSIAMGFRYSDLASID
WVSIFPIIITTVLGAFGSVKLAKKVKASSLQLGFAFLIFISIYMGFNPFDLF

>RXN01846 TRANSLATE of: rxn01846.seq check: 4543 from: 1 to: 282
MSIPGNVSVYVAQGGTGWGDAQYTTGESWDLQSFLENSTDYLMITIGSSLLALVGGAAVW
GFVNVMRKLFGGQSGQIQIWFTTILLIIVGGALP

>RXN01847 TRANSLATE of: rxn01847.seq check: 7155 from: 1 to: 735
MLIVLPPSETKTHGGSGKPLDFHHLSPFSLTKARQITLADLQALEVDEALKVLIGSEKLR
PEAESNRALETSPTMPAIFRYSGVLYDALDAATLPEKALERLAIGSALFGVIAH7DPIPH
YRLSGGTLPTKSGELPTMKARWGTISEALIDVNQLVIDLRSQTYQQLGRVKDAVTVRV
ESVMDEGSRKVVSHFNKHYKELARVLALSEKEAHTAEDVMSIAQAAGLVVEENPNHKT
LTLV

>RXN01874 TRANSLATE of: rxn01874.seq check: 6539 from: 1 to: 348
VIAYVASACCLPFGAFAGALLSKELSGHLQERVLLTHTVINFLGFVGFALGSLSLVFAA
IWRTKIRHNFTPWSVGIMAVSLPIIVTGILLNNGYVAATGLAAYVAWLLAMVWG

>RXN01875 TRANSLATE of: rxn01875.seq check: 5040 from: 1 to: 846
MRIAVTGATGSLGGHVDSLLNKGVAASDIAIVRNEEKAADLKARGIALGVATFEDEAA
LTAALGEGVDRLVFISGSEVGQRVAQHTNVINAAKAAGVT7FIAYTSLNLGTSKLALAPEH
IATEKLAEAGIDHALLRNGWYENYESSIGAAKATGKVFGAAGARVSAARAKDYAEAA
AVVITSNDQAGKVYELAGAPALTYPIAAGIGEIVGSEAEYVNL7SVEEYQNALEQAGVPA
EFAALLAGMDPIIAEGALYSDBTDLQDLIGRPSTSIWEALSS

>RXN01877 TRANSLATE of: rxn01877.seq check: 5596 from: 1 to: 1071
VPLRLATGGVLATLLIGGVTAATKKDIIVDNVGEQMSLVMTMSGTVEGVLAQAGVELGDQ
DIVSPSLDSSISDEDTVTRAKQVALVVEGQIQNVTTAVSVEDLLQEVGGITGADAVD
ADLSTFIPESGLKVSVPKPIIISINDGKVTVYSLAAQNVQAELELRDIELGAQQRINVP
LDQQLKNNAAIQIDRVNDTEITETVSFDAEPTYVDDPEAPAGDETVVEEGAPGTEVTRT
VTTVNVQEESSTVINEVEITAAPKATISRGTKTVAANSVWDQLAQCESGGNWAINTNGF
SGGLQFHPQWTLYAGGAFSGDASGASREQQISIAEKVQAAGGWAWPACTASLIGR

>RXN01879 TRANSLATE of: rxn01879.seq check: 6847 from: 1 to: 933
VKITAKAWAKTNLHLGVGPAHDDGFHELMTVFQTI7DLFDVTTLT7DEELVEEGSVVKQL
SVTGARGVPEDasNLAWRAVDALVKRRAEKTPLSAVSLHISKIPVAGGMAGGASDAAT
LRAVDWATIGPFGEDTLLVEAAELGSDVPFCLLGTMRGTCRGEQLVMDL7RGLKHLHWVAA
MAHGLSTPEVFKKHDELNPESHMDISDLSAALLTGNTAEVGGQWLNHDLTSAALSRLPELR
SVLQEGIRSGAHAGIVSGSGPTTVFLCESEHKAQDVKEALIDAGQVYAAT7ATGPAASTA
DQRGAHIITS

>RXN01896 TRANSLATE of: rxn01896.seq check: 5243 from: 1 to: 636
MTHAIFLDLGD7LVDHASAARAALHAWSP7VGVDT7DVERWIELDKWGFARFERGETTHLG
QRRDIRAYLNRELD7DATTCDIISGYLKAYEQNWTAY7PAKGVLDRAVATGAPGVGILNG
AAPMQQDKLDR7TGLGLPELVMLAAS7LDSAKPRPEMYARAL7HLGARTAT7IGDWD7NDV
AAPRELGNWALYLD7SGTDP7ADIHS7LDEL7H

>RXN01899 TRANSLATE of: rxn01899.seq check: 7424 from: 1 to: 786
MSRTLWAVSDLHVTFAQNQNTVDALMPQDPGDWLVIVAGDVAEKIPDVV7RTL7SALVKR7DT
V1WVPGNH7ELFN7RKT7DRVNGKARYALV7QLRAIGVITPEDPYPIFGGV7ICPLFTLYDY
SRP7LGL7AKQAL7AQAKIKL7DDELA7IAPYVDIPAWCAERV7YTEDRLKAT7GPKPVLVNH7
PLVIEPT7H7LFQKDIAL7CGWTAT7RDWAV7RNALMA7HGH7LHIPAETRV7DGVSH7EV7SLG
Y7FEKH7PHMKRP7PWP7FV7MQIN

>RXN01902 TRANSLATE of: rxn01902.seq check: 3503 from: 1 to: 1059
VQKRSRTGQTTWNGG7PPIENPGTSFILSAGDQANHS7WDEHSAYIS7PETLRN7YLA7VNG

NHDQYNYDAYNAMYPRPNQVDENYFFEYNNAFLSLSDNDYLDIDDDIAFLRDTVAAGHD
DKDWIVLTYHHSTFSQAYHMDARIKYQRELRTPVISELNVDLVGGHDIYTRSHLNMG
FTPVDAAGRAVVGETLNPKAGEVYVYATNSSSGSKFYDFQLGQRYDTGLDFQETVDQ
KKIRITYTAVWNQDQVQDYTNVELTPEGLTVTTKDAVSGELVDQFTLSKQDRDEESEVPE
DKDKGDNATGSSNLGLAAILAPVLAIFGFGVLFGVGGSLAEFFANLGVKMPF

>RXN01908 TRANSLATE of: rxn01908.seq check: 3792 from: 1 to: 846
MHSDFEHFPNGYGYTIRQDTPDAENPMTHHDTKDAALWVHNRPRGDTVADKPEGNEILL
IFAKPICGQHNDNDNPFVWSDGSDASLIRTKAYVAEHHPELIDISAKTITIGVSGQDW
LDVVCVTTAATCDELIPADSLIDIRQWAGFDVWTVIPDSQPGLAGIYADDPADALAYQ
ENFEDEPIWDLRSHDADKDAALAAASAAENHALARGTTPPVIRTQDIITNARYLMSDS
ADDNPEYDRALVELSAYLLSIDLDDRVAAEMTILGRFPVKEG

>RXN01909 TRANSLATE of: rxn01909.seq check: 5615 from: 1 to: 879
MANFRSKDKDGNVINPNASTKGVDLVNVVYDSAKHVTEKGNTVHFVDVQVQIPIPDADGT
RANANLAPQTMPHLHLDTKDQQRNTGVAYSDAQIQAQMTVAAGRNHMTPLLSKDGETVG
YSMLVKADVMFPKTKDGKSLPAVMNTKSLQSPGVPSDAMNIQQQQFMAVAMNRQAAEAQ
KAAQQAQTQAQAPOVAPQPVMMQNCQFQAPVPOQAPYAGAPVYADAVAHATAQQQAAAA
QAPQAPAGNPFNPQPPAVAAALAPQTPPVAALAPQTPQPPAAQFQMDNEPPF

>RXN01910 TRANSLATE of: rxn01910.seq check: 445 from: 1 to: 846
MAFFLLAVAGTVAPVAAAGWAKDKFLSNSQNNQQAQNQMSFQVNNQAQNSGENSEGFMG
QYGNLGAAGLAGAATGAGLAYSDFEDGQSLSSKARNMVGKLAGAGAGVFTKLANDAIQAE
GGSMKASAYSATAGGLGSYLKDGPGGVIKSAMASGAAGFGADKVDKLAESGHEGLADSL
SGAIQGGGLGYSTLGGVTGAGIGGATGGLAGLAQNYFGGGDDYSNAGASASGFSANQVNS
EISTEIPQFANLQGPQRSELEQLALPQESRSVDKSYDQGYEA

>RXN01911 TRANSLATE of: rxn01911.seq check: 9256 from: 1 to: 939
VFIIAGGLPLLIVYFVTVIIMVYVYALLRYEQRMSTGVYEEADPVEDMSVINWEGIKCDIA
SDIAARAEAKKAKKPVASDAVAVGNVYIASLRQHMLVETQRRYHHKLGRELHNDPQLEDY
GSLGLDCECRACVVAQKGLVTVHAHGVVQASARKKDRVIRAGDQIVAGWNNHQRQARR
KTSAAKQLERDAQRKRTQAEERDKIEKRKAQFEVAEQSGKAAAQRRAEKKAQARVD
ELVAQKQAQEQEKTHCKRDKQRAKKAQGRKVGAVDNSAVDDVLAYAEKTRSTAGCRDDDS
VVHVDMAAGVRDV

>RXN01930 TRANSLATE of: rxn01930.seq check: 8516 from: 1 to: 951
VISTNEIENIHSTRRDIEIALDESSTSEPKRFSEISHLYLALAEKGKISFPESFSLRELY
DHLMHGELKENELDGEIFRQGPVEIRDSRQKVIHSGFSPESQIIEGINAIKLAHSEEE
SNLVGIMMSHFMFESIHPPFYDGNRTGRYLLGIQLSKILSPATALLMSSAINQFRNKYYK
AFHVAEHRMLNRGDGTPFVISMLELLIAAQEGLIENIKQRIDFASLEDAIKLTRNSFFK
NHQINLNYILGQIQLFGKDETLSLESAKFLKVSATATRYFRTLREMLVHEVSKRPLR
FALTDKGREIVGLEVKI

>RXN01944 TRANSLATE of: rxn01944.seq check: 9781 from: 1 to: 972
VRTATLHVTSSAGEAATTINLTEDDGSFNWALPAADLTGKSNWFYTTATDGFNSVTTET
VRVTVDGANTDPLRLNLEENQWVSGTDDVIGASDVFGDKLELLIDDAVAVTNSLSAAPT
FAMEVETQTVDFFRNGILAGGEEELRIDQGTANTETISTVPVLYHINEDGTLTVSVYAGT
KAAPFIDLNENNDDQFIRNRLILPDGRLTLPAGISDSNAWLNMGDSAGKLDFDPAATFAL
PEDAFTGVAAHAWDTTQSTDGEHHTISREDGGEISRTIRVDNTEPALTSGVVEEQEELRG
TVEIDAQATDAGAGVKSVELLGD

>RXN01945 TRANSLATE of: rxn01945.seq check: 3307 from: 1 to: 1992
VQLPLTTGSIADLKEGHTLVIRAEDVEGNRTEKITFTSTPDENFISGDYAFSNGATVGVG
DKLFLARASDPGDTVMTFLEADSPKLDGSRVMSGTVEAGSVRAEAKMLERGDVE
KLSSLDLGLMEVTSDAALPYQLFEVDAADALAAADTEVRLNWAAGSAGRAQVIMYFDEGA
WVEVDRLTGDELEEFFTLQGVVNAEKFAIGGTVTVLQHSSEGFAGADHSTRNSDVTAAPH
DDVARSEYDFTLAWESDQTYNEEFHEHQNTIHIDYVLAERENKNIQFMFTGDVVDWDDQ
PAQWATANPEYQRLDDAGLPYSVLAGNHVGHGTSNDYTFESRHFGEQRYVDNPNWYGESYQ
DNRGHYDLFSAGGIDFINVAMGWGPDEEIAWMNEVLAKHPERVAAILNLHEFMTLTGGGLG
PIPQRLDEVAATNPNVSMIMSGHYHDAFQRTDSFDDGDDGVDDRTVTSMLFDYQGLPEG
GGQYLRLLHFDNQGGQKMMVRYTSPSLKDYNSDEPSLLGPAEDPNMYQEFVSYEQLGIKF

EGRTLIGDSFSADFLTSNEIGIVDEVPSGTIAFTNWKDVTEGRHSWYVRSEDPFGGVEIS
PVQSFIAEGEAGNAPGTGSSNGGSHGLWGALAEFFAGAAALAGAAIAFVPGIWDVYTN
AFKR

>RXN01960 TRANSLATE of: rxn01960.seq check: 2689 from: 1 to: 318
MPQHFQSNYRKAPVIMSAPLTIHDLNSTNSKLNKWLCTVLNSPNLTPCITVSVNHT
EGMISLVSEFGGHGLTEIANTQLVPVLELPKFNPFALATHLEAANN

>RXN01985 TRANSLATE of: rxn01985.seq check: 6664 from: 1 to: 1050
MRTSRVLAGILAATLTVSLAACSDSSETSSNSSSASQSSSDVSNAPVTEHAFGETT
IESKPERIATVWGSNHEVPLALGVTPVGFKEVWGDGDDNNGILPWVEETLSKLGSDPEVL
FDATDSIPFEEIANTAPDVLILASYSGITQEDYDQLSQIAFVVAYPEIAWGTSLDDEMIEMN
SKAIGLEQEGKDLIADLDAEVASAIIDANPELDAKPVFAFFDESDFSQIGVYTSIDPRMS
FLLDAGVQEAASVLKEHSSPDSFYEQVSAENPETFDDVDVVIITYGTEDDAANAELLKMQA
DPLLSRIIPATAEGKVVLGANGPLAASANESPLSPWGINDFAKLAELPK

>RXN01987 TRANSLATE of: rxn01987.seq check: 9043 from: 1 to: 213
MTFFPAQSRRLARSTTDKWIIGVAGGLAETYGWNPAYVRLAFVASVFLPLPGSQILFYALA
WLIIIPSRNRF

>RXN01988 TRANSLATE of: rxn01988.seq check: 4185 from: 1 to: 426
MMNKTHPASAKQTTELRLLTATVYFKALNEVHNVMQMIDPLTPVPVPIITGTSAVELYADA
REHLNNGATQVMI PVISPSNLTLSVVALGNEEVDALGHSEGAQVHSLLEIHTPKRSWPLS
ELYIDDNEGLAQVSRCFARLVG

>RXN01991 TRANSLATE of: rxn01991.seq check: 5467 from: 1 to: 873
MTNLLPHFFSTDVAAWEPTVVYSADKTTATATFKNIPSDISFSWTGIEALEFPSPGKTFE
HKVQGSVGEPAGAFTRDNYTEGELYKXRRHADLLSGDGLFGPNITDGGDGNLPSVDGDK
GDDGSDGSDGRDGVVAIDVDNADGTVTVTLSDGTTFTLDAGQDGKDLGLDGDGTGLTLE
SATPDEPGNITVYVLDGTEFTVRNGVDGSDGDKGDKGVNGTDGVDGSDGKGLVEVSRVTN
DNGSTVITYEDGSGQITTKPTPTNWLKLLDLLPLFNLFGLGGSVTSKSK

>RXN01996 TRANSLATE of: rxn01996.seq check: 8265 from: 1 to: 537
MSKLTGTWTLDPAPTEIKFVARHAMVTKVRGEFTTEYDTSIVVDAENPENSSAKVVIKTAS
VTTGNADRDAHVKDDFFAVDKFPEMTFEATSFVIKNENEGTVTGDLTIRDTSKVTLLDV
EVGGVAEDPFGNTRLGFEASTEINRKDFGVDFQAPLSTGGVLVSEKIKIEIDGSAIKAA

>RXN02007 TRANSLATE of: rxn02007.seq check: 3631 from: 1 to: 633
MSSDAEKASVELSEKXHPERTHILGAVVFLGISLLVIGAAPQYLFWLLALPVI FGYYWLK
SSTIVDEQGITANYAFKGGKVVAWEDLAGIFKGARTFARTTSDAEVTLPGVTFNLSRL
EAASHGRI PDATISKEAADGKVVVVQEDGSSVMMSSKEYLERQKALGKVPQLNFDDDDTD
GNTTQTSESVESQETGQAASETSHRDNPASQH

>RXN02014 TRANSLATE of: rxn02014.seq check: 217 from: 1 to: 507
MENIAEQAGVGAVATLYRNPDRFTLDMACAQYLFNVVISLQLQAISTFFPTDEGVWTSFN
QLLDFDRGLGSLVPALAPESLDDLPDEVSALRRTTEKNTTTLINLAKQHGHVHHDHAGTY
IVGLTISRIPITALATISENSHKALLGLYLSGLKHGMMANIGEDHGS

>RXN02019 TRANSLATE of: rxn02019.seq check: 8826 from: 1 to: 501
ETAPKATKVEASDLGLQAIPSTSLPSTSYSDIDDVVLGVAASTLSSGEIATKPRFVGTETLI
NSIATNVDSSLVIEINMVLPLSLAEPVLIPLQHGDTISVVSQDPDTGLPENIAAGGTVI
LAGGTPDSTLILALPQSIKVAQSLNTPLAVALTGDADNNTYTEE

>RXN02023 TRANSLATE of: rxn02023.seq check: 8728 from: 1 to: 768
MAPKQTPSPPEKNRNVLGVPLQRRQTEGTFDQRLLEMRADHNNKHADPWRVLRIQSEFVAG
FDALHEMPKAVTVFGSARIKEDHPYKAGVELGEKLVAAADVAVVTGGGPGLMEAPNKGAS
EANGLSVGLGIELPHEQHLNPNYVDGLNFRYFARKTMTFLKYSQAFVCLPGGGFTLDELFL
VRLCMVQTKGVNPNFPIVLIGTEFWAGLVWIRHRLVEEGMIDEKVDVRMDLTDLDQAVK
FIVDAHAGLVDARLHN

>RXN02032 TRANSLATE of: rxn02032.seq check: 9048 from: 1 to: 570

MPFLQISLLSIGVAADAFACSVVRGTAIQVNLFKRALVLGIFGVQAAAMPLIGWFIGRF
FAGITFIAEIDHWIAFALLGIVGTKMIWDAFQPEDDETIIVDGRVQFRPAIILGLATSID
ALAVGMGLAFVEVSILKVALSMGSIITFALSAGAWIGHGGGKFKWATILGGIILIGIG
ANIVYEHLSA

>RXN02039 TRANSLATE of: rxn02039.seq check: 6804 from: 1 to: 840
KASISNLSFWTSTSTTAPLWLVLVAVQAVMHGELYHVEVPTIALVIGFGAQLLIG
VMSYLLPSTMGSGASAVRTGTHILNTAGLFRWTLINGGLAIWLLTDSNWLVRVVSLLSIG
ALAVFVILLPKAVRAQRGVITKKREPIPTPEEPRNLQITAGISVLALILAAFGGLNPGVA
PVASSNEDVYAVTITAGDMVFIPDVIEVPAGKSLEVMTLNEDDMVHDLKFANGVQTGRVA
PGDEITVTVGDISMDGWCTIAGHRAQGMDELVKVAAPN

>RXN02044 TRANSLATE of: rxn02044.seq check: 4936 from: 1 to: 1383
MVPTPMGNSNISILGIYRQKIQRHLVSTLFRAYFPVITELIILLIVITLALAFDFTNGFH
DTGNAMATSIATGALKPKVAVALSASLNLVGAFSLSEVAVTTAKGVVDLDQDFLNSAWDS
HQLLLVVFAGLIGAIWNLTLWLLGIPSSSSSHALFGLGIGAAIASLFGGGVVWEGVLSKM
IIPALLAAVAVAGLVAAGITGFVAVYSITKAVGDNEKNRYFRWQIGSASLVLAHGTNDQAK
TMGVIFLSLVATGHLGTADIPFWVKATCALAIAIGTYLGGWRVIRTLKGLVEIDSPQG
MAAETSSAAIILTSSHFAGMALSTTHVATGSGIMGTGIRKGAQVRSVAGRMAMAVITLP
ASAIVGVFCVWVAHGIGLISDDLGLVLVAFALITLSGYIYKRSRRVPDPSNVNADWNE
ESNSVEPATPSAPAASEITEAPAAPAAQAVQDLNNENEVTK

>RXN02045 TRANSLATE of: rxn02045.seq check: 8713 from: 1 to: 261
MNFATIFGSI FEVTVLGILLGAGLPALFALGIRFAHSPSSNGTNALGKIATICFAIIAV
AIIAGILWVTKATIIYQYSGDFIDFTEG

>RXN02049 TRANSLATE of: rxn02049.seq check: 6577 from: 1 to: 609
VRYLLFIATITAGLSGFVVI IIAAWALGDSQSLEEFATYAGWGLFFAGTGVLTLGTQETTRA
VTAGSRGSGSGRGRAGSVVGFRLPFLFSFVVAIVLVVLGASAPLWIGQLLSNLQGVGVGLL
AVGLASYAIQATISGIFVRLPIVERVCLADFFGHRRAHGFNCCLRLVAGLSIAGVLDHHR
GINILAGHRAVLRFGAFRFGIGC

>RXN02050 TRANSLATE of: rxn02050.seq check: 1487 from: 1 to: 795
LDTGVRMVLTVAAWLLGYQLLAFLIITVVGSIWLVLCFGSVRSVLGSAVDVSRGVFI
RQALLAMAASGATAVLITGFPTLLKFTNPSAVAGGVSMAAVSYAVIITRAPLLVLPQQFQ
SAIIVRFVKGTSGLKTLAGPLAIVWAVGLVGAGLANLVGPWILDVVLQKELFAVFGWLL
AMLTIGATTTASLMVSGCAATAFERHGIYLTGWVAVTVVAVGFLLPGLDGLVAGLALIV
GPLCGLVHMGAFVGGDRNRVLTAG

>RXN02059 TRANSLATE of: rxn02059.seq check: 3288 from: 1 to: 495
MTQPRPDAAVSLEKKRPEGWPFVGSFETYPEAAQAVDILLSDNAFPVTELTIVGVDLIEVE
RVTGRLTWGRVIAGGMASGAWLGLFEGIVMALMSGWFSSIAAGIGMGLVFGIVGAAPY
AASKGKRDTSSQTIVAGRYDVICSPEAREAREMDIALKTRDLRQ

>RXN02066 TRANSLATE of: rxn02066.seq check: 2735 from: 1 to: 492
MFNSDTTANLQAKSRDRAGSKAKSRSPSFDVARDVLDVTRKTAQVKNNAKEFSVDHLS
ADAAMSVTERAQAESERLVNSGNDAYRRRAVAGQAEQDRLVSEAEVVRSTEEAHRIVD
ARLASLATECMPGPGEANLQRPESFVAKVESVVRVAVRKNQGR

>RXN02067 TRANSLATE of: rxn02067.seq check: 4916 from: 1 to: 456
VGWGEIFLLVVGLVIGPERLRLIQDARAALLAARTAIIDNAKQSLDSFGSEFDEIRK
PLTQVQYXSRMSPKTAITKALFDNDSFLLDDFDPKKIMAEGETEQAQRNKQAADNNANVV
ERPADGSTARPTQNDPKDGPNSYSGGVSWTDI

>RXN02075 TRANSLATE of: rxn02075.seq check: 2111 from: 1 to: 789
MYKVFEALDDLQVAVQRAYGVPMTGNCVVRQEVALLDDLDRDALPVELDDAQDVLDRHD
GVIREAEKAIALVDDAENEARNLLARATEESDAMVEDATKHAHSVVAKANDTADRIYSD
ARREANSVTERAQAESERLVNSGNDAYRRRAVAGQAEQDRLVSEAEVVRSTEEAHRIVD
AAHADSINKLRNECDDYVDTKLAEFETSLTTLRSVTAADRARSALRRGAGATGRELRDQPA
RGEYERDYERDYERDYERDRDY

>RXN02076 TRANSLATE of: rxn02076.seq check: 9502 from: 1 to: 534
 MKSPFIIVDAALLRGSALPEHLTQSGPSPTRIGPEMIAIEGGKVIVEAQIIPGLGGGLAV
 EADIEAQLLQCSRCRLRELTPTKTLHVSEVFAADPDFVTGEDAADDEDELPMVNDQDIDL
 LQSVIDEAGLTLPFNPVCEELGYGACQDDETPADPGVSEEEVEDEEKVDPWRAGLEKFL

>RXN02094 TRANSLATE of: rxn02094.seq check: 8559 from: 1 to: 717
 MAEHNAIITDAVHSDPAVLEDNAGFSGKYLIRALDKAAHMQTGAIEGYISWLKHNPEKT
 PAQLQVLVDKHFMRALTGSGAGVGMAAAVPGIFVGTALAVGAESLVFLDAAAFYTMASA
 HLRGDIIRHPPERRRGLILVVLGTAGKATVDAGVGLSKKNHAPGIAISRFINIGLMEVNN
 GRLMRYAVKEVSRFRSALIGLIKILPFGIGAVLGTMANRKIAKRTVGNAYDSLPLPTHF

>RXN02104 TRANSLATE of: rxn02104.seq check: 737 from: 1 to: 1122
 MSNSPTDVSTAPRIMIAPDSYKGTATASEAAQYLGEGLVLEILPNASITLAPMADGGEGT
 SSVFGGVQITLPTTNAAGRLTEASYTLDETNTAYIDIAAASGLPAVADDLVPTTGGDTYG
 TGVLIADAVTRGATRIALGLGGSATTAGSGILIALGAVPRNKEGYALRTGGADLILNDY
 IDTAEELNIPAAAVEWILLTDVDPATPGQGAATVFGPKGATEKDLSLLDAAHLHACAQL
 EVDGTFKPGMGAAGGIAIGLTWLSTLMHGNDDQIHIILPGAPLIARSNGIEDALPETDILLIT
 GEGRLDQSFTGKVVGTLHGLAKAHVDVLAVAAGIVEGGIPDDFLAVEMIKSSDVAQRLR
 DAGRRIAQEYVAQN

>RXN02107 TRANSLATE of: rxn02107.seq check: 3646 from: 1 to: 342
 MDLHKVAAAHAATLPLSTKEFPFGEHEVYKVRGKVFLLLTILNDEPIITLKSDPEIGAS
 LPSGFPITQAGYHMKNVHWLSIDGERITKDFIEGLVEESYELVISTLPKRRRP

>RXN02108 TRANSLATE of: rxn02108.seq check: 5369 from: 1 to: 609
 MGDMMKTRHIIHACVEISQGNDRIIIDPGTFGAPDLGATILVTHNHADHVDPELLKPGMT
 IYAPRSVAHSIPEVECHIEVHGGRNFTVGLSLEVGEHMLTHSMPAENVGVLINRGLV
 HPGDFTFQIKDVELALVPVNGPWKMLDVEGLKKFPKRFIGIHGDVINDRGLAINKKF
 LTHLGETYGESEYPLEEGESLEI

>RXN02114 TRANSLATE of: rxn02114.seq check: 7318 from: 1 to: 486
 SICYAWTTAFHALTPGLGGIAIGIWLGGVLCGLVIRKPGAAIFVEVVAACVSAAALASQF
 GISTEYSGLAQGGIAEIIIFALFLYRRYSLPTTMLAGMGAGGGAIFLEMFFYGNLAKTMSF
 NIIYSTTVLISGAILAGLLSWYLVRALARTGALDRFAAGREV

>RXN02121 TRANSLATE of: rxn02121.seq check: 4238 from: 1 to: 705
 MITSPFERELKLLNEGELGIVQQLVESSNIGFIVDLELDGDBGWAVYKPELGEQPLWDFP
 PGLYKRERAAAFVISEFLGWNIVPPTVIMHDAPAGVGVSQVWFIEENGEHYFPLFDTRADLH
 PQFVMAVFDLLCNNTDRKAGHVLLDGDHIWIGIDHGLCFCSVEPKLRVIVWDFAGCTIPDD
 LVTDEQLELLEDVPEELHQLLHPAEIDALQRRASRISRLPFLPQAKSHRQFPFWPLV

>RXN02138 TRANSLATE of: rxn02138.seq check: 8752 from: 1 to: 342
 MTAPSTNTGVILTESAASKAKALIDQEGRDDLSLRIAVPGGCSGLRYQLYFDDRTLDGD
 KEDIYGVGVRLVVDKMSPTYLLGAQIDFADTIEQQGFTIDNPNAGSSCACGDSFN

>RXN02151 TRANSLATE of: rxn02151.seq check: 8209 from: 1 to: 1188
 MDWPDIAGKISILGVLLHVLSLAIPGGQDTMMSHLNALLDPLRMPLFFMVSGFFAVKVLN
 QSGFELFRGLRWFLVLPYLLWTPVNLYLHRLLEGTVFTGRAPGTWEWYSGMSLSATNMWYF
 LYFLVIFNLFLWATRKLPAWAIVALVASLWLLMPAYSEIEILRKSIIYLPFTFLIGAYFRP
 LISRFAEAAATRPKAVFVAALVYVSGALGVISNGLRDSNHNHGAASVLMNMLRDTFAHALG
 GNLTFGDMHLPGMIIRIVSLPAGIVLCVWLGRKIPVGEFLKLIHRHTLPIYGLHATGSL
 LFFGFGLRWNFMEIDNFSDSLWHHTNTMMVIAFAFACMLGGYLYTILSRVPVLGWLTVPPK
 LPFEPDKTPAKAQADSHVKAQSAKAPMNASTSSKTYGI

>RXN02169 TRANSLATE of: rxn02169.seq check: 3541 from: 1 to: 846
 LDMQINRRGFLKATTGLATIGAASFMFPKANALGAIGKTVIYAAAGVPSAASIKNAGHLG
 AVRYYSQRRPGTESWMIKGPVTLAETRAFEQNGLKLTASVYQYGAETADWNKGAAGAATH
 APQAIALHVAAGGPKNRPIYVAIDNPNWSSEYTNQIRPYLQAFNVALSAAQYGLGVYGN
 NVINWAIADGLGEFFWMHNGSECKIHPRTTTHQIRIDKDTLDGVDGMDMNVYADWDGQW
 TPGNAVDDAIPITPGNSHTGGTGIDADTINQVKILGTLS

>RXN02180 TRANSLATE of: rxn02180.seq check: 4458 from: 1 to: 1458
 MTSKSTSTRGALDRYFKISERGSISGTEIRAGVVTFFAMAYIIILNPLLTGGTTPDVEGN
 TLGIAQVAAATATAAGVMTIAFGLIARYPFPIAGALGINTMVAVTLVSGEGGLTWPEAMGL
 VVLDDGVVIVILAVSGFRVAVFRAIPASMKAAISVIGIGLFIAMIGLVDAGFVRRIPDAAGT
 TVPVTGLIDGSIASWPTFVFVGVLLCGILVVRVRVGGGLFIGILGTTLLAI AEAI FDSG
 ASFENGAEANEGWSLAVPGLPDSFGGIPDLSIVGAVDLIGAFSRIGVVAATLLIFTLVLA
 NFFDAMGTMTALGKQGNLVDDEGNLPDIKKALVVEGAGAI VGGAFSSSNTVFADSSAGV
 ADGARTGLANVVTGSLFLAAMFLTPLYEIVPIEAAAPVLVVVGAMMGQVTEIDFSKFYI
 AFPAFLTI VIMPTYSIANGIGVGIFIMYAIMAAAAGKAKQVHVMWLVAGLFVVFFAIDP
 IMEAVG

>RXN02185 TRANSLATE of: rxn02185.seq check: 8940 from: 1 to: 579
 MGRHSTKTSSAFTKLAASTIAFGAAATIMAPSASAAPDSWDRLAQCESGGNWAINTNG
 YHGGLQFSASTWAAAYGGQEFATYAYQATREQQIAVAERTLAGQGWGAWPACASLGLNSA
 PTQRDLSTATTSTPEPAAAAPAVAEYNAPAAINAVGSTDLNTIKSTYGAVTGTLAQYGITV
 PAEVESYNAFVG

>RXN02186 TRANSLATE of: rxn02186.seq check: 5727 from: 1 to: 198
 MYDMANVEKKHFVDPAPWPEHNPADGHVVTLEISKVAGASSPWGDDKEFPVSAEETGYVHP
 YTRINR

>RXN02207 TRANSLATE of: rxn02207.seq check: 6831 from: 1 to: 798
 MRRRSRVSRLLPATALLASTALLSACTQGVTDSPDMGKATPAVSPASNPDCQVIEFNG
 ITDMEVTDGDI LGVRTEDALAI GTVSDFEAGSQVELVDVKQCGDLTATGGTFVLPADGV
 YLIDAKDPDLDELRAITDKPVTVAALTSDQLLVQGEDEELTIYREGEEPTFTFVAGNPT
 QLIAVPVDIRHDVAVRTWNENTTIQDVDPNDREGATLRVGLGVGQMGAGGEDGLLVVSDSE
 MGGQAIYNADDVIRLQNDPRHRRGT

>RXN02223 TRANSLATE of: rxn02223.seq check: 9117 from: 1 to: 501
 MSTYQDDRFPGPDPYAPLGEKPSFTLTSTDLENGAKLAEAQGGTDSPLQSWSDLPBGT
 KSLATCLDPAAPTAGAGFWHVAVENIPTVTVEIPTGAGDETGGIEGVVSLKGDGSKRGF
 YGAQPPAGHAPHRYLFAVHALDVEKLDIADPATPTGLGFNLVYHTLG

>RXN02226 TRANSLATE of: rxn02226.seq check: 1898 from: 1 to: 1056
 MTENQTPSSTSAPKPGPRPGPRGPRGPAQVAAKKAATVAPAPIAKTSNDPAKFRVEAD
 GSAYVTTSSAGERLIGSWQAGTPEEGLAHYGARFDDLATEVELMEQRLLISHPDDTSIRTK
 AEELKATLPTIAAIGLDGVEARLSKI INNSEANERAKEQKAKNRERAVARKEELAVEA
 ETLAENSSDWKVGADRI RAILDEWKS IHGIDRKT DDELMWKRYSRARDSFNRRRGAFEL
 DRTRASARKLKEELVERANALKESTEWNDTARAFRDLMTETWKAAGRAPREIDDKLWAAFK
 GAQDYFFDKRNAVAKERDQEFANATAKQQLIDEYDAQINPEQGGLDGARSKL

>RXN02238 TRANSLATE of: rxn02238.seq check: 4471 from: 1 to: 285
 VTNVSNETNATKAVFDPVPGITAPFIDEILLDKVTSKYALVIFAAKRARQINSFYHQADEG
 VFEFIGPLVTPQPGKPLSIALREINAGLLDHEEG

>RXN02254 TRANSLATE of: rxn02254.seq check: 1030 from: 1 to: 777
 IAAVEEGLWENLLQHRFGGHGALAGHALGNLVIAALTDLIGTSQHALLDQIAQLAGAKGR
 IIFVCAEPLDLEAEVSGSLDSARVMRQVRGQVAAVATPGQVRRVRIIPDNFENPAAIEA
 ILDAVLTLVPGSWFSSVIPHILVPGIVDALAQTKATKTIVVNLNLTSEPGETAGFSAERHI
 HVLRQHARNLQVDQVIVDAKTLSSQTERNHVERAARTLGAEVSFHDVQAEADGRGFRFTSIH
 DPAKLCAALLASFAGARKE

>RXN02271 TRANSLATE of: rxn02271.seq check: 4621 from: 1 to: 558
 MSFLNSAKTKTVALTATFVGAATLATPAIASADIVDNALALPSGEISCSQAEKYNTTEA
 DYNKVAQANALAMFDSRGFPQIQAALARVDEAANRCGLKGSTVAAQAEATEAAPAPAPA
 PQDNTGTSQTAPAPAPAPAPAAATPVVNLAPAGSPTFTTIEVPGVGVQLPLDYQIVQQFLA
 QFGIKI

>RXN02279 TRANSLATE of: rxn02279.seq check: 6646 from: 1 to: 1458
 LISLEKKQKQDANFFLSRLRQGYRAVDLFLESQTVDQLNNPDVQTYLTAELIRDDLRSWA
 VINQMALDNIDLVFYGEENDEPLAIAARKIIEETASHPELRFENLEAQFSEFTILLAQSPSE

NLDVARYQELRTOGQNFVQELALDSIFGQHAVVQDTGNGEAILDETIGYMIGAGMRETTAR
TASQPAQLYSFVGRQERSIEMARLAFEELQAAGLPHEEELRLGMQLAQVEPIELARELLE
KLLLPKFEQNLTLDELETEALLPLGATVAIHDQAAAAAILRHARENAAGFNFELAVQAM
TMTIDVLYTNMHEQLLEELNHSLPYAQMLDDQHAELKLLDSIAIVQADLGSSTALELTT
GTAMGLAETTAQKLIVQESLNRAYFTFARPEDCISGAADASALAMQNDPDSNAAQLEQC
AQYLPQLGHETDGLLESASFVRGEPTEQALYANALSSIIYEDFGDSAKSQYVQEQQAQE
KQOLLE

>RXN02296 TRANSLATE of: rxn02296.seq check: 7700 from: 1 to: 489
MRNQI IAAVAALVLLTAATPAIAATPATAGNGLYSIDMGDEKQLTCVLFDPESTEAHVVA
SCAATFVPTWKLLDGAHEQAQAKLEITQAQDGELSVTASQKPLITMTIAPTSTIKPTIVNR
LVVVPGENEVRFYATDPDVLVPLITPDSYEVLTDSAAKVKATL

>RXN02300 TRANSLATE of: rxn02300.seq check: 2962 from: 1 to: 333
GSTIFFGAIAGMTMYCEGVNDWLSQMHTATVTDATMTIFNEAGSNIGELKR

>RXN02301 TRANSLATE of: rxn02301.seq check: 2104 from: 1 to: 717
MDLALAQVSTVSGLYDALDLIGVLLNGIIGGTIARQGYDIIGFLFALFSALGGGMGR
DMLIQQGTVAADINQIYLALAFSGALIAMAVNFKGRVWELFKVHGDAIVLGWVAVTGSVK
AMNAGVAPLPSIFMGVLTAVGGGMVRDVATGQPTIFGGGTLYAVPATLSATSMVIFHSF
DQVILGMIISPFGLIALAVTAYWCGWVIFVNTDFAPVNLTVSQRLAMLSKAERKKDKQK

>RXN02302 TRANSLATE of: rxn02302.seq check: 9010 from: 1 to: 879
VATNRTSSAGVITSVLASALFGAIFFISSGAIEAKAETLVAVRWLLTAACYLLALLHPAGR
KVFEKEFWTLRSQPRQILYFIFLVVLTQLQLWFSWSPKSHALDASGLYLLFFIFLVIVG
RFFFADYITRLQWIAVGIALIAVTLKFVISAQLSWVTFAIAGYALYFAIRKYSGLNNAF
AYGAEVLALSPIAFFMLATVEDPLSNAMLSMVILAGLAGALAMALYLAASLTLLSMPMFG
LSYGEFILLVFAALLGETLNLSDAIVYSLACALALLGFDGIRRSRKNLETD

>RXN02303 TRANSLATE of: rxn02303.seq check: 6641 from: 1 to: 906
MAENNTFQETEQQDEARFREFEVGGKDRQLSEEEQLEQLGSYIDAHYFVPDTPFPWAGG
AGDDPDADRYIAHLPDRTHTAMIMLGGSLDHSMPGVAFIGGVSVDDVPEVGGAIHFHPSN
PTGRWAVSFHSGGWWRGSGDALEFQWRPEVAAAAELSGTTILDLDPYPLAPGNHLDMMNEV
VGKAVGYARHHNPVSTIGWYSSGAALAAINASLFDALVLTTPDLGSEVKLPAEIRGDAV
VPAAAAWPTTFVQIAAQDEIAERPGELGDATVKEYVSRHRISTPKVAREKITDVAEFLKT
VC

>RXN02307 TRANSLATE of: rxn02307.seq check: 9052 from: 1 to: 621
MSGTAIMYDITTVVPSKKEIAQAWTGYVDLQGSYRLVDTVDGEVGVGEVLISKDREGRLLIQI
PFSYRSAEINPEQTLSTLEHGVLGKRWVTNALGDPVAVREFIRTIITGDGGAARSDGVKG
YLDIKSGSDAESVDLQDKLTVTRQRAIGSVTINGERKQFSRLPLQLKNFRETAAGHT
ATTLRIVATHPEKDDVELLVAEFNWME

>RXN02314 TRANSLATE of: rxn02314.seq check: 2536 from: 1 to: 441
MEWYQVRRARQLLIVLFIAAMLGAASMVIGPFLNDRITIEGNSGRALAQVTVNGSYRTTV
DFQDENGILYSPATGLLPFTGLGEGQQRVWVYAKSDPDVLVKEGKWTLSIIPALSVAAV
ATATWSVLWLGVRGFRGRSDDANETTV

>RXN02337 TRANSLATE of: rxn02337.seq check: 408 from: 1 to: 1323
MSKLYAGARTNALRRTHQLTQSALADKLDLSTSYLNQLENDGRPLTAVLLQLMKVFDVE
ASYFTSPDRGTATATRIALETLAMNQGTMSMDLLDFADRFQQLAQHIIQPAEVDPTHSSA
HDFVRDYFATHKNYIDSLDRLEELATAIGQPLRVTRLAQLLDAEYNIIVRFRAPDITG
RRHFDPQSRQILLRQDLSEAQQCFQLAELTFLAHAELDTLTDDQPLPSEAIRLAKV
GLSQYFAAAVVMPTRFLEFAQDKHYDIELISEAFGVSFESACHRLSTLQRSAGSGVFFF
FVRSDRAGNTSKQSSAATFHFSRTDGTCLPLWALHRAFERQGNITRQVARMFDGRTYLWLA
RAVKGRTHGFGYPAAEFAGLGCDSIAPGLVYSQGLNLDPSAAEIGPGCRICPRENCV
QRAFPSPGQESIRPAFVQLLN

>RXN02339 TRANSLATE of: rxn02339.seq check: 8878 from: 1 to: 492
PTDNLFSYPAQRYDLLTLAFEVRIGDMQVINDMLAPPFVKLPEDPALGADPTLTSTAIAH

PDSPLVWAYRAENLIKASNDDEEKIQAYAFARTGYHRSLDRLRANGWKGWGPVPSHEPN
QGVILRAIASLALAAKLIGEDNEYDRCRQMLSDADPESVAVLLDK

>RXN02340 TRANSLATE of: rxn02340.seq check: 7304 from: 1 to: 1065
MKKSIVVFEVEGGSDKHFDGHRKDTMPFVNSINDAGWQAEVVYRPEWTEGLFEYVSENF
DGYISRVNPGNI PGGERGYFDLLTRLSEAGLVGMSPTPEEMMAYGAKDALVKLSQTDLPVS
DTEAYYDVETFFHKVFPFSLSGFERVLKQNRGSTSGGIWRVQVLVDKELAAIEPGTALPFD
TEIKCTEAVDNHTEVRKLGEFMDFCQDYIIGDNGMLVDMRMPRIVEGEIRILLVGPHPV
FVVHKKPAEGGDNFSATLFSGAKYTYDKPEQWQLIDLADARPVIAEKLGGDNITPLWT
ADFMGLGDVVGDGTYYVLGEINCSVGFTELDMDGIQQLVASEATKRTEEFAQLTV

>RXN02341 TRANSLATE of: rxn02341.seq check: 4129 from: 1 to: 486
MGNSLEKHIAEGDRIHVDLTSPLSAMLFPIFELIVITGICWMGIGFLDQLPGIDGTNEAD
SFPEGRNLLVGVWAVLAAWRFGFLPIRQRRLRVILSDRKLVLRRAGRLTGFDSIPLSYI
QRVQRRRNTLVLVGGVHRRPVYINQVPKARKVEALLKDLTFW

>RXN02360 TRANSLATE of: rxn02360.seq check: 7403 from: 1 to: 2433
MRGDVQKIKTKVYDGKHTLEIPVYQRNYDWEKQCSRLFDDLSEVVKENHROHFPGAVVG
PKQGSWTWVVIDGQQLRTTISLFMLALVHSLRASEVEEGFNAGYNIDLATLIEDDYLR
GNEGKILFKLKPVKNDNEAYQKLFGEPESEFIESNLTANYRYFRNLVKATDLTAQKLWEA
IEKLVRMYLDOLEFDDPQRIEFLNSTGLELSEADKVRNLVLMQDELKTQEKLYQQRWNP
IEVCVKFDTDNFIRWYLTLTARTPRKQDVVEEFKKFIRNSKLPVEFILLDDMYEYAKLYR
DLLGATTGFIAADRLKRFVPMVGVVLPFLLPVLKDAKDGIIITESDFGLVLKLVESYLF
RRFVAVASNALSKIFSTAYSIDIKKFWTPGQSYSSLLAYILKRRDGGSGRFPSPSEFRNF
ATKNFENWNNHNNRRYLDCLENADSNVDRIQTSLDEGSLSTEIMPRSLNDQWRAELRG
EYARHETWNNRIGNLTITGYNAYSNSSEYERKRTMENGFLVSPYRNNFIIKKQKHWSEE
QLIERTELLTQAALDYWLPKETFQPPQAVLPTESLDSDLSFRGREIVAFVEYEDYKETVT
SWADMLQSVLKVNLNFSRQELIALTNEEICLATSNNNSNSLREIDHGLFVDYDTSGTSVKI
GFLRRVFTQLGLEQALVFTLRPLANDVEPRDDELEVEVEKKYSDLTKFTQPLEEAENLE
GADTEVIPLESLKLEQLTAFSPENPQALGGLPVPEFLKQNVIEQLSAEHILAVLTQHFN
IASMCGDDYLLLELRSGRLRELLQRLLEELDS

>RXN02361 TRANSLATE of: rxn02361.seq check: 1002 from: 1 to: 651
MELLSHLLALDPASPRLTVYNNESTGARLDFAITLDNWSKVGNNMLLEELDEEGSLITI
DLFPVSWQAAMIMLGALATSVEVSFDDPEADAFITSLDRFSHYKXGSDVLVISEDPPFRGV
VEGGELNGAIDFGPTVRFYGDQFFQPTRLPELIQHSDDVPMVGARVLATGWSDELSFNH
QVLEPLAVGGSVAVITGLADIERLNIQATNEKTHRI

>RXN02367 TRANSLATE of: rxn02367.seq check: 8247 from: 1 to: 609
MSNAEINPVEYEINNHPGTALNPQCEDGANVEIITSREVPLGGPRAMTVHRTLPRQRORS
LIGAWCFVDHYGPDVSLTGMDMMASHPHGTGLQTVTWLFEGETVTHHDSGGNHAVLPGEV
NLMTAGAGICHCTEVSATSTTILHGLQLWTVLDPDKDREGPRRRFDHYAPEETILEGGSARVF
LGSFLGQTSVPVHTFTGSSCFRVH

>RXN02368 TRANSLATE of: rxn02368.seq check: 7600 from: 1 to: 675
IRVLAGATRVTYVEPWLAIPLFILAFASILIPFISKTKGLRDLDAWKIHTTQGDKKRA
MQQLIIIPATLAIIDIGLPTLFNAPPLASAAALFGGVYGASLAWAAYRADQLPRIRTKERL
AELSQNASLDVRSDDLVLVQEPESRELVRCLAHGAMDGTRVMARQVARVLDTEVDEHV
QVARLEQHGVLVSRSTIMFGGDPKGVFIEVSLKGISAIKALESGR

>RXN02381 TRANSLATE of: rxn02381.seq check: 8210 from: 1 to: 1023
RLSTNFRFLAGIAVIAACVAATPTAQAGSSGSSGSSAGSSGLWDLLEFPESHESFIE
MLDLDDSHITSHPDLTPDLYEEVFPDPQIGCEPAVVAVVARGSEQNLRIPARPSSES
PWTSGNCFEKKNFRSFFGRMEKHVREYESTGESLMKDVYVMGLNNIEYASLPLSSSEGSSE
LGTSISSGRDNVISAIDRESATGCTPKYLLAGSQGVILVDGYEEELIARDQYLTGLHI
ANPAQQVDDPTLVGHVEVTTGGLASSVEPVEDNPFVSYCLPGDIVCDRSEFQFSAGSSSI
AAAQSLSTGNIRPGRVHVQYFVTTPQWDEQIFDEVASWIEAA

>RXN02383 TRANSLATE of: rxn02383.seq check: 712 from: 1 to: 636
MPVRVIVDSSACPTHVAEDLDITVINLHVMNNGEERSTSGLSLELAASVYARQLRERGSD
DGVLALHISKELSSWAAVTAADVDDDSVRVVDTSGLMVGAVGAAAMAAARMAKOGASL

QECYDIADVDTLKRSETWIYLRHIDEIWKSGRISTATAMVSTALATRPIMRFGNGRMEIAA
KTRTQSKAFKVLVLAQIRADGEPVFIAIGQN

>RXN02387 TRANSLATE of: rxn02387.seq check: 2544 from: 1 to: 762
VWMCLEPTWIKAGQDAVDLALSAADVPSGTYLIVMHSGGGRSKSMVKKLEKVAUVVHDAK
LKDRDRPGWVKQEFKNHKVQVTPDVIHALLEGVGSDLRELASAVS QLVEDTQGNVTVEKV
RAYYYVGAEVSGFDIADSACAGQMSKAVASTRRALQLGTSFVALAAALSMKMGVQIARLYS
TRGRINGEELAKELGMPFVFVEKTAKVARNWSGDAVSEAVILMADLDAAVKQSGSDPEFA
IESAVRRVAELARR

>RXN02398 TRANSLATE of: rxn02398.seq check: 7197 from: 1 to: 1602
VVEVKKNRLVLAPLTASLVFCNLAVANAWEAESEPVVINEVESNSDPVGVWVELANDT
NNNSIDISGWSLVDDKEDLENALVLPGEETIESGGYFYIYTDSDADYPTNNFTGGQEFYFG
LGKDDTIVTLRNAEGEVVATYSWKDLGEHAENTYGRIPDMTGDFANTGVPTPGAKNVAAEG
SGEEGVVANAQLPFHNVEITPIHLGGDFTEGDMSGVDFDANSTAWIANNDIGKLYSLAH
DIANNTYKLTGEWETGYPEGGGEPDAEGIVAATNGDIYLSERNADKNVSRPSILRFAT
PTGKTGVQNAQGEWDLSEFVGDIQPNNGGLEAIAQLEDNIFVVGVEETGDVIVVDSADQP
VLVQRYESSFDGVMSLDYNAATKQLSVVCEACDGLSEILEWDGEKLYKSDDKIYERFAN
LGNWANEGCFGTYSSELKCEGNTVSVTSYLVWADDAATNEGTSLSNAQVINGDCGVDNIPG
ESSSDNSSSDFATGSIAGAFATAVLAVVGITAGALGGFFQQLIAAFPALQQVIRF

>RXN02406 TRANSLATE of: rxn02406.seq check: 9586 from: 1 to: 549
METLAAQARTLLLEKMGVAPTHASFVESIAKAIPILSLLTLVTIVNGISSGNFPQPPALE
QVRTDVVNKNYERNLKLGLVSI SPELELHTAAQTIAQRNADSDSEKVPDPEGNLVVLQQ
NLFPYANANADTIVDRFLNSPDHVKLLLANDYEAIGVGVAYKGDHAWIVVEFTVAPADSV
STE

>RXN02407 TRANSLATE of: rxn02407.seq check: 3013 from: 1 to: 372
MNRQNLHYDQEVKAVESVSSLMNMSPPASPLATPDVLEDDVHTLSLENLFWLCIVWDDPV
NLMSYVTVYFQTVLFGSKKRATELMMQVHTEGKAVVSSGEKDKVGEDVKLHTAGLWATM
QQAG

>RXN02408 TRANSLATE of: rxn02408.seq check: 1367 from: 1 to: 912
MLIDVAGFLGHVTKDGTGCSVVIAPNGAFAGVDVRGGGPGTRETDLLEPHNSVQQAHAV
VLCCGSAGFLAAADGVMTALENRGIFPVRPEGPVPIVPGAVIFDVLGDPKNRPTAAD
GEQAVENAFAGTHNGSGSVGAGTGATAGRLRGFGQSSRRVKGKTYAAGVNAVPGVEVVD
LTTGALFGRPEVMGVGDKLSAAETLNTTIGVVATDAPVTKAQAKRLALVAHDGLARAV
RPSHSPMDGDTFFAMSGDGSVTPVELAELSAHAADCVQDAI IDAILTASPLGLKSKFR
ELLP

>RXN02409 TRANSLATE of: rxn02409.seq check: 5850 from: 1 to: 537
MQQWKKKGLMRQARYAVVFEPFMEVRLGDLSAAVSEALIQRAQSVPKDPLAEMTGMTSG
HKEAPTDPALARLLPDFQHEGDEYDGDNSFRLSLHEGDI TRAKLENLRVINDALPGDGN
VAVTASEEEHAWLAALNDIRLYVASGDVRGGEAAEDRENLVQNLAYNQESLLEAMMN

>RXN02428 TRANSLATE of: rxn02428.seq check: 3176 from: 1 to: 1134
MAATLDLPDPTDPIAYAMFACHFTGSRFTPAAARVSKTLAESGVACLRDFPGLSQSEGGF
SKTTFNNSVDDIVAAQWLTETHYSAPQLLIGHSLGGAASLKAAATKISCLKAVATIGAPFD
PAHAVLHFADRICDVEDDQGAUTLQLGGRDVTISREFLEDLAENVNEDHLRLRKLPLLLH
SPTDQTVGVNNAQLIFRVTRYPKSLMTLDKADHLLTKDGTQAQRAARIANWVEPYLVPE
VCEDDLPEFVAEASTIKASKYGAAIRTGGHNFTDRKDSQGGKNGLFTPTSLVSLAALAN
SQTIKQAAIDNRKIGLDDVKVTISQEQSADHGQIKLRKRISLIGNLSDADSASLRAASNS
CSITQLLAQGIVIDDEVN

>RXN02454 TRANSLATE of: rxn02454.seq check: 5811 from: 1 to: 1242
MKESMSITSSTYASALLTLPWGTPLQWPDNLIAALPRGISRHIVRFVGINRGIVAVKEI
GARTAHHEYKMLRELQRLGAPSVRPAVITGRHPAEEDYGELTAALVTHELFESLPYREI
FSRHILTVESEKLIRALSVLVRMHLLNFYWGDDVLSNTLFRDRAETYSAYLVDAETGEF
QPNLSERSSRLVDVDIRVNIIGELMDLQAGECLDKSIDVIALGGLVESSSYLEWLTETLAE
ESVDASEYWRLSERIDRLNLGLFQVGLKVTDKDSRQVVRIRPVVDPGHVRAELLSLTG
LSVEEHQAQRLLSGIQAYQAVECGPHVGLTQAAHLWMTNEYEPTIAAVPVEMLDKLEPAQ

IFHEIVDHRWFLAQERGGAVTLPEATASYLESVLPARRDEARLLSTNPSDEDLS

>RXN02457 TRANSLATE of: rxn02457.seq check: 8018 from: 1 to: 1110
 MFYFTVNNPQDPLSTEIVETNRRLDAFWHRLRPKDDDLATAINKICVRTGLSRKLIAC
 LFSICFLPLYPNFHKLVEKLGHLDMARINAITKAGEKVPSEKRELFDAYLVDTLPRAEA
 QCLQPASSISAMMRKFIQAHCPCDDKASATNDGSIYRRNNKGGISITVDATASEVTEIK
 AALEQMSKDKDCTPGTSLHHIIRGLPTKVVLNTYGTQDSPYLEGGTWLSKEQSEFWKTR
 TSSSRMDAAHFSYTTAYATPREMRVYIKGLRITCSVPGSCVAVENCQLDHIIPWEGGG
 TTPWNIHPLCVFHHIQKTEGRLQCYPLPDGTVLFLVDGIPVFSIPDGPGLSKNKNTWGTKE
 GKYMERIRIAA

>RXN02460 TRANSLATE of: rxn02460.seq check: 7527 from: 1 to: 504
 LRVIYPATFSTLRGLNESRVITARSGYGFVTPALLDFTYTDGDEEIIAHAAFPQDAEASI
 RLLAIGDEETFPYRRVVSVVDVDSVVTYQPENGESVVKLSPAHLNDDVAIHIHIDEAS
 EADTKKAEIVIDESDLGEEDAELTVGDAQDNFMAWYDPEELPFVIELL

>RXN02464 TRANSLATE of: rxn02464.seq check: 6833 from: 1 to: 1200
 MAAKLQPLKRTKKDLIATGVITALAVIGVGTVWATAPIRGSELTPADEPFPIGSTLDAIP
 ETLESHWRDLDLTNHNKPLITGGVIFTADGNTIKTYTPDGALLWSYRDKELCSLSVGFQ
 AAVATYKTIIGCGDVTAINANDGQYQATRSALISDHPVAPISNSDRIGRLGTERLELWRSO
 LVRTIEYGDVEAPQESGQQPHPECSITSAMTRKDLLAITEPCPDGSSYLRFMGTTTPDDSR
 TPEITQDIETDGRIVAIGQSVAAVYTNDSPPRIVSYNDNGELVGEQAVDEVEFPDPFPQ
 SATADLPHMSWFGDSLVLFSPQLNVRQSFNDALGTGIALNGSLLYPTAEGITVANWD
 TGEVQRTIPVDRAGYDGEVALGVVGQVIVEKRGSSEIVALG

>RXN02465 TRANSLATE of: rxn02465.seq check: 154 from: 1 to: 399
 MPASIRWGGVALIQSTIGFGYAFFLIYREATGETDPSIVYETDNANTWVGVTGAFFII
 VFGTVVAGAINMMKGHRWGRGAVVMLNIILLPAAYYMEIEGRFSWAIVTGISALFVLGAL
 FNKRAVLWANNEI

>RXN02466 TRANSLATE of: rxn02466.seq check: 2914 from: 1 to: 87
 VEGEQEQTFITYVIEIEDGVNTAAAYGGDDA

>RXN02505 TRANSLATE of: rxn02505.seq check: 6513 from: 1 to: 171
 VAGTHAVYNETLSENEFSMCRKNEPLVIELENISIDRIVISTDAHRYADELMAAV

>RXN02510 TRANSLATE of: rxn02510.seq check: 1304 from: 1 to: 636
 MDSSDSHVQGDVYDQGLGEPDRLERLWAPYRMSYINTRSGGKQSTAKRDPFIEVPKMS
 DEDGLIARGELVYCVLNLNLYPNAGHMMVIFPRKEKNLEDLSLAESAELMLFTQTATAIKAL
 KQVSNPDVNVGLNLKASGGSGVDHLHVHVVPWWSGDANFMTVIDGVKVLPTLRQTRA
 MLAQAWGTIDGAPGTVDPTLTSAIRTAAPKEH

>RXN02519 TRANSLATE of: rxn02519.seq check: 317 from: 1 to: 1629
 VEDEQSLGATLPDVTGASSINDRDTDASGLEPEKIRRFARLRLIGTMGALMIAFGALG
 AGALPVNNPNYPVDFPGGNFMSRMLQTSMSIVLIGVFLVAVLMAPLVGIPEKRSNGRT
 ASVLSMLRRTFGAWVAPIMLTAPLFTQDIYSYLAQGSVTAQGMDAYAGGPLELLGPDNH
 LARSVPFIWAQSPSPYGPVALSIAASISVITNDSIVGGVLAHRIASLLGVVAAGWAITML
 ARRCRVSEASFYGLVNLPLLIHLIGGIHNESILLGFLLVGLELGLRGTDRITGLWGP
 AWTYITLSGVLISACGLVKVTGFGILGFGVMALARAFHARGHRHVVAIGVAGLVQVAALV
 ITVVVLSVITIGSLWNTGQGGGAATIRSMWMTTINIGVISGPIGMNLGLDHTAAMLVVT
 RAAGTAAVAAMFVMRMLFATYRGHIAHVGGLGVAFTFVLVILFPVVHPWYMLVAIVPLASWA
 NRLFPQGLVIAYSTAFSFFVLPRGLALPVGTVFSIFYGAALGFSILLVWWSLRRNPTF
 GLH

>RXN02520 TRANSLATE of: rxn02520.seq check: 9529 from: 1 to: 684
 VGDVVKGNDAHTGDTRRKILLILLERAPVIASDIAEQQLSTVGVRRHLDNLVNEULA
 EAANPRQNPYEPKMRGRPAKTYRLTDKGRSIFGHEYDSLAAAALATLREVGGDDAVRQFA
 RKRIETIVEGITPADVTQDSIEDTAKSLVEAFSRFAGYAATVDATRNLGLQCHHCPISTV
 ATEFPPELCEAEHQAVSELLGQHTQPLATTADGHGICTTINIALTPIKHS

>RXN02534 TRANSLATE of: rxn02534.seq check: 3127 from: 1 to: 804

MNSPNADIILVNVKLSKFDIENIMLVGARCDDIHHQQKYRQDTAGRRTKDQVDFALALESW
DDFNLLKQQFSPTGNWQGITIGNIPVDLVFGNINENPGEVLRSKRGHLLNVAGFEKVEFV
QAEVLPLNDADIKLSTVPGTLAKLHAWLDRKENNIKDASDLALILSWYEDDETLLNWR
YFALENQCYIGEPEAMAELLGLDTGRILGHKETQALLDRFNEQSPPELNQFAESLEAPP
EHSHPLERRRIQVEALLGLRDSLGIDE

>RXN02537 TRANSLATE of: rxn02537.seq check: 3878 from: 1 to: 462
MLALKSSLEGIATSLTAVAGALHESNTDRLOQSQWQLEMTSASSLIQGGIKLVLYPNRPT
VNIVQMKHTASTLFNTADFLRLTEGYVDVLEKQADKSITLTVMLRYIASLSSLLDLMA
REINALCTAITPEPLKHLGDFGLTPPQQSTSFIV

>RXN02538 TRANSLATE of: rxn02538.seq check: 5301 from: 1 to: 672
VNAPPEIRALAEAHPEMDQILEAGDGLSVASFGDIDRATTVTTIVAGVGSNNPGEWNTYVD
RARTVSASTGSATVLMGLGYQAPASIPAAVSGAAANRAAADLQRFQAAQLQRNPHGRKVV
GYSYGSYVVGKAASSGELSADALVLVGSFGAGVSHSSQLGAPVAVTGSADPIGFAGTQY
DEIHTDTPDALTFGATVWDS PSTHSGYWNDEFLNGVAEVVRGK

>RXN02555 TRANSLATE of: rxn02555.seq check: 3981 from: 1 to: 603
MGEQFPFGDKNIRVSDTERSAAALAGQFYAEGRLSLEETDDRCEAVADATRGDLNAIFY
DLFPNQIAVVDRESEQTYTATEVAELHRKGARPRAGILGLTTLVIAITGTAAFASTTAFATV
LLALIPVIFMLVYMKIGPESWHAPTPRQLQRKRMIELREKEKLDLMELKAQRKERTHAL
TNRALDAAETAFTNFKPWKKNK

>RXN02564 TRANSLATE of: rxn02564.seq check: 3452 from: 1 to: 1002
MAEVAEPAGSAGSQSTKQFVVGTAAVVITAAAFSISQASGGEDIRSNMTLIPAAAGG
GWDTFQREQQQSMRVNKIVNNIQQVNI PGAGGTIALGKLSMTAFTMLVGGTGTHIAAII
QDFTPAKIQDVTPIARVVEEFDIITVPADSPYNTLEELIEGKADPAGVSWTGGGSDQL
VMTEALASAGIDPKQTTTIPSDGGGEAIIQALLNGTAKASTGGFADMYFQVEAGRLKVLGI
AAEERLPGSDIPTLVEQGYDVTLTNNRAMFAPPLSDDQIAELRAIVAESVETAEWQSAV
ERNYMNNASLEGEELDQFVEDEIDRIDQLFKEMG

>RXN02568 TRANSLATE of: rxn02568.seq check: 2134 from: 1 to: 1653
MDGTSPPQNKISTTPPAGNAIPAPGGAIPPAKTEQDAVPPPTVAALKPVPGSSIPAPGRA
LPTVPAPGSSVPAPRASAPAVPNVPAAPGAAPVAPGISIPAPASAPGSAITPTGTAIAPV
GSATVPVAPGVSAPGASVPSIPVPGSVTPPAPGISAPGGALPTPGSAPPTPGGALPTPGE
ALPVPVAPGAPGASGIPSPGLPTPGVPTPGASLPVPGAPDAPGTPSIPAPAGFQAPGIPA
APGAPAPAAAHAKPVFQDAEKRPRTDEAGNAKKELPLRVRLAQPIITRKQWAMTLGVVLV
AIVVAAIAVVLAKWAFTEWLQDFVEKYPGKYDNPEGAPVGIPTWLSWQHFFNMFFMVLII
IKTGIEINRRRPPKGYWTPKKGGKKISLTWLIHVLVDLLWINGAVFIILLFATGQWMRI
VPTSWDFVPNALSGALQYVSLDWTENGWANYNSLQELTYFTTVPFIAAPLSIVSGFRMSS
YWPKNNAITMKNLIPIGFARALHMPVMVYIYVICIHVFLVLATGALRNFNMHYAGQDVVN
WVGFGWFVASL

>RXN02593 TRANSLATE of: rxn02593.seq check: 9101 from: 1 to: 597
MEAMATTITVPSPTHSPAQIREITLSAAEKEDDVGDFGVPTTHPRNVTIEVDDDELINDCLG
WLDDVALASGLGIQYNDVLYRGDEDISFTVQTKNDDARIGASRLGLEHQLNVLAGSSG
DSGSDGYLKIAHFDDLNDPDESSYIFARSLAEVDGWTLEFGVAGVKNTITVSSDDAIT
TILRWMGEDIRDLNWTRA

>RXN02606 TRANSLATE of: rxn02606.seq check: 7692 from: 1 to: 1371
MQEIHITMKHMDALIDPSAAAFKATLPFAELLEKHNNKALFDAALAKSAERADAGRII
GKTSHIDALAYLLDISKSEAFRRTKRAEEHYGNPSPEPSSSEELAKETPEEKLAREEKEQ
DLAEQAEANRLAREHGISAEKQDTRIYELEKINDNTSLSRASLRKLAMQEATSRTPEDLR
NWTNRNKVIRINPTAKDPLAAVKKRSLSIGRQDHGGAKASLYLDAGKALLKSLMSKAP
GHLLDDS LAEDKRTKPRQYDAFADILHRAHSDLLPARSGVGTIILVLSAKDVNTLKASG
PDHRYPTSTGILKLTPLILRLGAAYQDFVTVLDSSEGRPLHLARTQRTASLYQRLALPAS
ELVCTREGDCSPFEDNEIHHIRSLWDGGPTDIENITNICPHDHGNNNDQRDGDKNMGHMN
IDPTTGRVGYQPADRRKPMRFNNTAAAESGGAQART

>RXN02610 TRANSLATE of: rxn02610.seq check: 4081 from: 1 to: 927
MRKTITVIAVLIVLALIGVGIVQYVNTSDSDFIGQPGEPGTGTETTEFPFQDWCFAVEV

IAAPGTWESAANDDPINPTANPLSFMLSITQPLQERYSAADDVKVWTLPTYTAQFRNNINSQW
 EMSYDDSRNEGTAKMNEELINTHNECFATEFIIVGFSQGAIVIAGDVAARQISEQGVIPAD
 SVRGFWALIADGRREPFGVGQFPGFTVDVGIGAENVTLQPLNLLVQVIPGATMRGGRAGGPGV
 LNDNRQDICAPNDAICDAPVNVGNALDRALAMVSAANGVHALYATNPDPVFGTTTNAWVVD
 WATNLDNG

>RXN02624 TRANSLATE of: rxn02624.seq check: 3015 from: 1 to: 1296
 VLI PHGVAVLLVI ILAVASLMFTNSSMVNL SATIAQLWLSNLNGAVDGSGEVIVSLPTLP
 GFTFLWAI AARIHRAVKDRVSIADLVGLAALVGLI PLALT AIAAFMLFDASSVLNVEVPP
 ITRLLRVMFLHLSALFLGMGPRLLKQALARRYGAPEWLIDAITQAFRLIAFTGTVLSVSLV
 VMTAINHSAFTATMQGYDDASVVALIVLSILYLPNNMIFAMCNLIGSPLYFGDASISVF
 SVHSVLPPLPLILAALPSEALSVAVALLVIPAIATWVCVRNPMRLAVNNTAAVISALCF
 LVLAVFAGGTGLGVYNYVGNLLASVGLVFVYFALVGLLIAGIDKLRNPVEVKSVAKAVAV
 EPEPEEVEDEEHVEEVEDEEEVEEGVEEVEDDAEDPEENPEEEESDEEIEETETE
 EETNDGSEADER

>RXN02626 TRANSLATE of: rxn02626.seq check: 9067 from: 1 to: 1005
 MSTQVELKTPKSEDRAAYIAALGFPVLVIIGIIGFTASDVNLINISSWVNPPLGIMFESM
 GLTLKPFVDALVAKRPLVLIIGVIAQFVIMPLIALLVVVWLQPAEIAAGVILVGCAPGG
 TSSNVVSYLSRGDVALSVMTSISTLLAPIFTPLTLWLAGQYMLNNAOMVASVIVQVVL
 IPVVGGLVVRILFPTLIGKVLPLLPWISVIAISLIVAIVVAGSRDKILEAGLLVLAUVII
 HNTLGSYGLYAAKFTGQPAARRTTAIEVGMQNSGLADGLASQYMSPMALPGAIFSVW
 HNLSGALLALCRASDKRAAEKVASEKAASEKAAS

>RXN02656 TRANSLATE of: rxn02656.seq check: 1781 from: 1 to: 840
 MIFGVLAYLQWGMFPFAFFELLPLPAGPFEILAHRLIWTAVLMMIISFTSGWKELKSADRQ
 TWLRIILSSLFIAGNWLIYVIAVNSGQVTEAALGYFINPLLSVVLGIVFFKEQLRKLQIS
 AVVIAAAGVLVLTFLGDKPPYLAITLAFITFGIYALKKKQKMSAASSLCAETLVLLPTAV
 IYILGLEASGHSTFFNNGSGHMLLICSGLVTAPELPLMFLAALAIPLSTVGMQLYLPFT
 MQMLNALFVVNESVEPMRWFGFVFIWIAVTIITDLSLLK

>RXN02673 TRANSLATE of: rxn02673.seq check: 5852 from: 1 to: 633
 MAALVLVLVIALIIVAVVALRGSSSEPEEEQPNNAVTVSSMESSATSSSSSESTTEAT
 TEEETSSAEPTATSSVAADAKKTCESDLVISASTNQPTSGSAQPELFMAVHNPTAVDC
 EIDLEENKLRFEVYNLATNARIWSDVDCNPAVEDGTSVFPAGEDRYFQATWSRTTSAPNQ
 CNNRTDVAGGYLHTTVGNNPSPAVTFNLT

>RXN02680 TRANSLATE of: rxn02680.seq check: 5186 from: 1 to: 1284
 MRLNKRPLAALSGLLSAAALLAGCSTSGTAETTTTTVSSAAASTTTSTSSASSSSSSSS
 SSSSDSSSTAETISNTAEAAQAFSLSTLSTEEQDAVLVDYDAEEKSTGWSNFPVTFVQRSG
 VNLTDLTTEEQAAALNVLKNLLNDDAQMIEDIMASDQYLNDESNTTEDSLGQYIYAFEG
 DPSSSDSDSIQFGGHHIGINTTFSDGAITFPAHLTGTPQSEWNTNEDGETVAHLSNMNYETA
 FAFYDLAEQQQAQLYQGEELDSMVCAPGSTCDYPTGTGLKSGDLDTEQKELLIDVIANW
 VGLADEETTETELDAIRETLDDTYINWSGATEYDTSFGDGIYFQISGPKVYIEFANQQQS
 AGADIDGVIITAGWGHITIRDPDNDYANSVTQEAASGMGGPGNGGEMPSGDMPTGE
 MPSPGAPSN

>RXN02693 TRANSLATE of: rxn02693.seq check: 9728 from: 1 to: 1776
 MVSPLRLASLLTTRLATLKPAKLPATHLASLGAQVIAELVPGIRMSPNRRRILPANMGAG
 FIGAETAMMWALSPSLLPKPWWVTAAANLAVLQAVGHAATGIHSLPRNRRVSRYLIYNA
 THIAETAITLTITTVGLIRHRTQIRLIGQKNFGPKETIAGISVGTGLYCALLITGELTGL
 SINEVKLLIERFLPPWISFIAAVSVITLTTLTLADRVLLRRLIHNSAIAQAHLNRMVFPFG
 TEQPEWEPERSGSFWSYKQWAGVGSQGRAVLSGGPRKDDIITVTRLSDTETHEPIRFIGM
 VPGRSLSDQVDLVIHEMRRTGALRRDHIINNSTGTWITDWSAHTFEFLTGNGCNVTISM
 QYSYLPALSADWYKNDNGPINAARMILDAVLHELDPQTGSRPKPLFAGESLGAYGLAEVW
 GDVEKLLGTADGVLLSGAPRFSDDAMNLRTRDASSERLPVIDSGRHIRFAGEPEKHLDM
 PATWQFPRMIVAQHASDPVWVWNAELFIRREPLWTKPKQDQDVQFPRLRWMPFVTGQVQA
 LDLFSTSVPGGHHNYHEEFIDYWAALLDREVTELRHSIAYWIRANRHIK

>RXN02696 TRANSLATE of: rxn02696.seq check: 3394 from: 1 to: 456
 MSMLKKTKEFFGLAPYEAHEHDAYADEPRYEGTAAYAPEYRERYGYAPAPAPVAPSP

APRSYQSTIVPVELHSFEDAQVIGGAFRDGDVAVFDMSSLRSREARRIVDAAGLCFALR
GRMQKIDSVTFVAVPELSNISTSELEAARIR

>RXN02697 TRANSLATE of: rxn02697.seq check: 1664 from: 1 to: 1527
MTLFQRITNPVVLGGLAGVLLLLGSGGGAIYRGGVLDALGLNFLAFGHAQGSINTVLW
VGQLLLLGAWVHLGRRLFKKKVADDTADAADLGLVKRTLYAMVPLI FAAPMMSRDVYSY
LMQAGMLRDEGDEPYTEGAANVPGLMLLEVSHDWRNTT PYGFLHLWIGDMITTVVGNVNT
LGVVAYKILSIIGLAVTGWSTVIRIAQHFGANPAIALWIGVANPVMIIHMGGMHNESLMV
GLSVSGLLLALKKRFVAGVALIAVAVSLKATAAIALPFVVMIGMHFAGFLATKKGKDS
TLKQVPAFFATGAAGVAVTGVVVSIAITWASGASWGWISEISGNSKVINPLAFPSLVASV
ITMVAEVFPVDDFDYNAVNVNVRISMLIMLGGVVCWWLFRQNERAVTGTAAAYAVAFV
FNSVTLFPWYASLISLGTFKPPMMLIRFAAGASVFIALMFTGSGNHQLYNIVTVIIAAI
IAWLATVVIDDTPATTATEKPSPTVS

>RXN02720 TRANSLATE of: rxn02720.seq check: 5443 from: 1 to: 702
LERREELQVRLLQVQARIDATLNEHNRPESVRLLPVTKFHPVEDIKIQEFGVTVAGEN
REQERAKALELPMDMFHMIGQIQSKKANSIARWAAVHVSVDSEKIAEALGRGVVALGDR
GDRTSDELPCFQILSLDGDPSRGGTPLSQVTQLADICISDTHLRFEGMLCVPLGLGWPEK
AFSQARDVLSGLEEHFDRSLEFSAGMSGDLVAAIKHGSTIVRVGTIELGNRPLA

>RXN02744 TRANSLATE of: rxn02744.seq check: 343 from: 1 to: 804
MSKFPFENSALRGSSRFPAFTTTPAPKRATPAKMLAAQGMESLFLRHGEQQLLSIIIP
VALIALANFDPIPGENSLDKTFPFALATAAMSAGFTGQAI SLAFDRRYGALKRTGASGVP
AWTIIIFGKVIIVAVTIVQII FLGVLTALLGWSAPVGGVLFVGIITLVGVSSFTALGMIM
GGTLLSELVLALANLIWIVLSGLAAWAVFSPSVNAEGVLSTIPSVALSQGMVDAENGELP
WLQILGVWLIITGVAANKLFNFSASR

>RXN02770 TRANSLATE of: rxn02770.seq check: 2969 from: 1 to: 1566
MLVAALVMTSCGDGEPEPTSHQTSLEFYAVNSSLATTNAASLLGVANDAGLLAARVYPGV
YVQGPSPQMIPNTDLASTQVLPGINRQVIYITINEDATYSDDGPVVCDELLSATAGQMPE
LFQSHVPLTSQIERVDCVSGSKVATVVFKEDELGERWRYLFEQGDLLPAHAVASKAGMTLE
ELNQALDKDKDEALTEPARVWSEGFQLSQFDPPELTAFGPYKVDSVGFEFVKLVLRVNEFY
SGDQAVEAEITMWPKGSLSAIAIDNGNLQIAHVVAWESEFPWNRRDPLNPYDIKEEVGVL
TEQLTLASAGVFIYAAEARQAFACVDQEAVAASSSISGIDVPAGVGHVSRHQNPVHVQI
GDLPAQHMAVDINAAALAGQSIRIGYDGPDERKAAMVEAIRQSCPEAGITTVIDASQEA
SLNDSRTEVSEWGEYQYFEGTLDVAVLRTVDPHREYENANTIGTDAESTRRTEQLWAEV
PSIPLAQPRVFIIDRTVGNVVNTDLAGIOWNMNRWSRSEE

>RXN02781 TRANSLATE of: rxn02781.seq check: 9745 from: 1 to: 1191
VVAALVEGFLLPWTWERGLSDAALKFVFEQGPDAAREVLGTIAASTISVTGLFISITLVVL
QLVSSQFSRMLNGFLNRNIRVQATLAMFLGTFFVFSLTIVIRYVWSEDEIDITGEVPRASVS
AFLLVLGCLGLFALIRLITFSMRVANAISEIGETMALAARIYFVQSDDAGFPVQGGFWS
PRPGDPREIRVRGNHGLSVWIDYRKLVSWSSTEHQAVITVDRPVGDFLVEQGPLLRVWWDG
ELSDRDRVLHSAIEVTERELHQDVAFGLRQLVDIADRLSPGINDPATAQCCQVEIHR
IFRYLTVTIEPSPYIADDDGRVRVHVQFQRIADMLVEYVREIRHEYGADSAMIPRLLTMY
EDLVTAADHSLPAVERARGILODETDDEDRSDTANV

>RXN02782 TRANSLATE of: rxn02782.seq check: 837 from: 1 to: 1299
MPTLLIDTHPLHAQLLDPLGELLTAGSNKKVQWQCPKHSNHIWTSVNNRTNAKNPRC
PYCATSRVLAGFNDLATTTHPLAVQLVDQDIIVTISAGSGKQLWQCVVNPFKHQLWATPN
NRTSTKSASSGCPYCANRAVLVGDNDFATTYPELAAQLVDQSAATTAGHNPVEMICC
KHEPFFTWKTSPLRVRQNTQCPVCSERTIVAPALNDLATHPKLAQIADQGPFGSVGAAA
IIPITISRGSTQLTWQCSKNHDDQWVATVKDRVRGTDCTCANTGTSRKEALEIEVIRAL
FPNTDQDQGALINGRTGNQASPSPTDLIPSKNLATEFNGLYHWSLEFKIDKHYHANKSA
LAEQAGVQLTHVWEDDWNLRDIDIRMIHAKHLATHNLSAVLPTETTSRVATTAFVHVS
HCRWLSLVHALLHS

>RXN02812 TRANSLATE of: rxn02812.seq check: 3189 from: 1 to: 339
VWAVAINAGNGISEDQARAASDFSSFSFDTGNADNSALESVLTQASSESAETTEAQPSE
TPVEPAAASPSDTIINLDTSSNMDRVVDGSGQETHTVTSRTLIANLARETGAQG

>RXN02817 TRANSLATE of: rxn02817.seq check: 7091 from: 1 to: 399
MILGVPIQYLLYSLWNWIVDTGFDVAIILVLAFILIPRIGRLAMRIKRRVESAADADTTK
NQLAFAGVGYVYIAQIVAFMFLAVSAMQAFGSLAGAAIPATIASAAIIGLGAQSIADFLA
GFFILTEKQFGVG

>RXN02818 TRANSLATE of: rxn02818.seq check: 4037 from: 1 to: 606
SYSRKFLTQVWIRDNVGDYKGLTDTAFRKLQRDLAYLRVRGVPIEQFTVTSGIAEGGQA
YRLAQDSYKLPVEVFTPDEAAVLGMAGEMGHNLGLAFARSGWTKLAAAGAQDRLSTSTA
LTNAGDLGSLSAKTLDAIIKARQLGKQISFEYRRAPKDAFSLRHMDPWLGVPERDRIYLV
GFDLDRQEARTFRITRVNRNKL

>RXN02825 TRANSLATE of: rxn02825.seq check: 7394 from: 1 to: 1839
MKLAPRMMRSPKTPFAALASLALVIGLGQVPIAAQAEYRTASDGLNWGFQSRFNYIQ
TGVAKGSITLGDGASDNGGNFAFTPRNTGTTVTSDSQGTVEFNGSVHFLGHQAEDKWIQD
TTMSDIKMFVNGSSAQVLVDLVAREFKGTTYYDIGEYIISDDIVLADVSNLSAADFSQDS
IDLSTGTTDLTAAGAQAQFGGFYETGEALDPTGGSLSITSTTAPSTSTSTSTSGGTAD
CSSGALGVVTTGTNDGMLGTIQEVNNTFAIWNNLIVNTERMFCNIDTLKARFDTDDSSDS
ATSSTSGTTASTGTTAATAGTTGTTGTASTASGTSSTSGTAAVAGTTFTPDNGVCT
ASGSLGVQASQAQWGVKASQFNYIRGSIANGSWTLNGVGFNDQOQFQSGNSGASVAENKTL
GSINFPFSIHFTGHGILDMQIANIEISFNNGSGLIADVVSDDMGNSNTRYGRTVVGTGL
NFSALNVSATEASGSASVSLSQSGSAFADFTPTGTQLDPIFSFATLGGDASCATGSTST
TGAAATANTDTEGAGEESTTPANQNSQFQIRQAAADSTGLDTTMTMLLILAAFFVAGG
SMTRFTVGNPTGK

>RXN02838 TRANSLATE of: rxn02838.seq check: 4352 from: 1 to: 528
NTGKGGGLTVPLGDGQGRYIAKFSTAFVGVSENEFANLALAEATGMEVPAEVLVGRQF
EGVPEFEAMTDGLVLLVRRFDRAGDGVVRHMDFAQVGLYPARKYDQASHDIAAVLG
SAVSIAAGLEFVRRLLALSVVMGNGDMHLKNWSLIYRGRGDVPALAPVYMMSTVY

>RXN02840 TRANSLATE of: rxn02840.seq check: 7123 from: 1 to: 150
MTVISGALNVLLPDATDWQVYEAGSVFNVPGHSEFHLQVAEPTSYLCRYL

>RXN02841 TRANSLATE of: rxn02841.seq check: 2452 from: 1 to: 435
MFTAFKSNPTTIKKVLSELINGDDAALNELERHVTNESVRARELPNVQYKATACRNFAIS
KLVQNLRRINKAQNPRGVTHATVILLKEDGSDGEEQWRIPKATIPFDMLRSPDFNH
NRLKNRPLMVESQYPWGVFLIKMN

>RXN02846 TRANSLATE of: rxn02846.seq check: 4539 from: 1 to: 750
VLTIIVLLASVLIGALLQRTMGLGVGLVTGPVLTSLGLPLAGVTMNVGLSIINAVNNAW
SVRKRTDWAKEFRILAGALVLGSVPAAVAVYFLNGFWLLIFVGAMVLLALGVSLFTEKFA
LKQEAFLPMVIFGMIGFMSTVAGIAGPSLTVYARLSRWYDRDFATLHVPVLLVANTVSF
LKLVLILGGLDFGGAPAWLWIGAVAMIFVGAWLGEIVNAKVSFPMKRIATLLAAAGAAV
VLFRGIMELV

>RXN02847 TRANSLATE of: rxn02847.seq check: 8481 from: 1 to: 1089
LALTARGFLNSERSQTRWKTHTFTQKVPKSGYRYDLGLRGIAIAFVVLVHVFVGVKVS
VDVFLLLSGYFFLGSQRLYADRPDSINPWWPIWRTLRLLLPALVLVLGVSMVLILAWVP
RLQPTIEIANQAVASLFYVQNWELASQGAAYGAASAESVFPFHLWSMAVQGOQFYLLFAILL
MAIILIRRYREYSAVRLATPVLAVLTVSFSAIILWHFIDQSVNYYSTFTFRFELGLGA
LVLVHAPRILISAKTKSILAAGVLFMVLTSTGTFMDGAETFPGPALYILGACLVILGDG
KISVFLSRKMWLWLGDIAPPLYLHWWPLLIIFTALFNQEEPISWLGIAVIMLSGLAQLT
NKY

>RXN02849 TRANSLATE of: rxn02849.seq check: 4597 from: 1 to: 282
SPYPMVISTDASNVTVTRIMGVDTTSVESINNGRWSTTPQNTVRVSGSDCVPSTGAPGF
TTSDFRITSLSGNEITRETVTIVYDPSPNVVC

>RXN02911 TRANSLATE of: rxn02911.seq check: 602 from: 1 to: 459
MRTSKKEMILRTAIDYIGEYSETLSYDLSAEATGLSKSLGIYHFPSSRHALLGMHELLA
DMDKELRDIRDPEDEPLERLRAVVVTLAENVSRPELVLLMDAPSHPGFLNARWTVNHQW
IPTDDLENDHAHKRAVYSGAARSWPLRLHLS

>RXN02914 TRANSLATE of: rxn02914.seq check: 6261 from: 1 to: 543
 MVGNSIWIASLLGLSALISTYPAILNLLQLVGGGYLTWMGIGAVRSWWTKRSTQQAAD
 SQAVENTLVTATAASVGVWPAIRSGIATNLSNPKAVLFFGVSFAQFVRPDMGIGWSIFIG
 VFLTLTGLLWFVGFVAVLVRKLAAGLTRNGAII DLLTGVIFIGLGMFMI FEGVVGIGGRVV
 G

>RXN02921 TRANSLATE of: rxn02921.seq check: 4157 from: 1 to: 471
 VSALEESIRIATIAAKAADEKKADDIAVIDVSDMIAITDCFVVASADNERQVGAIVVEIE
 DDMTKACGFEPKRREGNRENKRWLLDYGLVVIHVQQAEREFGYGLDRLYRDCPLIEIEGLE
 TFKRESSWSDEADIRNIDSIDELPLPAEYEPGYEDD

>RXN02924 TRANSLATE of: rxn02924.seq check: 3999 from: 1 to: 549
 VPSVASISERATFILTADHFLRSCSKVIYVRGENFTATATTSLSVFGTDLGLIKLDGKAP
 TMPLPLFADKPLRVGMKTTTFGGGLPSATVAKEIHGRVISAIPHGVSRRNITRVHHGAL
 IENSPEKAVKXGDSGGPVLVNGRVAGIQSMISDPGGFNTGVATAASLIQHMPALAAQALELL
 EHS

>RXN02927 TRANSLATE of: rxn02927.seq check: 3221 from: 1 to: 468
 VADEGSILAWFPCGDEAPVLVVTLCFAIFGEVVVAEVSATGLVAVEGVDTHFAEVEDVVG
 YACCVFENLVHLIGAAGDAHVLPEVIAEGTDLVDAILEVYVSGNATGEVQDIARLAVVV
 LRSVNVVTDPLWAVAHEAVNASLCTNRNCLCFWCIL

>RXN02928 TRANSLATE of: rxn02928.seq check: 382 from: 1 to: 693
 VAGRCNTHWAGVWLANCLFVHGEEVGVTLADGLVSEALGGVAEVQCVSVVQRNSTETSI
 DLLGDRTGNSVNTWDEVTCEVVAALQEVVALILRDGVNIAVIVRFLRGPDAAVVTVQRHGHQ
 NGLGLPGGVHRQAGWVELDERWGREVCAGFVCTHDGRGVGLQGQGGHVHVAVATGCQDN
 GMAGVCGELAGQVAHQAFALFTVTFGDNVDNVHFMGDEFYGAEVDLAL

>RXN02931 TRANSLATE of: rxn02931.seq check: 8393 from: 1 to: 225
 MQPYPRNPPIEKRRQEVNRNSRNAVSVGGGIVGGAALWLVEGSAFFMGLGLIIAVVGGFY
 YYNKVQKIINEKDRY

>RXN02932 TRANSLATE of: rxn02932.seq check: 938 from: 1 to: 972
 VSKTEEGRSAAIIYAFPTFILLGAIIFIPPEFPIPLTNYINIFLTIMFTMGLTLITVP
 DFQVMVLRKPLPILIGVVAQFVIMPFLLAIVVAKMFNLNPAVALGMLLMSVPGGTSSNVIA
 FLARGDVALSVMTTSVSTIVSPIMTPFLLMLLAGTETAVDGGGMAWTLVGTVLLPVIIGL
 VLRVFLNKWIDKILPILPYSILGIGGVVFGAANAERLVSGLIVFVAVIVHNVGLVYV
 VGYLTGRVFKFPEAANRTMAIEIGTQSAGLASGMAGRFTPEAALPGAAVALVHNITGAV
 YVGLVRNRPLTKASRKKEVAVSS

>RXN02934 TRANSLATE of: rxn02934.seq check: 3200 from: 1 to: 306
 VGADDEFDFEIDAPEAGFALVDAGGVSFVEFPHAGFEGEVVTVVVGEGDLLAECVLSV
 FCGVGLAFAAPDADEREEREESVVEVGAEVSGVVVRDKVT

>RXN02936 TRANSLATE of: rxn02936.seq check: 3720 from: 1 to: 198
 VVAPFQLVGLVSVQLRSSFSEPAATEEAEDTEAESPTTPTGLPAAAASIATLDNASSLFF
 SRGIHV

>RXN02939 TRANSLATE of: rxn02939.seq check: 7866 from: 1 to: 1602
 MNLHSLERIQISSGTISERKTWIFPTAARSFNQNLVHPQSIEDIAQTGVILAMENLQRT
 EVESVEYPTDLNPAWGTGPAISWPLKDPSIDFPDPLHSSISELPQSDNPRHLRVSISLD
 AVEGAFPRYRIGDSIRIPLVFARDTFPMSGLETTTRAWIEAATEMDIHNTWPIILITGDGW
 TALSHSKPIRHEAELKGWFFHSLFGSEMPITDLKIERIYGGGLGTFDSGATRQELTDTD
 DAYTENGSWLLEIVDATLDGAIPPPQQPQFASITHIVDEQLVVLGQMLPVLRCDWLE
 TCKYLGQTYVPIVSVSHSRQLQFSEGLIHXYENAWSLNPGRVRLAEPQWPIEPVIELDVPA
 PWELQESFPDGLYSLTDGEQTLGRSTPAGQLEICVISLNDGSRILNAGRVEDLYFVQVFWG
 MTVFLNSNFQVQSAEEHQLGAKRERWITQEGVAAKFTFEDEIVFLDQISESEITRWKTPE
 GYFTEVRILSPNHNILVPTTGS DYLPVPSSVSVFRDQQWSNKKFEDSVSEI

>RXN02950 TRANSLATE of: rxn02950.seq check: 7742 from: 1 to: 324

MTVFNVLHDAPAPQPDKNRPGVKRLQLGGDGANLIAFTFSFGQSLPDHRAAHPIVTAFSG
QLTFSYGEETFELSPGVTVHLEAGVTHRVDCPPEAPGDASNAVNYAHW

>RXN02951 TRANSLATE of: rxn02951.seq check: 852 from: 1 to: 609
MSSLTARKASGDGSEKKKPLFRARLFLTHPPHKQVNSDLADIREGLGLGVDDSHEGSK
PSNDHSLHKEPIEIVMPETSMARLIFYAPMDMGQTDPGCEVVWIAWAPADGPPQPPRKRAI
VVVGRNRNALLLGLISCNPEHRTDEWDIGSGSWDPGRGRQSWVRLDRVLEVPGLGIRQ
GTVVPPGRFERIANRLRDNFNWV

>RXN02957 TRANSLATE of: rxn02957.seq check: 2405 from: 1 to: 291
MQTAGGGRVYTSLMDEKSLSPFLGLPGRENIGLRHWHGLSTMLRVLNGIVYVLLFATG
LWQGIPTSWDVFFPEAWETLKVYLGFRAFGIEHTPL

>RXN02967 TRANSLATE of: rxn02967.seq check: 8901 from: 1 to: 318
MDLLVVAVHEGGQPRQSDCNAPGCAHTWLCAINFQLGAGVVEGGVEKRNVFEGGTFLGPE
YGGRALRAGGGVDIGEQDPFDGGCGDVEFGGIDVIEVDEVGATGS

>RXN02971 TRANSLATE of: rxn02971.seq check: 4841 from: 1 to: 312
LIAIVALVALVWLFNRSDSGSTTTTSGQECISGNLSLPVCGDSTAEEELVNKNDDSSP
VSRDFCVAEAVDGNVPAATYLFAGSRSDATAAETAGVASSS

>RXN02978 TRANSLATE of: rxn02978.seq check: 8219 from: 1 to: 1509
VIDRFPVLFELYNTAKEVYVSLIDQVTGENTILKKDDGWRDQFMIESFFAYDSADATS
WSGKNMNSYWFVSDLISNISFAERSLESFSWALRDLSDLSSSETFEGLEEINLKFSELQ
ENYTNLELPFPQSAADVDEVEQYLQAEVTRQGRDQYQWSPFPIPKPDSYIIDHALAVYTD
VLGAIEQGEELREEVEVQQAQDEVSNNWNPLEDSYDYLQDHRGRPVQDLREMEELVRLCLM
LDQEEWGAEARIRKLVESVEWEDTQAISSLIEHQYWDGGRFRPLPHKFSGLDEPEPLP
MTRKMLIATNHPDVLRVNIADYQQHRRRIATQKVECYKEVLALYPEILKKFDDSFVNHR
WYRAFDREGQLLYIGETINPLVRLREHAGLGSINHAHRLRVSFWFSTMTAFHLESCFTQ
AEAKEKEALYIKLEQPRYNKTHNSARLAVSEEGVPVNEVPSRNDPRNVGWKGRHVRVPPML
PIVARVVDSTTREGYAFYEDNR

>RXN02995 TRANSLATE of: rxn02995.seq check: 169 from: 1 to: 1566
LNHAKVNHGPGQATLPETAEGQVRYTEVKTGYCQMNVHDSERLSGLLEEAGYVAAPEDTT
PDVLFVNTCAVRENADMRLYGTGLNLRVSKYKPNPMQIAGVGCLAQKDQDVTVVKAPVVD
VVFETHNIGSLPTLLQRAEHNAQAEVEIVDSLEQFPVSLPAKRESAYAGVSVSVGVCNNT
CTFCIVPSLRGKEQDRRPGDILAEVQALVDQGVTEVTLLGQNVNAYGVNFVPELDERDS
AFSKLLRACGIEGLERVFTSPHAEFTSDVIDAMAETPNICPOLHMPLOQSGSDKVLKE
MRRSYRSKKFLSILDEVRAKIPHASITTDIVGFGTEEDFQATLDVVKKARFTSAYTF
QYSPRPGTFAEYENQLPKEVVQERYERIMVVGQVCEENQKLGITTVELLVQAGGGRK
NDATKRMGSRARDGRLVHFAFEGDIDGEIRPGDFVTVTVTEAKPFPLIADSGVQTHRRTK
AGDNSAVGQVPTTAPIGVGLGLPIGAPKVPATESACCSIN

>RXN02997 TRANSLATE of: rxn02997.seq check: 4243 from: 1 to: 729
PLPGQPFEGEALTLINALLHHAENVASNPWKRTTFTAHMHPPGNSADCDYCLVLQRRG
VYKAHEEIQQTIPLPQSGDWSAGEFTVVDVEGTAFPSALIPSIVELQHRAALDVPNGHNSV
APAQWDEHRIAQQSERILKTGTLFTVLFAEGSTVAAAMSSIAIPGSPNPIAQEQLGTIVH
PDFRGRGLGTAVKLAGLSLSRCHPEIQRVATSNVADNHAMLAINRSIGATEIARTTLWE
KKL

>RXN03001 TRANSLATE of: rxn03001.seq check: 9853 from: 1 to: 453
MDWLTIPFLVNEILAVPAFLIGIITAVGLGAMGRSVGQVIGGAIKATLGPLLIGAGATL
VTASLEPLGAMIMGATGMRGVVPTNEAIAIGIAQAEYGAQVAVMLMLGFAISLVLARFTNL
RYVLNGHHVLLMCTMLTMVLATGRVDWIF

>RXN03005 TRANSLATE of: rxn03005.seq check: 972 from: 1 to: 768
MSHKFSRRFAFATAAISTSAFATTAAPSIAIEPVLMSHCRRFRQRNFRKLPLRLGLQGLF
AHLCHRTLDWNRRDATGGATVNEGDYTNFTLTGTSNVDVDETEKQGLNYEGTVAFASDAHG
FNITLSNPQITVEGDTATLSAELSDNAAPEETSTTRVDVAEFELTAPEVSETDADITYTW
TDASGTFLLETLPPEELSRVAGQADALSFSITVDKASENPSSDDVATGSSSSFLSTILNLF
QQLASPLKLFGSLSS

>RXN03009 TRANSLATE of: rxn03009.seq check: 8107 from: 1 to: 348
VANIASYGLWEGSTSTPIEQLVPAGKSSFLRVRSFYRRI DGQAVQARLKEIINTAENP
LPRLDIPGKERTAQYPENPDTFAQKAAQEILDEFRTPLIGEEAAHVETKTKTIFWK

>RXN03010 TRANSLATE of: rxn03010.seq check: 697 from: 1 to: 237
VPTDNLFLIVAGIAWVLGALISVLSIGKYSMAVNERKSTGFYTEVPWKKALFTATAVLLV
FAVVSALDIALVWGQSW

>RXN03011 TRANSLATE of: rxn03011.seq check: 6364 from: 1 to: 201
MAYETDSLNRRTLGPASAVVGIAGAVAVVGVSMISGQDVTPTGNAVTTADDALLGGPE
YGSREAD

>RXN03012 TRANSLATE of: rxn03012.seq check: 8240 from: 1 to: 570
TTINIIITNGAAPHTNLNRAEIHDLPLTASDSELTRPSQESVLYDHESETVLRITVIVP
ADLHVAMKHLAKKHNLTVEISRILLQRYIDRNINHVEQNQAESDMVEVFASQPTNATAM
IPVPGTSFRQIFIKHSTGFWKNDHDLVDLQASKTPRVRDRSVLPQQLHRALLSDADMA
RLAAQLTKDH

>RXN03017 TRANSLATE of: rxn03017.seq check: 6478 from: 1 to: 1539
MLDSLKNRFTKAGSHGVGEGAVSGDAVFKPLRKEERLASVIQETEPGAAVEVMRNDAF
ALPGETGWVVMLLPTHDSQFGGLNAKEKNREDKGTIINLVVNDIHSVVTPELLDSVGL
VIPADSFDRMDEFDLLRNKARWHYGVAIEPDTGELVVFKVPKNSASARGDIFSEVGD
VLSGAADLEDVVDVEVIATFLEVINETSEVDIDDEGDGVPGYLEGVNAAGVITDOLIREK
LDVDSYSSAEIIDNIVHVFTKLQGGHHVAPQVPLHSADVVDVDAQESHDVTVIESPDDV
ALAEQVVDVPFSDGFGIIDAETVEPEDEVEVEATADAPFGDVAEDDPFGSDDEPDFGAS
DVVAAPAPVAGMSDEQIQALIRGVSESQAKTGSELNALRELAQALANPVQDSQAALA
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                                     Met Ser Thr Gln Thr
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atc acc atc aca gtc cta gaa acc gcc acc atc ttt gac ggc cct gaa 163
ile thr ile thr val leu glu thr ala thr ile phe asp gly pro glu
                                     10                               15                               20

acc atc tac cgc tat gac ctg gct gcc gaa ggc atc ctt gat gga tgg 211
thr ile tyr arg tyr asp leu ala ala glu gly ile leu asp gly trp
                                     25                               30                               35

gct cac tct gct gtg ctg gat caa gtg aaa caa ata gca ggt gaa aac 259
ala his ser ala val leu asp gln val lys gln ile ala gly glu asn
                                     40                               45                               50

tgg ccg act gtt gag atc gtg gtg gat ggc acc gac aac gta gtc aat 307
trp pro thr val glu ile val val asp gly thr asp asn val val asn
                                     55                               60                               65

gca ctc acc tcc atg ttt gct tcc aaa ggc gtg acc tgc ggt ggg gtt 355
ala leu thr ser met phe ala ser lys gly val thr cys gly gly val
                                     70                               75                               80                               85

gga gta gaa gca cct ccc gtt gcg gag gaa cca ccg aaa att aaa cgg 403
gly val glu ala pro pro val ala glu glu pro pro lys ile lys arg
                                     90                               95                               100

ccc acg agt gga aaa caa gtc cgc cag ttc tac ggc atc aag cca cta 451
pro thr ser gly lys gln val arg gln phe tyr gly ile lys pro leu
                                     105                               110                               115

cac ctg ttg ttg gtc agc ata ttg gtt ggt tct att gct ggt att tgg 499
his leu leu leu val ser ile leu val gly ser ile ala gly ile trp

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120	125	130	
gtg att tgc ggt ttc act ggg cca gtg gac tca cgg ccg gta gat aag			547
Val Ile Ser Gly Phe Thr Gly Pro Val Asp Ser Arg Pro Val Asp Lys			
135	140	145	
gtg gcg gag att tca acg cag ggg gag acg tgc ata agc aat caa ccc			595
Val Ala Glu Ile Ser Thr Val Gly Glu Thr Ser Ile Ser Asn Gln Pro			
150	155	160	165
caa ccc cag ccc acc gtg ctc gtg acc gag gac ctg ctt att gag gcg			643
Gln Pro Gln Pro Thr Val Leu Val Thr Gly Asp Leu Leu Ile Glu Ala			
170	175	180	
cca ttt ggt ttt gaa atg cga agc gac gaa cag tgc cgc tac ctg gaa			691
Pro Phe Gly Phe Glu Met Arg Ser Asp Glu Gln Ser Arg Tyr Leu Glu			
185	190	195	
ggc ccc gac ccg aat ctg cgc atc cac gtg ggc gtc gat ccg ctg cac			739
Gly Pro Asp Pro Asn Leu Arg Ile His Val Gly Val Asp Pro Leu His			
200	205	210	
ggc gcg gac gcc gcg ctg gtt gcc gaa gag ctg cgc cgc ctg atc acc			787
Gly Ala Asp Ala Ala Leu Val Ala Glu Glu Leu Arg Arg Leu Ile Thr			
215	220	225	
gag gat cct tgc ctg gag gaa att ccc gca ggg gag tgg gcc gag aaa			835
Glu Asp Pro Ser Leu Glu Glu Ile Pro Ala Gly Glu Trp Gly Glu Lys			
230	235	240	245
acc acc atc gac tac cgc gaa aca ccc gcc gat gcc tct cat gtg ctg			883
Thr Thr Ile Asp Tyr Arg Glu Thr Pro Gly Asp Gly Ser His Val Leu			
250	255	260	
tgg gtg acc tgg ttt gac acc gac cga caa ctc aac gtt ggg tgc cat			931
Trp Val Thr Trp Phe Asp Thr Asp Arg Gln Leu Asn Val Gly Cys His			
265	270	275	
agc aaa gcc gcc gaa acc ctt gtt cac aag gca caa tgc cga aat gtg			979
Ser Lys Ala Ala Glu Thr Leu Val His Lys Ala Gln Cys Arg Asn Val			
280	285	290	
att gag cat ctg acg ctg aaa tgatgccggt ttctatccgg aat			1023
Ile Glu His Leu Thr Leu Lys			
295	300		
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<211> 300			
<212> PRT			
<213> Corynebacterium glutamicum			
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Met Ser Thr Gln Thr Ile Thr Ile Thr Val Leu Glu Thr Ala Thr Ile			
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Phe Asp Gly Pro Glu Thr Ile Tyr Arg Tyr Asp Leu Ala Ala Glu Gly			
20	25	30	
Ile Leu Asp Gly Trp Ala His Ser Ala Val Leu Asp Gln Val Lys Gln			
35	40	45	

```

Ile Ala Gly Glu Asn Trp Pro Thr Val Glu Ile Val Val Asp Gly Thr
  50                      55                      60

Asp Asn Val Val Asn Ala Leu Thr Ser Met Phe Ala Ser Lys Gly Val
  65                      70                      75                      80

Thr Cys Gly Gly Val Val Glu Ala Pro Pro Val Ala Glu Glu Pro
      85                      90                      95

Pro Lys Ile Lys Arg Pro Thr Ser Gly Lys Gln Val Arg Gln Phe Tyr
      100                    105                    110

Gly Ile Lys Pro Leu His Leu Leu Leu Val Ser Ile Leu Val Gly Ser
      115                    120                    125

Ile Ala Gly Ile Trp Val Ile Ser Gly Phe Thr Gly Pro Val Asp Ser
      130                    135                    140

Arg Pro Val Asp Lys Val Ala Glu Ile Ser Thr Gln Gly Glu Thr Ser
      145                    150                    155                    160

Ile Ser Asn Gln Pro Gln Pro Gln Thr Val Leu Val Thr Glu Asp
      165                    170                    175

Leu Leu Ile Glu Ala Pro Phe Gly Phe Glu Met Arg Ser Asp Glu Gln
      180                    185                    190

Ser Arg Tyr Leu Glu Gly Pro Asp Pro Asn Leu Arg Ile His Val Gly
      195                    200                    205

Val Asp Pro Leu His Gly Ala Asp Ala Ala Leu Val Ala Glu Glu Leu
      210                    215                    220

Arg Arg Leu Ile Thr Glu Asp Pro Ser Leu Glu Glu Ile Pro Ala Gly
      225                    230                    235                    240

Glu Trp Gly Glu Lys Thr Thr Ile Asp Tyr Arg Glu Thr Pro Gly Asp
      245                    250                    255

Gly Ser His Val Leu Trp Val Thr Trp Phe Asp Thr Asp Arg Gln Leu
      260                    265                    270

Asn Val Gly Cys His Ser Lys Ala Ala Glu Thr Leu Val His Lys Ala
      275                    280                    285

Gln Cys Arg Asn Val Ile Glu His Leu Thr Leu Lys
      290                    295                    300

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<210> 3

<211> 513

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(490)

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<400> 3

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ggagacgtcg ataagcaatc aacccaacc ccagcccacc gtg ctc gtg acc gag 115
Val Leu Val Thr Glu
1 5

gac ctg ctt att gag gcg cca ttt ggt ttt gaa atg cga agc gac gaa 163
Asp Leu Leu Ile Glu Ala Pro Phe Gly Phe Glu Met Arg Ser Asp Glu
10 15 20

cag tgc cgc tac ctg gaa ggc ccc gac ccg aat ctg cgc atc cac gtg 211
Gln Ser Arg Tyr Leu Glu Gly Pro Asp Pro Asn Leu Arg Ile His Val
25 30 35

ggc gtc gat ccg ctg cac ggc gcg gac gcc gcg ctg gtt gcc gaa gag 259
Gly Val Asp Pro Leu His Gly Ala Asp Ala Ala Leu Val Ala Glu Glu
40 45 50

ctg cgc cgc ctg atc acc gag gat cct tgc ctg gag gaa att ccc gca 307
Leu Arg Arg Leu Ile Thr Glu Asp Pro Ser Leu Glu Ile Pro Ala
55 60 65

ggg gag tgg ggc gag aaa acc acc atc gac tac cgc gaa aca ccc ggc 355
Gly Glu Trp Gly Glu Lys Thr Thr Ile Asp Tyr Arg Glu Thr Pro Gly
70 75 80 85

gat ggc tct cat gtg ctg tgg gtg acc tgg ttt gac acc gac cga caa 403
Asp Gly Ser His Val Leu Trp Val Thr Trp Phe Asp Thr Asp Arg Gln
90 95 100

ctc aac gtt ggg tgc cat agc aaa gcc gcc gaa acc ctt gtt cac aag 451
Leu Asn Val Gly Cys His Ser Lys Ala Ala Glu Thr Leu Val His Lys
105 110 115

gca caa tgc cga aat gtg att gag cat ctg acg ctg aaa tgatgccggt 500
Ala Gln Cys Arg Asn Val Ile Glu His Leu Thr Leu Lys
120 125 130

ttctatccgg aat 513

<210> 4
<211> 130
<212> PRT
<213> Corynebacterium glutamicum

<400> 4
Val Leu Val Thr Glu Asp Leu Leu Ile Glu Ala Pro Phe Gly Phe Glu
1 5 10 15

Met Arg Ser Asp Glu Gln Ser Arg Tyr Leu Glu Gly Pro Asp Pro Asn
20 25 30

Leu Arg Ile His Val Gly Val Asp Pro Leu His Gly Ala Asp Ala Ala
35 40 45

Leu Val Ala Glu Glu Leu Arg Arg Leu Ile Thr Glu Asp Pro Ser Leu
50 55 60

Glu Glu Ile Pro Ala Gly Glu Trp Gly Glu Lys Thr Thr Ile Asp Tyr
65 70 75 80

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Arg  Glu  Thr  Pro  Gly  Asp  Gly  Ser  His  Val  Leu  Trp  Val  Thr  Trp  Phe
                85                      90                      95

Asp  Thr  Asp  Arg  Gln  Leu  Asn  Val  Gly  Cys  His  Ser  Lys  Ala  Ala  Glu
                100                105                110

Thr  Leu  Val  His  Lys  Ala  Gln  Cys  Arg  Asn  Val  Ile  Glu  His  Leu  Thr
                115                120                125

Leu  Lys
    130

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<210> 5
<211> 561
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(538)
<223> FRXA01639

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                                     Met Ser Thr Gln Thr
                                     1                      5

atc acc atc aca gtc cta gaa acc gcc acc atc ttt gac ggc cct gaa 163
Ile Thr Ile Thr Val Leu Glu Thr Ala Thr Ile Phe Asp Gly Pro Glu
                10                15                20

acc atc tac cgc tat gac ctg gct gcc gaa ggc atc ctt gat gga tgg 211
Thr Ile Tyr Arg Tyr Asp Leu Ala Ala Glu Gly Ile Leu Asp Gly Trp
                25                30                35

gct cac tct gct gtg ctg gat caa gtg aaa caa ata gca ggt gaa aac 259
Ala His Ser Ala Val Leu Asp Gln Val Lys Gln Ile Ala Gly Glu Asn
                40                45                50

tgg ccg act gtt gag atc gtg gtg gat ggc acc gac aac gta gtc aat 307
Trp Pro Thr Val Glu Ile Val Val Asp Gly Thr Asp Asn Val Val Asn
                55                60                65

gca ctc acc tcc atg ttt gct tcc aaa ggc gtg acc tgc ggt ggg gtt 355
Ala Leu Thr Ser Met Phe Ala Ser Lys Gly Val Thr Cys Gly Gly Val
                70                75                80                85

gga gta gaa gca cct ccc gtt gcg gag gaa cca ccg aaa att aaa cgg 403
Gly Val Glu Ala Pro Pro Val Ala Glu Glu Pro Pro Lys Ile Lys Arg
                90                95                100

ccc acg agt gga aaa caa gtc cgc cag ttc tac ggc atc aag cca cta 451
Pro Thr Ser Gly Lys Gln Val Arg Gln Phe Tyr Gly Ile Lys Pro Leu
                105                110                115

cac ctg ttg ttg gtc agc ata ttg gtt ggt tct att gct ggt att tgg 499
His Leu Leu Leu Val Ser Ile Leu Val Gly Ser Ile Ala Gly Ile Trp

```

```

120          125          130
gga ttt cgg gtt tca ctg ggc cag tgg act cac ggc cgg tagataaggt 548
Gly Phe Arg Val Ser Leu Gly Gln Trp Thr His Gly Arg
135          140          145
ggcggagatt tca 561

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<210> 6
<211> 146
<212> PRT
<213> Corynebacterium glutamicum

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<400> 6
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 1          5          10          15
Phe Asp Gly Pro Glu Thr Ile Tyr Arg Tyr Asp Leu Ala Ala Glu Gly
          20          25          30
Ile Leu Asp Gly Trp Ala His Ser Ala Val Leu Asp Gln Val Lys Gln
          35          40          45
Ile Ala Gly Glu Asn Trp Pro Thr Val Glu Ile Val Val Asp Gly Thr
          50          55          60
Asp Asn Val Val Asn Ala Leu Thr Ser Met Phe Ala Ser Lys Gly Val
          65          70          75          80
Thr Cys Gly Gly Val Gly Val Glu Ala Pro Pro Val Ala Glu Glu Pro
          85          90          95
Pro Lys Ile Lys Arg Pro Thr Ser Gly Lys Gln Val Arg Gln Phe Tyr
          100          105          110
Gly Ile Lys Pro Leu His Leu Leu Val Ser Ile Leu Val Gly Ser
          115          120          125
Ile Ala Gly Ile Trp Gly Phe Arg Val Ser Leu Gly Gln Trp Thr His
          130          135          140
Gly Arg
145

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<210> 7
<211> 6470
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
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<223> RXN01590

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Trp Gly Gln Lys Asp His Trp Gly Lys Ala Pro Leu Gly Asp His Asp
 1          5          10          15

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gct gtg cgt atc tat agg caa gca gaa gcc ttg atg aaa cag cgc gca 96
Ala Val Arg Ile Tyr Arg Gln Ala Glu Ala Leu Met Lys Gln Arg Ala
20 25 30

gca aac aat aag ggc tta gac ctc aat gat gaa gcg acc tat ggc gcc 144
Ala Asn Asn Lys Gly Leu Asp Leu Asn Asp Glu Ala Thr Tyr Gly Ala
35 40 45

atc atg ttt gcg tct ttc gat gat gcc ttc gcc gct gat gcc gaa gct 192
Ile Met Phe Ala Ser Phe Asp Asp Ala Phe Ala Ala Asp Ala Glu Ala
50 55 60

cat ggc tgt gta cac cga cca cag ttc gcg aag gta act agg cga aat 240
His Gly Cys Val His Arg Pro Gln Phe Ala Lys Val Thr Arg Arg Asn
65 70 75 80

att ctt aat tca ccg caa tac acg gcg att aag tca tct tat gac gcg 288
Ile Leu Asn Ser Pro Gln Tyr Thr Ala Ile Lys Ser Ser Tyr Asp Ala
85 90 95

ctg gtg cag cag gat ctc gtg gcc caa cag cag cag gca caa gcg cta 336
Leu Val Gln Gln Asp Leu Val Ala Gln Gln Gln Gln Ala Ala Leu
100 105 110

cag caa gct gct tat gag caa gag cag gca gct att ttc cag gca cgt 384
Gln Gln Ala Ala Tyr Glu Gln Glu Gln Ala Ala Ile Phe Gln Ala Arg
115 120 125

gat caa gca aca ttc cag gct gaa caa acg ctc gcg caa gag tcc gtt 432
Asp Gln Ala Thr Phe Gln Ala Glu Gln Thr Leu Ala Gln Glu Ser Val
130 135 140

gcg caa tca gag ggt gtg ggt tta cct gtc att gat ccg atg gag agc 480
Arg Gln Ser Glu Gly Val Gly Leu Pro Val Ile Asp Pro Met Glu Ser
145 150 155 160

tat ttc ccg gag tac gcc ttc tat gaa ggt gtc gag atg ttt ggt acc 528
Tyr Phe Arg Glu Tyr Ala Phe Tyr Glu Gly Val Glu Met Phe Gly Thr
165 170 175

tgg ggt acg cac gtt gat gct ggt gtg tcg cag ttt agc acc tct gat 576
Trp Gly Thr His Val Asp Ala Gly Val Ser Gln Phe Ser Thr Ser Asp
180 185 190

ggc cgt gcg atc cga gcg ctt gtt gat gag cat ctc gca acc tat gaa 624
Gly Arg Ala Ile Arg Ala Leu Val Asp Glu His Leu Ala Thr Tyr Glu
195 200 205

cca gta gag cag cgg ggg agt act cag gca ttc ttc gcc tct gtc aat 672
Pro Val Glu Gln Arg Gly Ser Thr Thr Gln Ala Phe Phe Ala Ser Val Asn
210 215 220

gct gcc ttt gct gag gtg gca cct cac gca gca ccc atg ttt agt gcg 720
Ala Ala Phe Ala Glu Val Ala Pro His Ala Ala Pro Met Phe Ser Ala
225 230 235 240

att gct cgc gag ggt gag ggt tca aag ggg tac cag gcg ctg cgt cac 768
Ile Ala Arg Glu Gly Glu Gly Ser Lys Gly Tyr Gln Ala Leu Arg His
245 250 255

cgt ttc gac aag atg gtc ggc act gca att gga cct aat ggt ttg cct 816

Arg Phe Asp	Lys Met Val Gly Thr Ala Ile Gly Pro Asn Gly Leu Pro	
	260 265 270	
gag gga cct gat ctg ggt ggt cgt cgt tta cct att tgg cct tat gat	864	
Glu Gly Pro Asp Leu Gly Gly Arg Arg Leu Pro Ile Ser Pro Tyr Asp		
	275 280	
cca cgc tgg tca gac cgc gaa gta gtc cgt gtg cac ggt acc aag ctg	912	
Pro Arg Trp Ser Asp Arg Glu Val Arg Val His Gly Thr Lys Leu		
	290 295 300	
cta tca ctg tcc gaa gag agt gtt ggc atg atc agg gac ctt gat cta	960	
Leu Ser Leu Ser Glu Glu Ser Val Gly Met Ile Arg Asp Leu Asp Leu		
	305 310 315 320	
gca acg atc cac cta caa gat aat gat gtt tac gag ggc act cat cga	1008	
Ala Thr Ile His Leu Gln Asp Asn Asp Val Tyr Glu Gly Thr His Arg		
	325 330 335	
gaa gac gac act aaa ggc ggt gtg cga ccg ttg act caa tgg gtc aat	1056	
Glu Asp Asp Thr Lys Gly Gly Val Arg Pro Leu Thr Gln Trp Val Asn		
	340 345 350	
ggt gaa gct att gcc tgg cgc act atc acc gag aat gac cag atg cga	1104	
Gly Glu Ala Ile Ala Trp Arg Thr Ile Thr Glu Asn Asp Gln Met Arg		
	355 360 365	
ctg ccc aat att ggt cag ttt atg acg gct aaa gaa tac cgt gcc gca	1152	
Leu Pro Asn Ile Gly Gln Phe Met Thr Ala Lys Glu Tyr Arg Ala Ala		
	370 375 380	
gcg tca tgg ctg cgt gct gga ctc att gat acc gca gat gtt gcg agt	1200	
Ala Ser Trp Leu Arg Ala Gly Leu Ile Asp Thr Ala Asp Val Ala Ser		
	385 390 395 400	
cag aaa att gac ccc aac aag gtc atg tct gat gag ggt atc gcg cgc	1248	
Gln Lys Ile Asp Pro Asn Lys Val Met Ser Asp Glu Gly Ile Ala Arg		
	405 410 415	
tgg gaa gct att ttg acg tat ctg tgg gat gag ggt gtg gat ttt agg	1296	
Ser Glu Ala Ile Leu Thr Tyr Leu Ser Asp Glu Gly Val Asp Phe Arg		
	420 425 430	
atc gag cca gat cgt gag ccg gga cag ctt aaa gtg cgt att gag ggc	1344	
Ile Glu Pro Asp Arg Glu Pro Gly Gln Leu Lys Val Arg Ile Glu Gly		
	435 440 445	
acc cgt att gat att cgt ctc act gat act cgc gcc aat gaa cag tgg	1392	
Thr Arg Ile Asp Ile Arg Leu Thr Asp Thr Arg Ala Asn Glu Gln Trp		
	450 455 460	
gtg ggt cgt gtc tat gat tct ggc act gtg att aag tat tcc gcc gaa	1440	
Val Gly Arg Val Tyr Asp Ser Gly Thr Val Ile Lys Tyr Ser Ala Glu		
	465 470 475 480	
caa aca gcg gaa gaa cgt cta cga gct cgt gag cgc atg gag aac ggt	1488	
Gln Thr Ala Glu Glu Arg Leu Arg Ala Arg Glu Arg Met Glu Asn Gly		
	485 490 495	
gat gga acg tgg aca ccg gct act gat tat gaa cca agc cca act gaa	1536	
Asp Gly Thr Trp Thr Pro Ala Thr Asp Tyr Glu Pro Ser Pro Thr Glu		

500										505										510										
gtt gtc gat ctc gtg aaa ttt gct ctc ggt cga gag gtt gag cga cag	1584																													
Val Val Asp Leu Val Lys Phe Ala Leu Gly Arg Glu Val Glu Arg Gln																														
515 520 525																														
gat ggc aaa ggt ctt gtt ggt gtg cct aat gct cga cac cca cgt gct	1632																													
Asp Gly Lys Gly Leu Val Gly Val Pro Asn Ala Arg His Pro Arg Ala																														
530 535 540																														
tta gag cag gca cag gat gca tat ttc act aag aat cgt tcc gca ttc	1680																													
Leu Glu Gln Ala Gln Asp Ala Tyr Phe Thr Lys Asn Arg Ser Ala Phe																														
545 550 555 560																														
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Met Val Arg Glu Gly Leu Ser Ile Val Gln Asp Ala Arg Asp Arg Ser																														
565 570 575																														
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Ala Gly Pro Gly Lys Trp Phe Asp Asn Glu Ala Lys Ala Ser Glu Trp																														
580 585 590																														
ctt ggt aac aat atc gcc ctt act cgt gcg cgt gtg gcc gaa gag ctc	1824																													
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595 600 605																														
ggc gtt gaa gaa ctg att gcg ctt tct gca cag tac gcc gat gat cct	1872																													
Gly Val Glu Glu Leu Ile Ala Leu Ser Ala Gln Tyr Ala Asp Asp Pro																														
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Asp Phe Met Pro Ala Phe Ala Gly Glu Asp Glu Leu Met Ala Ile Lys																														
625 630 635 640																														
cag gac tat tgg gcg atg ctg cga ggt gag gaa acc gat ctg ctt aac	1968																													
Gln Asp Tyr Trp Ala Met Leu Arg Gly Glu Glu Thr Asp Leu Leu Asn																														
645 650 655																														
cct ggg gtt aac cgc gat gat tat atg gct gct atc cgc gat ggt gat	2016																													
Pro Gly Val Asn Arg Asp Asp Tyr Met Ala Ala Ile Arg Asp Gly Asp																														
660 665 670																														
cat gag cag att gct gcg atg acc tca gca atg aat gct gtg acc gtg	2064																													
His Glu Gln Ile Ala Ala Met Thr Ser Ala Met Asn Ala Val Thr Val																														
675 680 685																														
gag gat cgt gtg cgt cag cac gcg gcc ctt gtt ctt gat gat tat gtc	2112																													
Glu Asp Arg Val Arg Gln His Ala Ala Leu Val Leu Asp Asp Tyr Val																														
690 695 700																														
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Gly Thr Val Glu Pro Asp Pro Val Thr Gly Leu Arg Phe Asn Pro Val																														
705 710 715 720																														
aca gtt gct cag cac atg ccg agt gct aaa tcc ctg tgg tca aac cat	2208																													
Thr Val Ala Gln His Met Pro Ser Ala Lys Ser Leu Trp Ser Asn His																														
725 730 735																														
gac gat att att gcc gcg ttg cga gcg act tcg att act ggc gat gaa	2256																													
Asp Asp Ile Ile Ala Ala Leu Arg Ala Thr Ser Ile Thr Gly Asp Glu																														
740 745 750																														

ctg cgc ggt gac gaa ttc tat aac gat gtt att aat caa cag ttg ctc	2304
Leu Arg Gly Asp Glu Phe Tyr Asn Asp Val Ile Asn Gln Leu Leu	
755 760 765	
aaa ttt aat cct gag acc gcg cag aaa atg gtt aat aac cct gat ctt	2352
Lys Phe Asn Pro Glu Thr Ala Gln Lys Met Val Asn Asn Pro Asp Leu	
770 775 780	
gac cgc cag ttg gct cga ttt ggc act gtc att gcc gag act att tcc	2400
Asp Pro Gln Leu Ala Arg Phe Gly Thr Val Ile Ala Glu Thr Ile Ser	
785 790 795 800	
cgc aat ggt gct gat gtg gtc gat att gct gtt gac gat aac ggt gtg	2448
Arg Asn Gly Ala Asp Val Val Asp Ile Ala Val Asp Asp Asn Gly Val	
805 810 815	
gtg cgg tgg acc gca cag cga cgt gtt ggt gcg aag gat agt cgt gca	2496
Val Arg Trp Thr Ala Gln Arg Arg Val Gly Ala Lys Asp Ser Arg Ala	
820 825 830	
gta gat agt aag ggg cag gtt cgc ggt gaa cgc acc cgt cat gtg cag	2544
Val Asp Ser Lys Gly Gln Val Arg Gly Glu Arg Thr Arg His Val Gln	
835 840 845	
ggt gag ata ggt cag att ttt act cgc ggt gag cat ggt gaa att gtc	2592
Gly Glu Ile Gly Gln Ile Phe Thr Arg Gly Glu His Gly Glu Ile Val	
850 855 860	
acc aaa ttt aat ggt ggc gag aac tat atg ttt gcc cct ggc tac acc	2640
Thr Lys Phe Asn Gly Glu Asn Tyr Met Phe Ala Pro Gly Tyr Thr	
865 870 875 880	
gcg tct gtg gta cca caa aag cct ggt gag aca aag agt tta gaa gag	2688
Ala Ser Val Val Pro Gln Lys Pro Gly Glu Thr Lys Ser Leu Glu Glu	
885 890 895	
cgt acc aag ctc aaa ggc tat gag cag gtg atg tca gag gcg ttg gtg	2736
Arg Thr Lys Leu Lys Gly Tyr Glu Gln Val Met Ser Glu Ala Leu Val	
900 905 910	
tac cgt gtg cga gaa gat ttg atg ttc act gag cga tcc cga gtg ggt	2784
Tyr Arg Val Arg Glu Asp Leu Met Phe Thr Glu Arg Ser Arg Val Gly	
915 920 925	
gct aca acc agc atc aac agt gca tat aag cga ctg tat gac aat cgc	2832
Ala Thr Thr Ser Ile Asn Ser Ala Tyr Lys Arg Leu Tyr Asp Asn Arg	
930 935 940	
ttc cct gtg gac ttc ttc gag gcg agc gcc gaa gaa ggt ttg agc gat	2880
Phe Pro Val Asp Phe Phe Glu Arg Ser Ala Glu Glu Gly Leu Ser Asp	
945 950 955 960	
gag tgg cgt gct gcg ttg ctt gag act gcg agt ttg cgt gtg cgc tac	2928
Glu Trp Arg Ala Ala Leu Leu Glu Thr Ala Ser Leu Arg Val Arg Tyr	
965 970 975	
gac aac tct att cgt gat ggt gcg aat gtg atg gag gat att cga gca	2976
Asp Asn Ser Ile Arg Asp Gly Ala Asn Val Met Glu Asp Ile Arg Ala	
980 985 990	

cag cag cgt ggt ttt gat gcg cgt aat gat aac tcc cgt gat gcg ctg Gln Gln Arg Gly Phe Asp Ala Arg Asn Asp Asn Ser Arg Asp Ala Leu 995 1000 1005	3024
gtg ctt acc ggt ggg cgt aac att tct gta ctt gat gtt gat gcg ggt Val Leu Thr Gly Gly Arg Asn Ile Ser Val Leu Asp Ala Gly 1010 1015 1020	3072
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tct gtt cgc tat ttg ttg cct tct gcg aag gtg ggc gct gat ggc atg Ser Val Arg Tyr Leu Leu Pro Ser Ala Lys Val Gly Ala Asp Gly Met 1045 1050 1055	3168
att acc cct ggt gat ccg gct gat cga gta cct gtt gca gcg cat cca Ile Thr Pro Gly Asp Pro Ala Asp Arg Val Pro Val Ala Ala His Pro 1060 1065 1070	3216
gaa tca tgg gcg atg ggc ttt gac cca cat gac cgt cag aac atg act Glu Ser Trp Ala Met Gly Phe Asp Pro His Asp Arg Gln Asn Met Thr 1075 1080 1085	3264
ttc tcg aac atc atg cag gct agc gct gtg act ggt ggt gca cgc act Phe Ser Asn Ile Met Gln Ala Ser Ala Val Thr Gly Gly Ala Arg Thr 1090 1095 1100	3312
gcg atg ata cag ctg ggc ggt tgg aac ttt gaa gat ggc att att gtc Ala Met Ile Gln Leu Gly Gly Trp Asn Phe Glu Asp Gly Ile Ile Val 1105 1110 1115 1120	3360
tct gcc gat ttt gcg aat acc cat gtt att cgc gat acg gaa gat gag Ser Ala Asp Phe Ala Asn Thr His Val Ile Arg Asp Thr Glu Asp Glu 1125 1130 1135	3408
atg cgc ccc ttg gtt gcc ggc gat aag ctg tct gat ttt cac ggt aat Met Arg Pro Leu Val Ala Gly Asp Lys Leu Ser Asp Phe His Gly Asn 1140 1145 1150	3456
aag ggt gtg acc gct ctt gtt gtt gat cca gcg atg agt gat gct gat Lys Gly Val Thr Ala Leu Val Val Asp Pro Ala Met Ser Asp Ala Asp 1155 1160 1165	3504
gca cgt gca gca ggg ctg gaa tca gag gtg gcg ttt ttc cga gac aac Ala Arg Ala Ala Gly Leu Glu Ser Glu Val Ala Phe Arg Asp Asn 1170 1175 1180	3552
cct gat cta gag gtt gtc atg agt ccg ttt tct gcc att tct cgt ttt Pro Asp Leu Glu Val Val Met Ser Pro Phe Ser Ala Ile Ser Arg Phe 1185 1190 1195 1200	3600
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ttc agg aat aat gat ggt tct act cgt gtt caa cca ggt gcc tct ggt Phe Arg Asn Asn Asp Gly Ser Thr Arg Val Gln Pro Gly Ala Ser Gly 1220 1225 1230	3696
gat ctc aac ttc atc gtc acg cat atg gct gtt gat gcg aaa acc aat	3744

Asp	Leu	Asn	Phe	Ile	Val	Thr	His	Met	Ala	Val	Asp	Ala	Lys	Thr	Asn	
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Val	Tyr	Asp	Glu	Glu	Ala	Val	Arg	Glu	Gly	Gln	Gly	Arg	Lys	Ala	Ser	
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Ser	Gln	Leu	Ala	Trp	Val	Leu	Gln	Ala	Gln	Glu	Cys	His	Glu	Ile	Met	
		1265				1270					1275				1280	
gag	cac	ttt	tat	ggc	aac	aac	gtc	tct	gca	ttg	gct	aac	ttc	cag	gaa	3888
Glu	His	Phe	Tyr				Gly	Asn	Asn	Val	Ser	Ala	Leu	Ala	Asn	
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tat	ctt	cgc	gtc	acg	ggg	ctt	gat	gtc	acc	cgg	tat	ggt	gag	ttg	cgc	3936
Tyr	Leu	Arg	Val	Thr	Gly	Leu	Asp	Val	Thr	Pro	Tyr	Gly	Glu	Leu	Arg	
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Glu	Gly	Phe	Ser	Glu	Ser	Asn	Glu	Gln	Arg	Asn	Ile	Ile	Glu	Met	Pro	
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agc	att	tac	gat	gag	aac	ggt	gag	ctg	aat	aat	cgt	gtt	aat	cgt	gca	4032
Ser	Ile	Tyr	Asp	Glu	Asn	Gly	Glu	Leu	Asn	Asn	Arg	Val	Asn	Arg	Ala	
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cag	gtg	cgc	gaa	gct	ttt	gtt	gag	cag	atc	agt	cgc	gct	ggt	ggt	gtt	4080
Gln	Val	Arg	Glu	Ala	Phe	Val	Glu	Gln	Ile	Ser	Arg	Ala	Gly	Gly	Val	
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Met	Glu	Ile	Pro	Phe	Gln	Leu	Gln	Leu	Arg	Asn	Gly	Ala	Gln	Leu	Glu	
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gag	tca	cct	aat	aat	cca	gac	atg	tat	cag	ttg	cca	cta	ctg	agc	cgc	4176
Glu	Ser	Pro	Asn	Asn	Pro	Asp	Met	Tyr	Gln	Leu	Pro	Leu	Leu	Ser	Pro	
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cat	ttg	cgc	agt	gat	gag	gat	tta	gcg	gac	ggt	agt	acc	tct	cga	cat	4224
His	Leu	Arg	Ser	Asp	Glu	Asp	Leu	Ala	Asp	Gly	Ser	Thr	Ser	Arg	His	
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gag	tac	acc	acg	cgg	tat	atg	gct	att	ttt	gat	acg	tgc	tac	aag	ctg	4272
Glu	Tyr	Thr	Thr	Arg	Tyr	Met	Ala	Ile	Phe	Asp	Thr	Cys	Tyr	Lys	Leu	
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gca	gaa	gag	caa	gcc	aag	att	gac	gca	ttg	cgc	cag	gag	gaa	gcg	cag	4320
Ala	Glu	Glu	Gln	Ala	Lys	Ile	Asp	Ala	Leu	Arg	Gln	Glu	Glu	Ala	Gln	
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cac	ggc	acg	ttg	cct	cgt	gct	gcg	gaa	aag	cga	ctg	agc	gag	tca	cag	4368
His	Gly	Thr	Leu	Pro	Arg	Ala	Ala	Glu	Lys	Arg	Leu	Ser	Glu	Ser	Gln	
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aag	ttt	gtt	gat	caa	gca	cag	aaa	aag	gtg	cag	gca	agc	ttt	gat	gga	4416
Lys	Phe	Val	Asp	Gln	Ala	Gln	Lys	Lys	Val	Gln	Ala	Ser	Phe	Asp	Gly	
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Ile	Ala	Asn	Asp	Ile	Val	Ala	Ser	Arg	Ile	Glu	Thr	Lys	Asn	Asn	Val	

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Phe Lys Asp Gly Phe Met Ser Ala Arg Gln Ser His Ser Ala Thr Ala			
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Val Trp Thr Thr Gly Asp Pro Arg Leu Ser Val Asp Glu Val Ala Met Asn			
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tct tcg atg gca cgt gaa ctc ggc gtt ctc gat aac ggt tat gca atg			4608
Ser Ser Met Ala Arg Glu Leu Gly Val Leu Asp Asn Gly Tyr Ala Met			
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Val Trp Arg Asp Pro Val Ile Arg Asp Gly Gly Val Arg Tyr Leu Arg			
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Val Val Ile Asn Asp Asp Leu His Gly Val Ala Val Asn Pro Val Ser			
1555	1560	1565	
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Val Lys Ser Phe Asp Gly Asp Phe Asp Gly Asp Ser Val Gly Leu Val			
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Gly Asn Leu Pro Lys Lys Ala His Glu Glu Ala Leu Ser Arg Leu Thr			
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gtt gag gca aac atg ctt gat ctt ggt gat ggt aag cgt atg gag gac			4848
Val Glu Ala Asn Met Leu Asp Leu Gly Asp Gly Lys Arg Met Glu Asp			
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ggc act atg ttt tat ggg cta act ctg cat gac agc ctc gat gta cag			4896
Gly Thr Met Phe Tyr Gly Leu Thr Leu His Asp Ser Leu Asp Val Gln			
1620	1625	1630	
gta gcg cag cac cat gat ccg gca atg gcc gag aac atg aag gtt att			4944
Val Ala Gln His His Asp Pro Ala Met Ala Glu Asn Met Lys Val Ile			
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Val Ser Glu Leu Asn Arg Tyr Gln Arg Glu Tyr Glu Ala Gly Glu Ile			
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Ser Arg Glu Glu Leu Leu Glu Val Asn Arg Ala His Met Asp Asp Leu			
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aat gag cac tat gca cag gct ttt gcc aac cgc gat ggt ttg gtg acc			5088
Asn Glu His Tyr Ala Gln Ala Phe Ala Asn Arg Asp Gly Leu Val Thr			
1685	1690	1695	
ttg cgt ttt gac ggt atg gaa aac cat atg gct tct gtt gcg cag tgc			5136
Leu Arg Phe Asp Gly Met Glu Asn His Met Ala Ser Val Ala Gln Cys			
1700	1705	1710	
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Phe Glu Thr Gly Ala Lys Gly Ser Pro Gly Lys Leu Lys Glu Tyr Ala			
1715	1720	1725	

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 Thr Tyr Ile Gly Ala Asp Pro Ala Gln Gly Phe Lys Asp Val Gly Gln
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cca acg cca gaa gcg ctg cgt agc cac tat gag ggt tgc cag aag gcg 5280
 Pro Thr Pro Glu Ala Leu Arg Ser His Tyr Glu Gly Ser Gln Lys Ala
 1745 1750 1755 1760

act gca att aag gtg ctc ttt acc ggt gtg gct ggt aaa aaa gag cag 5328
 Thr Ala Ile Lys Val Leu Phe Thr Gly Val Ala Gly Lys Lys Glu Gln
 1765 1770 1775

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 Glu Met Val Ala Leu Cys Arg Asn Leu Gly Leu Thr Lys Glu Ala Met
 1780 1785 1790

gct gca tca gca ccg gca cag cag tgc att ctg cag gcg aag cac gac 5424
 Ala Ala Ser Ala Pro Ala Gln Ser Ile Leu Gln Ala Lys His Asp
 1795 1800 1805

ccg att gac gcg ctc tat cgt gca gaa act ctt atg gga cca gta ggt 5472
 Pro Ile Asp Ala Leu Tyr Arg Ala Glu Thr Leu Met Gly Pro Val Gly
 1810 1815 1820

gat ctc tac caa ggt cgc aag atg cgt cgt ggt gag aat gag caa ggt 5520
 Asp Leu Tyr Gln Gly Arg Lys Met Arg Arg Gly Glu Asn Glu Gln Gly
 1825 1830 1835 1840

cgc tat gag tgg gaa gtc gtt agg gac gag aac cac cag cct atc cag 5568
 Arg Tyr Glu Trp Glu Val Val Arg Asp Glu Asn His Gln Pro Ile Gln
 1845 1850 1855

gcc acc aag gat gaa tgg gta cag cag tac atg gag atg tac gcc gat 5616
 Ala Thr Lys Asp Glu Trp Val Gln Gln Tyr Met Glu Met Tyr Ala Asp
 1860 1865 1870

gac aag ggt atg ggt gtc tgc gtt ggc gtt gac cag gtg gag aag atc 5664
 Asp Lys Gly Met Gly Val Ser Val Gly Val Asp Gln Val Glu Lys Ile
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 Ala Glu Glu Phe Ser Asp Glu Gln Gly Tyr Met Arg Val Leu Ser His
 1890 1895 1900

gat gag cta ccc act gag att aag cca cta gca ctt gat cag ctt gcc 5760
 Asp Glu Leu Pro Thr Glu Ile Lys Pro Leu Ala Leu Asp Gln Leu Ala
 1905 1910 1915 1920

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 Tyr Gly Asp Lys Lys Asn Arg Phe Asp Leu Leu Cys Glu Met Ala Lys
 1925 1930 1935

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 Gln Gln Val Asn Ile Tyr Asp Gly Asp Ala Tyr Asp Phe Ala Pro Arg
 1940 1945 1950

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 Val Val Arg Ala Asn Met Lys Ala Met Glu Asp Ala Ala Arg Phe Gly
 1955 1960 1965

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 Ser Phe Glu Arg Val Pro Gln Arg Ser Gly Phe Arg Ile Glu Arg Arg
 1985 1990 1995 2000

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 Val Pro Ala Glu Val Gly Thr Gly Ile Ala Ala Pro Ala Pro Leu Pro
 2005 2010 2015

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 Asp Ala Gly Val Gln Gly Asn Tyr Val Gln Gln Gln Val Pro Ala Thr
 2020 2025 2030

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 Lys Ile Gly Asn Tyr Gly His Gln Gly Pro Ala Met Gly Ala Gln Gln
 2065 2070 2075 2080

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 Pro Val Val Pro Gln Gln Gln Asn Ile Pro Pro Val His Asn Pro Val
 2085 2090 2095

cca cag aat tct gtt ccg cct act ccg gtt gtg ccg aag cca ggt aca 6336
 Pro Gln Asn Ser Val Pro Pro Thr Pro Val Val Pro Lys Pro Gly Thr
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 2115 2120 2125

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 Phe Asp Thr Ser Arg Tyr Asn Gln Gln Glu Pro Pro Gln Arg Gln Asp
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 20 25 30

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 35 40 45
 Ile Met Phe Ala Ser Phe Asp Asp Ala Phe Ala Ala Asp Ala Glu Ala
 50 55 60
 His Gly Cys Val His Arg Pro Gln Phe Ala Lys Val Thr Arg Arg Asn
 65 70 75 80
 Ile Leu Asn Ser Pro Gln Tyr Thr Ala Ile Lys Ser Ser Tyr Asp Ala
 85 90 95
 Leu Val Gln Gln Asp Leu Val Ala Gln Gln Gln Gln Ala Gln Ala Leu
 100 105 110
 Gln Gln Ala Ala Tyr Glu Gln Glu Gln Ala Ala Ile Phe Gln Ala Arg
 115 120 125
 Asp Gln Ala Thr Phe Gln Ala Glu Gln Thr Leu Ala Gln Glu Ser Val
 130 135 140
 Arg Gln Ser Glu Gly Val Gly Leu Pro Val Ile Asp Pro Met Glu Ser
 145 150 155 160
 Tyr Phe Arg Glu Tyr Ala Phe Tyr Glu Gly Val Glu Met Phe Gly Thr
 165 170 175
 Trp Gly Thr His Val Asp Ala Gly Val Ser Gln Phe Ser Thr Ser Asp
 180 185 190
 Gly Arg Ala Ile Arg Ala Leu Val Asp Glu His Leu Ala Thr Tyr Glu
 195 200 205
 Pro Val Glu Gln Arg Gly Ser Thr Gln Ala Phe Phe Ala Ser Val Asn
 210 215 220
 Ala Ala Phe Ala Glu Val Ala Pro His Ala Ala Pro Met Phe Ser Ala
 225 230 235 240
 Ile Ala Arg Glu Gly Glu Gly Ser Lys Gly Tyr Gln Ala Leu Arg His
 245 250 255
 Arg Phe Asp Lys Met Val Gly Thr Ala Ile Gly Pro Asn Gly Leu Pro
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 Glu Gly Pro Asp Leu Gly Gly Arg Arg Leu Pro Ile Ser Pro Tyr Asp
 275 280 285
 Pro Arg Trp Ser Asp Arg Glu Val Val Arg Val His Gly Thr Lys Leu
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 Leu Ser Leu Ser Glu Glu Ser Val Gly Met Ile Arg Asp Leu Asp Leu
 305 310 315 320
 Ala Thr Ile His Leu Gln Asp Asn Asp Val Tyr Glu Gly Thr His Arg
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 Glu Asp Asp Thr Lys Gly Gly Val Arg Pro Leu Thr Gln Trp Val Asn
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 Gly Glu Ala Ile Ala Trp Arg Thr Ile Thr Glu Asn Asp Gln Met Arg

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370					375					380					
Ala	Ser	Trp	Leu	Arg	Ala	Gly	Leu	Ile	Asp	Thr	Ala	Asp	Val	Ala	Ser
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Gln	Lys	Ile	Asp	Pro	Asn	Lys	Val	Met	Ser	Asp	Glu	Gly	Ile	Ala	Arg
			405						410					415	
Ser	Glu	Ala	Ile	Leu	Thr	Tyr	Leu	Ser	Asp	Glu	Gly	Val	Asp	Phe	Arg
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Ile	Glu	Pro	Asp	Arg	Glu	Pro	Gly	Gln	Leu	Lys	Val	Arg	Ile	Glu	Gly
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Gln	Thr	Ala	Glu	Glu	Arg	Leu	Arg	Ala	Arg	Glu	Arg	Met	Glu	Asn	Gly
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Asp	Gly	Thr	Trp	Thr	Pro	Ala	Thr	Asp	Tyr	Glu	Pro	Ser	Pro	Thr	Glu
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Leu	Glu	Gln	Ala	Gln	Asp	Ala	Tyr	Phe	Thr	Lys	Asn	Arg	Ser	Ala	Phe
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Met	Val	Arg	Glu	Gly	Leu	Ser	Ile	Val	Gln	Asp	Ala	Arg	Asp	Arg	Ser
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Gln	Asp	Tyr	Trp	Ala	Met	Leu	Arg	Gly	Glu	Glu	Thr	Asp	Leu	Leu	Asn
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Pro	Gly	Val	Asn	Arg	Asp	Asp	Tyr	Met	Ala	Ala	Ile	Arg	Asp	Gly	Asp
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His	Glu	Gln	Ile	Ala	Ala	Met	Thr	Ser	Ala	Met	Asn	Ala	Val	Thr	Val
			675				680						685		

Glu Asp Arg Val Arg Gln His Ala Ala Leu Val Leu Asp Asp Tyr Val
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 Gly Thr Val Glu Pro Asp Pro Val Thr Gly Leu Arg Phe Asn Pro Val
 705 710 715 720
 Thr Val Ala Gln His Met Pro Ser Ala Lys Ser Leu Trp Ser Asn His
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 Asp Asp Ile Ile Ala Ala Leu Arg Ala Thr Ser Ile Thr Gly Asp Glu
 740 745 750
 Leu Arg Gly Asp Glu Phe Tyr Asn Asp Val Ile Asn Gln Gln Leu Leu
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 Lys Phe Asn Pro Glu Thr Ala Gln Lys Met Val Asn Asn Pro Asp Leu
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 Asp Pro Gln Leu Ala Arg Phe Gly Thr Val Ile Ala Glu Thr Ile Ser
 785 790 795 800
 Arg Asn Gly Ala Asp Val Val Asp Ile Ala Val Asp Asp Asn Gly Val
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 Val Arg Trp Thr Ala Gln Arg Arg Val Gly Ala Lys Asp Ser Arg Ala
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 Val Asp Ser Lys Gly Gln Val Arg Gly Glu Arg Thr Arg His Val Gln
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 Gly Glu Ile Gly Gln Ile Phe Thr Arg Gly Glu His Gly Glu Ile Val
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 Thr Lys Phe Asn Gly Gly Glu Asn Tyr Met Phe Ala Pro Gly Tyr Thr
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 Ala Ser Val Val Pro Gln Lys Pro Gly Glu Thr Lys Ser Leu Glu Glu
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 Arg Thr Lys Leu Lys Gly Tyr Glu Gln Val Met Ser Glu Ala Leu Val
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Val Leu Thr Gly Gly Arg Asn Ile Ser Val Leu Asp Val Asp Ala Gly
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 Phe Ser Asn Ile Met Gln Ala Ser Ala Val Thr Gly Gly Ala Arg Thr
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 Glu Gly Phe Ser Glu Ser Asn Glu Gln Arg Asn Ile Ile Glu Met Pro
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 Ser Ile Tyr Asp Glu Asn Gly Glu Leu Asn Asn Arg Val Asn Arg Ala

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Gln Val Arg Glu Ala Phe Val Glu Gln Ile Ser Arg Ala Gly Gly Val		
1345	1350	1355 1360
Met Glu Ile Pro Phe Gln Leu Gln Leu Arg Asn Gly Ala Gln Leu Glu		
1365	1370	1375
Glu Ser Pro Asn Asn Pro Asp Met Tyr Gln Leu Pro Leu Leu Ser Pro		
1380	1385	1390
His Leu Arg Ser Ser Asp Glu Asp Leu Ala Asp Gly Ser Thr Ser Arg His		
1395	1400	1405
Glu Tyr Thr Thr Arg Tyr Met Ala Ile Phe Asp Thr Cys Tyr Lys Leu		
1410	1415	1420
Ala Glu Glu Gln Ala Lys Ile Asp Ala Leu Arg Gln Glu Glu Ala Gln		
1425	1430	1435 1440
His Gly Thr Leu Pro Arg Ala Ala Glu Lys Arg Leu Ser Glu Ser Gln		
1445	1450	1455
Lys Phe Val Asp Gln Ala Gln Lys Lys Val Gln Ala Ser Phe Asp Gly		
1460	1465	1470
Ile Ala Asn Asp Ile Val Ala Ser Arg Ile Glu Thr Lys Asn Asn Val		
1475	1480	1485
Phe Lys Asp Gly Phe Met Ser Ala Arg Gln Ser His Ser Ala Thr Ala		
1490	1495	1500
Val Trp Thr Gly Asp Pro Arg Leu Ser Val Asp Glu Val Ala Met Asn		
1505	1510	1515 1520
Ser Ser Met Ala Arg Glu Leu Gly Val Leu Asp Asn Gly Tyr Ala Met		
1525	1530	1535
Val Trp Arg Asp Pro Val Ile Arg Asp Gly Gly Val Arg Tyr Leu Arg		
1540	1545	1550
Val Val Ile Asn Asp Asp Leu His Gly Val Ala Val Asn Pro Val Ser		
1555	1560	1565
Val Lys Ser Phe Asp Gly Asp Phe Asp Gly Asp Ser Val Gly Leu Val		
1570	1575	1580
Gly Asn Leu Pro Lys Lys Ala His Glu Glu Ala Leu Ser Arg Leu Thr		
1585	1590	1595 1600
Val Glu Ala Asn Met Leu Asp Leu Gly Asp Gly Lys Arg Met Glu Asp		
1605	1610	1615
Gly Thr Met Phe Tyr Gly Leu Thr Leu His Asp Ser Leu Asp Val Gln		
1620	1625	1630
Val Ala Gln His His Asp Pro Ala Met Ala Glu Asn Met Lys Val Ile		
1635	1640	1645
Val Ser Glu Leu Asn Arg Tyr Gln Arg Glu Tyr Glu Ala Gly Glu Ile		
1650	1655	1660

Ser Arg Glu Glu Leu Leu Glu Val Asn Arg Ala His Met Asp Asp Leu
 1665 1670 1675 1680
 Asn Glu His Tyr Ala Gln Ala Phe Ala Asn Arg Asp Gly Leu Val Thr
 1685 1690 1695
 Leu Arg Phe Asp Gly Met Glu Asn His Met Ala Ser Val Ala Gln Cys
 1700 1705 1710
 Phe Glu Thr Gly Ala Lys Gly Ser Pro Gly Lys Leu Lys Glu Tyr Ala
 1715 1720 1725
 Thr Tyr Ile Gly Ala Asp Pro Ala Gln Gly Phe Lys Asp Val Gly Gln
 1730 1735 1740
 Pro Thr Pro Glu Ala Leu Arg Ser His Tyr Glu Gly Ser Gln Lys Ala
 1745 1750 1755 1760
 Thr Ala Ile Lys Val Leu Phe Thr Gly Val Ala Gly Lys Lys Glu Gln
 1765 1770 1775
 Glu Met Val Ala Leu Cys Arg Asn Leu Gly Leu Thr Lys Glu Ala Met
 1780 1785 1790
 Ala Ala Ser Ala Pro Ala Gln Gln Ser Ile Leu Gln Ala Lys His Asp
 1795 1800 1805
 Pro Ile Asp Ala Leu Tyr Arg Ala Glu Thr Leu Met Gly Pro Val Gly
 1810 1815 1820
 Asp Leu Tyr Gln Gly Arg Lys Met Arg Arg Gly Glu Asn Glu Gln Gly
 1825 1830 1835 1840
 Arg Tyr Glu Trp Glu Val Val Arg Asp Glu Asn His Gln Pro Ile Gln
 1845 1850 1855
 Ala Thr Lys Asp Glu Trp Val Gln Gln Tyr Met Glu Met Tyr Ala Asp
 1860 1865 1870
 Asp Lys Gly Met Gly Val Ser Val Gly Val Asp Gln Val Glu Lys Ile
 1875 1880 1885
 Ala Glu Glu Phe Ser Asp Glu Gln Gly Tyr Met Arg Val Leu Ser His
 1890 1895 1900
 Asp Glu Leu Pro Thr Glu Ile Lys Pro Leu Ala Leu Asp Gln Leu Ala
 1905 1910 1915 1920
 Tyr Gly Asp Lys Lys Asn Arg Phe Asp Leu Leu Cys Glu Met Ala Lys
 1925 1930 1935
 Gln Gln Val Asn Ile Tyr Asp Gly Asp Ala Tyr Asp Phe Ala Pro Arg
 1940 1945 1950
 Val Val Arg Ala Asn Met Lys Ala Met Glu Asp Ala Ala Arg Phe Gly
 1955 1960 1965
 Ile Pro Asp Val Glu Ile Gln Ser Ile Ser Ala Gln Gln Ser Leu Ala
 1970 1975 1980

Ser Phe Glu Arg Val Pro Gln Arg Ser Gly Phe Arg Ile Glu Arg Arg
1985 1990 1995 2000

Val Pro Ala Glu Val Gly Thr Gly Ile Ala Ala Pro Ala Pro Leu Pro
2005 2010 2015

Asp Ala Gly Val Gln Gly Asn Tyr Val Gln Gln Gln Val Pro Ala Thr
2020 2025 2030

Pro Pro Val Met Pro Val Thr Pro Pro Ala Gln Gln Pro Val Ser Pro
2035 2040 2045

Ala Gln Thr Asp Phe Arg Gly Val Gly Gln Pro Leu Asp Gln Gly Gly
2050 2055 2060

Lys Ile Gly Asn Tyr Gly His Gln Gly Pro Ala Met Gly Ala Gln Gln
2065 2070 2075 2080

Pro Val Val Pro Gln Gln Gln Asn Ile Pro Pro Val His Asn Pro Val
2085 2090 2095

Pro Gln Asn Ser Val Pro Pro Thr Pro Val Val Pro Lys Pro Gly Thr
2100 2105 2110

Gly Asn Pro Phe Thr His Gly Gly Ala Asn Asn Gln Phe Met Gly Arg
2115 2120 2125

Phe Asp Thr Ser Arg Tyr Asn Gln Gln Glu Pro Pro Gln Arg Gln Asp
2130 2135 2140

Gly Gly Phe Glu Leu
2145

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<223> FRXA01590

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Gly Phe Lys Asp Val Gly Gln Pro Thr Pro Glu Ala Leu Arg Ser His
20 25 30

tat gag ggt tcg cag aag gcg act gca att aag gtg ctc ttt acc ggt 144
Tyr Glu Gly Ser Gln Lys Ala Thr Ala Ile Lys Val Leu Phe Thr Gly
35 40 45

gtg gct ggt aaa aaa gag cag gaa atg gtg gca ttg tgc cgc aat ctt 192
Val Ala Gly Lys Lys Glu Gln Glu Met Val Ala Leu Cys Arg Asn Leu
50 55 60

ggt ctg acc aag gaa gct atg gct gca tca gca ccg gca cag cag tcg	240
Gly Leu Thr Lys Glu Ala Met Ala Ala Ser Ala Pro Ala Gln Gln Ser	
65 70 75 80	
att ctg cag gcg aag cac gac ccg att gac gcg ctc tat cgt gca gaa	288
Ile Leu Gln Ala Lys His Asp Pro Ile Asp Ala Leu Tyr Arg Ala Glu	
85 90 95	
act ctt atg gga cca gta ggt gat ctc tac caa ggt cgc aag atg cgt	336
Thr Leu Met Gly Pro Val Gly Asp Leu Tyr Gln Gly Arg Lys Met Arg	
100 105 110	
cgt ggt gag aat gag caa ggt cgc tat gag tgg gaa gtc gtt agg gac	384
Arg Gly Glu Asn Glu Gln Gly Arg Tyr Glu Trp Glu Val Val Arg Asp	
115 120 125	
gag aac cac cag cct atc cag gcc acc aag gat gaa tgg gta cag cag	432
Glu Asn His Gln Pro Ile Gln Ala Thr Lys Asp Glu Trp Val Gln Gln	
130 135 140	
tac atg gag atg tac gcc gat gac aag ggt atg ggt gtc tcg gtt ggc	480
Tyr Met Glu Met Tyr Ala Asp Asp Lys Gly Met Gly Val Ser Val Gly	
145 150 155 160	
gtt gac cag gtg gag aag atc gcg gaa gaa ttc tct gat gag cag ggt	528
Val Asp Gln Val Glu Lys Ile Ala Glu Glu Phe Ser Asp Glu Gln Gly	
165 170 175	
tat atg cgt gtg ctt agc cat gat gag cta ccc act gag att aag cca	576
Tyr Met Arg Val Leu Ser His Asp Glu Leu Pro Thr Glu Ile Lys Pro	
180 185 190	
cta gca ctt gat cag ctt gcc tat ggc gat aag aag aac cgc ttt gat	624
Leu Ala Leu Asp Gln Leu Ala Tyr Gly Asp Lys Lys Asn Arg Phe Asp	
195 200 205	
ttg ttg tgc gag atg gca aag cag cag gtc aac atc tac gac ggt gat	672
Leu Leu Cys Glu Met Ala Lys Gln Gln Val Asn Ile Tyr Asp Gly Asp	
210 215 220	
gct tat gac ttt gcc cct cgt gtg gtg cgc gcc aat atg aag gca atg	720
Ala Tyr Asp Phe Ala Pro Arg Val Val Arg Ala Asn Met Lys Ala Met	
225 230 235 240	
gag gat gca gcg cgt ttt ggt atc cct gat gtg gag att cag tcg att	768
Glu Asp Ala Ala Arg Phe Gly Ile Pro Asp Val Glu Ile Gln Ser Ile	
245 250 255	
tct gca cag cag tca ttg gcg agc ttt gag cga gtc cca caa cgt tct	816
Ser Ala Gln Gln Ser Leu Ala Ser Phe Glu Arg Val Pro Gln Arg Ser	
260 265 270	
ggt ttc cgt att gag cgt cgt gtg ccg gca gaa gta ggt aca ggg att	864
Gly Phe Arg Ile Glu Arg Arg Val Pro Ala Glu Val Gly Thr Gly Ile	
275 280 285	
gct gca cca gca ccg cct tta cct gat gca ggt gta cag ggg aat tat gtt	912
Ala Ala Pro Ala Pro Leu Pro Asp Ala Gly Val Gln Gly Asn Tyr Val	
290 295 300	
cag cag cag gtg cct gcg acc ccg cca gtt atg cct gtc aca cct ccg	960

Gln Gln Gln Val Pro Ala Thr Pro Pro Val Met Pro Val Thr Pro Pro
305 310 315 320

gca cag caa cct gtt tgc cct gct cag acg gac ttc cgg ggc gtt ggt 1008
Ala Gln Gln Pro Val Ser Pro Ala Gln Thr Asp Phe Arg Gly Val Gly
325 330 335

cag cca ctc gac cag ggc gga aaa atc ggg aat tat gga cat cag gga 1056
Gln Pro Leu Asp Gln Gly Gly Lys Ile Gly Asn Tyr Gly His Gln Gly
340 345 350

cct gca atg ggg gcg caa cag cca gtt gtg cct cag cag cag aat att 1104
Pro Ala Met Gly Ala Gln Gln Pro Val Val Pro Gln Gln Gln Asn Ile
355 360 365

cgg cct gtg cat aat ccg gta cca cag aat tct gtt ccg cct act ccg 1152
Pro Pro Val His Asn Pro Val Pro Gln Asn Ser Val Pro Pro Thr Pro
370 375 380

gtt gtg ccg aag cca ggt aca gga aac ccg ttt act cat ggt ggt gcg 1200
Val Val Pro Lys Pro Gly Thr Gly Asn Pro Phe Thr His Gly Gly Ala
385 390 395 400

aac aat cag ttt atg ggt cga ttt gat aca agc cgt tac aac caa cag 1248
Asn Asn Gln Phe Met Gly Arg Phe Asp Thr Ser Arg Tyr Asn Gln Gln
405 410 415

gaa cca cca caa cga cag gat ggc ggg ttt gag ctc taaataatgg 1294
Glu Pro Pro Gln Arg Gln Asp Gly Phe Glu Leu
420 425

cagtagattt cag 1307

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<212> PRT
<213> Corynebacterium glutamicum

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Gly Phe Lys Asp Val Gly Gln Pro Thr Pro Glu Ala Leu Arg Ser His
20 25 30

Tyr Glu Gly Ser Gln Lys Ala Thr Ala Ile Lys Val Leu Phe Thr Gly
35 40 45

Val Ala Gly Lys Lys Glu Gln Glu Met Val Ala Leu Cys Arg Asn Leu
50 55 60

Gly Leu Thr Lys Glu Ala Met Ala Ala Ser Ala Pro Ala Gln Gln Ser
65 70 75 80

Ile Leu Gln Ala Lys His Asp Pro Ile Asp Ala Leu Tyr Arg Ala Glu
85 90 95

Thr Leu Met Gly Pro Val Gly Asp Leu Tyr Gln Gly Arg Lys Met Arg
100 105 110

Arg Gly Glu Asn Glu Gln Gly Arg Tyr Glu Trp Glu Val Val Arg Asp
 115 120 125
 Glu Asn His Gln Pro Ile Gln Ala Thr Lys Asp Glu Trp Val Gln Gln
 130 135 140
 Tyr Met Glu Met Tyr Ala Asp Asp Lys Gly Met Gly Val Ser Val Gly
 145 150 155 160
 Val Asp Gln Val Glu Lys Ile Ala Glu Glu Phe Ser Asp Glu Gln Gly
 165 170 175
 Tyr Met Arg Val Leu Ser His Asp Glu Leu Pro Thr Glu Ile Lys Pro
 180 185 190
 Leu Ala Leu Asp Gln Leu Ala Tyr Gly Asp Lys Lys Asn Arg Phe Asp
 195 200 205
 Leu Leu Cys Glu Met Ala Lys Gln Gln Val Asn Ile Tyr Asp Gly Asp
 210 215 220
 Ala Tyr Asp Phe Ala Pro Arg Val Val Arg Ala Asn Met Lys Ala Met
 225 230 235 240
 Glu Asp Ala Ala Arg Phe Gly Ile Pro Asp Val Glu Ile Gln Ser Ile
 245 250 255
 Ser Ala Gln Gln Ser Leu Ala Ser Phe Glu Arg Val Pro Gln Arg Ser
 260 265 270
 Gly Phe Arg Ile Glu Arg Arg Val Pro Ala Glu Val Gly Thr Gly Ile
 275 280 285
 Ala Ala Pro Ala Pro Leu Pro Asp Ala Gly Val Gln Gly Asn Tyr Val
 290 295 300
 Gln Gln Gln Val Pro Ala Thr Pro Pro Val Met Pro Val Thr Pro Pro
 305 310 315 320
 Ala Gln Gln Pro Val Ser Pro Ala Gln Thr Asp Phe Arg Gly Val Gly
 325 330 335
 Gln Pro Leu Asp Gln Gly Gly Lys Ile Gly Asn Tyr Gly His Gln Gly
 340 345 350
 Pro Ala Met Gly Ala Gln Gln Pro Val Val Pro Gln Gln Asn Ile
 355 360 365
 Pro Pro Val His Asn Pro Val Pro Gln Asn Ser Val Pro Pro Thr Pro
 370 375 380
 Val Val Pro Lys Pro Gly Thr Gly Asn Pro Phe Thr His Gly Gly Ala
 385 390 395 400
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 Glu Pro Pro Gln Arg Gln Asp Gly Gly Phe Glu Leu
 420 425

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 <213> *Corynebacterium glutamicum*

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 <223> FRXA01542

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 gct gtg cgt atc tat agg caa gca gaa gcc ttg atg aaa cag cgc gca 96
 Ala Val Arg Ile Tyr Arg Gln Ala Glu Ala Leu Met Lys Gln Arg Ala
 20 25 30
 gca aac aat aag ggc tta gac ctc aat gat gaa gcg acc tat ggc gcc 144
 Ala Asn Asn Lys Gly Leu Asp Leu Asn Asp Glu Ala Thr Tyr Gly Ala
 35 40 45
 atc atg ttt cgc tct ttc gat gat gcc ttc gcc gct gat gcc gaa gct 192
 Ile Met Phe Ala Ser Phe Asp Asp Ala Phe Ala Ala Asp Ala Glu Ala
 50 55 60
 cat ggc tgt gta cac cga cca cag ttc gcg aag gta act agg cga aat 240
 His Gly Cys Val His Arg Pro Gln Phe Ala Lys Val Thr Arg Arg Asn
 65 70 75 80
 att ctt aat tca ccg caa tac acg gcg att aag tca tct tat gac gcg 288
 Ile Leu Asn Ser Pro Gln Tyr Thr Ala Ile Lys Ser Ser Tyr Asp Ala
 85 90 95
 ctg gtg cag cag gat ctc gtg gcc caa cag cag cag gca caa gcg cta 336
 Leu Val Gln Gln Asp Leu Val Ala Gln Gln Gln Ala Gln Ala Leu
 100 105 110
 cag caa gct gct tat gag caa gag cag gca gct att ttc cag gca cgt 384
 Gln Gln Ala Ala Tyr Glu Gln Glu Gln Ala Ala Ile Phe Gln Ala Arg
 115 120 125
 gat caa gca aca ttc cag gct gaa caa acg ctc gcg caa gag tcc gtt 432
 Asp Gln Ala Thr Phe Gln Ala Glu Gln Thr Leu Ala Gln Glu Ser Val
 130 135 140
 cgc caa tca gag ggt gtg ggt tta cct gtc att gat cgc atg gag agc 480
 Arg Gln Ser Ser Glu Gly Val Gly Leu Pro Val Ile Asp Pro Met Glu Ser
 145 150 155 160
 tat ttc cgg gag tac gcc ttc tat gaa ggt gtc gag atg ttt ggt acc 528
 Tyr Phe Arg Glu Tyr Ala Phe Tyr Glu Gly Val Glu Met Phe Gly Thr
 165 170 175
 tgg ggt acg cac gtt gat gct ggt gtg tgg cag ttt agc acc tct gat 576
 Trp Gly Thr His Val Asp Ala Gly Val Ser Gln Phe Ser Thr Ser Asp
 180 185 190
 ggc cgt gcg atc cga gcg ctt gtt gat gag cat ctc gca acc tat gaa 624
 Gly Arg Ala Ile Arg Ala Leu Val Asp Glu His Leu Ala Thr Tyr Glu

195	200	205	
cca gta gag cag cgg ggg agt act cag gca ttc ttc gcc tct gtc aat Pro Val Glu Gln Arg Gly Ser Thr Gln Ala Phe Phe Ala Ser Val Asn 210 215 220			672
gct gcc ttt gct gag gtg gca cct cac gca gca ccc atg ttt agt gcg Ala Ala Phe Ala Glu Val Ala Pro His Ala Ala Pro Met Phe Ser Ala 225 230 235 240			720
att gct cgc gag ggt gag ggt tca aag ggg tac cag gcg ctg cgt cac Ile Ala Arg Glu Gly Glu Gly Ser Lys Gly Tyr Gln Ala Leu Arg His 245 250 255			768
cgt ttc gac aag atg gtc ggc act gca att gga cct aat ggt ttg cct Arg Phe Asp Lys Met Val Gly Thr Ala Ile Gly Pro Asn Gly Leu Pro 260 265 270			816
gag gga cct gat ctg ggt ggt cgt cgt tta cct att tgg cct tat gat Glu Gly Pro Asp Leu Gly Gly Arg Arg Leu Pro Ile Ser Pro Tyr Asp 275 280 285			864
cca cgc tgg tca gac cgc gaa gta gtc cgt gtg cac ggt acc aag ctg Pro Arg Trp Ser Asp Arg Glu Val Val Arg Val His Gly Thr Lys Leu 290 295 300			912
cta tca ctg tcc gaa gag agt gtt ggc atg atc agg gac ctt gat cta Leu Ser Leu Ser Glu Glu Ser Val Gly Met Ile Arg Asp Leu Asp Leu 305 310 315 320			960
gca acg atc cac cta caa gat aat gat gtt tac gag gcc act cat cga Ala Thr Ile His Leu Gln Asp Asn Asp Val Tyr Glu Gly Thr His Arg 325 330 335			1008
gaa gac gac act aaa ggc ggt gtg cga cgg ttg act caa tgg gtc aat Glu Asp Asp Thr Lys Gly Gly Val Arg Pro Leu Thr Gln Trp Val Asn 340 345 350			1056
ggt gaa gct att gcc tgg cgc act atc acc gag aat gac cag atg cga Gly Glu Ala Ile Ala Trp Arg Thr Ile Thr Glu Asn Asp Gln Met Arg 355 360 365			1104
ctg ccc aat att ggt cag ttt atg acg gct aaa gaa tac cgt gcc gca Leu Pro Asn Ile Gly Gln Phe Met Thr Ala Lys Gly Tyr Arg Ala Ala 370 375 380			1152
gcg tca tgg ctg cgt gct gga ctc att gat acc gca gat gtt gcg agt Ala Ser Trp Leu Arg Ala Gly Leu Ile Asp Thr Ala Asp Val Ala Ser 385 390 395 400			1200
cag aaa att gac ccc aac aag gtc atg tct gat gag ggt atc gcg cgc Gln Lys Ile Asp Pro Asn Lys Val Met Ser Asp Glu Gly Ile Ala Arg 405 410 415			1248
tgg gaa gct att ttg acg tat ctg tgg gat gag ggt gtg gat ttt agg Ser Glu Ala Ile Leu Thr Tyr Leu Ser Asp Glu Gly Val Asp Phe Arg 420 425 430			1296
atc gag cca gat cgt gag cgg gga cag ctt aaa gtg cgt att gag ggc Ile Glu Pro Asp Arg Glu Pro Gly Gln Leu Lys Val Arg Ile Glu Gly 435 440 445			1344

acc cgt att gat att cgt ctc act gat act cgc gcc aat gaa cag tgg	1392
Thr Arg Ile Asp Ile Arg Leu Thr Asp Thr Arg Ala Asn Glu Gln Trp	
450 455 460	
gtg ggt cgt gtc tat gat tct ggc act gtg att aag tat tcc gcc gaa	1440
Val Gly Arg Val Tyr Asp Ser Gly Thr Val Ile Lys Tyr Ser Ala Glu	
465 470 475 480	
caa aca gcg gaa gaa cgt cta cga gct cgt gag cgc atg gag aac ggt	1488
Gln Thr Ala Glu Glu Arg Leu Arg Ala Arg Glu Arg Met Glu Asn Gly	
485 490 495	
gat gga acg tgg aca ccg gct act gat tat gaa cca agc cca act gaa	1536
Asp Gly Thr Trp Thr Pro Ala Thr Asp Tyr Glu Pro Ser Pro Thr Glu	
500 505 510	
gtt gtc gat ctc gtg aaa ttt gct ctc ggt cga gag gtt gag cga cag	1584
Val Val Asp Leu Val Lys Phe Ala Leu Gly Arg Glu Val Glu Arg Gln	
515 520 525	
gat ggc aaa ggt ctt gtt ggt gtg cct aat gct cga cac cca cgt gct	1632
Asp Gly Lys Gly Leu Val Gly Val Pro Asn Ala Arg His Pro Arg Ala	
530 535 540	
tta gag cag gca cag gat gca tat ttc act aag aat cgt tcc gca ttc	1680
Leu Glu Gln Ala Gln Asp Ala Tyr Phe Thr Lys Asn Arg Ser Ala Phe	
545 550 555 560	
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Met Val Arg Glu Gly Leu Ser Ile Val Gln Asp Ala Arg Asp Arg Ser	
565 570 575	
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Ala Gly Pro Gly Lys Trp Phe Asp Asn Glu Ala Lys Ala Ser Glu Trp	
580 585 590	
ctt ggt aac aat atc gcc ctt act cgt gcg cgt gtg gcc gaa gag ctc	1824
Leu Gly Asn Asn Ile Ala Leu Thr Arg Ala Arg Val Ala Glu Glu Leu	
595 600 605	
ggc gtt gaa gaa ctg att gcg ctt tct gca cag tac gcc gat gat cct	1872
Gly Val Glu Glu Leu Ile Ala Leu Ser Ala Gln Tyr Ala Asp Asp Pro	
610 615 620	
gac ttc atg ccg gct ttt gct ggt gag gat gag ctc atg gcg ata aag	1920
Asp Phe Met Pro Ala Phe Ala Gly Glu Asp Glu Leu Met Ala Ile Lys	
625 630 635 640	
cag gac tat tgg gcg atg ctg cga ggt gag gaa acc gat ctg ctt aac	1968
Gln Asp Tyr Trp Ala Met Leu Arg Gly Glu Thr Asp Leu Leu Asn	
645 650 655	
cct ggg gtt aac cgc gat gat tat atg gct gct atc cgc gat ggt gat	2016
Pro Gly Val Asn Arg Asp Asp Tyr Met Ala Ala Ile Arg Asp Gly Asp	
660 665 670	
cat gag cag att gct gcg atg acc tca gca atg aat gct gtg acc gtg	2064
His Glu Gln Ile Ala Ala Met Thr Ser Ala Met Asn Ala Val Thr Val	
675 680 685	

gag gat cgt gtg cgt cag cac gcg gcc ctt gtt ctt gat gat tat gtc	2112
Glu Asp Arg Val Arg Gln His Ala Ala Leu Val Leu Asp Asp Tyr Val	
690 695 700	
ggc acg gtg gag cct gat cct gtt acc ggc ttg cgt ttt aat ccg gtg	2160
Gly Thr Val Glu Pro Asp Pro Val Thr Gly Leu Arg Phe Asn Pro Val	
705 710 715 720	
aca gtt gct cag cac atg ccg agt gct aaa tcc ctg tgg tca aac cat	2208
Thr Val Ala Gln His Met Pro Ser Ala Lys Ser Leu Trp Ser Asn His	
725 730 735	
gac gat att att gcc gcg ttg cga gcg act tcc att act ggc gat gaa	2256
Asp Asp Ile Ile Ala Ala Leu Arg Ala Thr Ser Ile Thr Gly Asp Glu	
740 745 750	
ctg cgc ggt gat gaa ttc tat aac gat gtt att aat caa cag ttg ctc	2304
Leu Arg Gly Asp Glu Phe Tyr Asn Asp Val Ile Asn Gln Leu Leu	
755 760 765	
aaa ttt aat cct gag acc gcg cag aaa atg gtt aat aac cct gat ctt	2352
Lys Phe Asn Pro Glu Thr Ala Gln Lys Met Val Asn Asn Pro Asp Leu	
770 775 780	
gac ccg cag ttg gct cga ttt ggc act gtc att gcc gag act att tcc	2400
Asp Pro Gln Leu Ala Arg Phe Gly Thr Val Ile Ala Glu Thr Ile Ser	
785 790 795 800	
cgc aat ggt gct gat gtg gtc gat att got gtt gac gat aac ggt gtg	2448
Arg Asn Gly Ala Asp Val Val Asp Ile Ala Val Asp Asp Asn Gly Val	
805 810 815	
gtg cgg tgg acc gca cag cga cgt gtt ggt gcg aag gat agt cgt gca	2496
Val Arg Trp Thr Ala Gln Arg Arg Val Gly Ala Lys Asp Ser Arg Ala	
820 825 830	
gta gat agt aag ggg cag gtt cgc ggt gaa cgc acc cgt cat gtg cag	2544
Val Asp Ser Lys Pro Gly Gln Val Arg Gly Glu Arg Thr Arg His Val Gln	
835 840 845	
ggt gag ata ggt cag att ttt act cgc ggt gag cat ggt gaa att gtc	2592
Gly Glu Ile Gly Gln Ile Phe Thr Arg Gly Glu His Gly Glu Ile Val	
850 855 860	
acc aaa ttt aat ggt ggc gag aac tat atg ttt gcc cct gcc tac acc	2640
Thr Lys Phe Asn Gly Gly Glu Asn Tyr Met Phe Ala Pro Gly Tyr Thr	
865 870 875 880	
gcg tct gtg gta cca caa aag cct ggt gag aca aag agt tta gaa gag	2688
Ala Ser Val Val Pro Gln Lys Pro Gly Glu Thr Lys Ser Leu Glu Glu	
885 890 895	
cgt acc aag ctc aaa ggc tat gag cag gtg atg tca gag gcg ttg gtg	2736
Arg Thr Lys Leu Lys Gly Tyr Glu Gln Val Met Ser Glu Ala Leu Val	
900 905 910	
tac cgt gtg cga gaa gat ttg atg ttc act gag cga tcc cga gtg ggt	2784
Tyr Arg Val Arg Glu Asp Leu Met Phe Thr Glu Arg Ser Arg Val Gly	
915 920 925	
gct aca acc agc atc aac agt gca tat aag cga ctg tat gac aat cgc	2832

Ala Thr Thr Ser Ile Asn Ser Ala Tyr Lys Arg Leu Tyr Asp Asn Arg	
930 935 940	
ttc cct gtg gac ttc ttc gag cgc agc gcc gaa gaa ggt ttg agc gat	2880
Phe Pro Val Asp Phe Phe Glu Arg Ser Ala Glu Gly Leu Ser Asp	
945 950 960	
gag tgg cgt gct cgc ttg ctt gag act gcg agt ttg cgt gtg cgc tac	2928
Glu Trp Arg Ala Ala Leu Leu Glu Thr Ala Ser Leu Arg Val Arg Tyr	
965 970 975	
gac aac tct att cgt gat ggt gcg aat gtg atg gag gat att cga gca	2976
Asp Asn Ser Ile Arg Asp Gly Ala Asn Val Met Glu Asp Ile Arg Ala	
980 985 990	
cag cag cgt ggt ttt gat cgc cgt aat gat aac tcc cgt gat gcg ctg	3024
Gln Gln Arg Gly Phe Asp Ala Arg Asn Asp Asn Ser Arg Asp Ala Leu	
995 1000 1005	
gtg ctt acc ggt ggg cgt aac att tct gta ctt gat gtt gat gcg ggt	3072
Val Leu Thr Gly Gly Arg Asn Ile Ser Val Leu Asp Val Asp Ala Gly	
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Lys Gly Phe Phe Asp Pro Met Met Thr Gly Met Ala Ala Asn Gln Gly	
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Ser Val Arg Tyr Leu Leu Pro Ser Ala Lys Val Gly Ala Asp Gly Met	
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Ile Thr Pro Gly Asp Pro Ala Asp Arg Val Pro Val Ala Ala His Pro	
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gaa tca tgg gcg atg ggc ttt gac cca cat gac cgt cag aac atg act	3264
Glu Ser Trp Ala Met Gly Phe Asp Pro His Asp Arg Gln Asn Met Thr	
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Phe Ser Asn Ile Met Gln Ala Ser Ala Val Thr Gly Gly Ala Arg Thr	
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Ala Met Ile Gln Leu Gly Gly Trp Asn Phe Glu Asp Gly Ile Ile Val	
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tct gcc gat ttt gcg aat acc cat gtt att cgc gat acg gaa gat gag	3408
Ser Ala Asp Phe Ala Asn Thr His Val Ile Arg Asp Thr Glu Asp Glu	
1125 1130 1135	
atg cgc ccc ttg gtt gcc ggc gat aag ctg tct gat ttt cac ggt aat	3456
Met Arg Pro Leu Val Ala Gly Asp Lys Leu Ser Asp Phe His Gly Asn	
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Lys Gly Val Thr Ala Leu Val Val Asp Pro Ala Met Ser His Ala Asp	
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gca cgt gca gca ggg ctg gaa tca gag gtg gcg ttt ttc cga gac aac	3552
Ala Arg Ala Ala Gly Leu Glu Ser Glu Val Ala Phe Phe Arg Asp Asn	

1170	1175	1180	
cct gat cta gag gtt gtc atg agt ccg ttt tct gcc att tct cgt ttt			3600
Pro Asp Leu Glu Val Val Met Ser Pro Phe Ser Ala Ile Ser Arg Phe			
1185	1190	1195	1200
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Asn Gly Gly Thr Ala Arg Glu Leu Met Thr Asn Pro Gln Asp Val Val			
	1205	1210	1215
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Phe Arg Asn Asn Asp Gly Ser Thr Arg Val Gln Pro Gly Ala Ser Gly			
	1220	1225	1230
gat ctg aac ttc atc gtc acg cat atg gct gtt gat gcg aaa acc aat			3744
Asp Leu Asn Phe Ile Val Thr His Met Ala Val Asp Ala Lys Thr Asn			
	1235	1240	1245
gtc tat gat gaa gaa gct gtt cgt gag gcc caa gga cgt aaa gcg tct			3792
Val Tyr Asp Glu Glu Ala Val Arg Glu Gly Gln Gly Ala Ser Lys Ala Ser			
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tct cag ctg gcg tgg gtg ctg caa gcc cag gaa tgt cat gag att atg			3840
Ser Gln Leu Ala Trp Val Leu Gln Ala Gln Glu Cys His Glu Ile Met			
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gag cac ttt tat ggc aac aac gtc tct gca ttg gct aac ttc cag gaa			3888
Glu His Phe Tyr Gly Asn Asn Val Ser Ala Leu Ala Asn Phe Gln Glu			
	1285	1290	1295
gat ctt cgc gtc acg ggg ctt gat gtc acc ccg tat ggt gag ttg cgc			3936
Tyr Leu Arg Val Thr Gly Leu Asp Val Thr Pro Tyr Gly Glu Leu Arg			
	1300	1305	1310
gag ggg ttc agc gag tcc aat gag cag cgc aat atc atc gag atg cca			3984
Glu Gly Phe Ser Glu Ser Asn Glu Gln Arg Asn Ile Ile Glu Met Pro			
	1315	1320	1325
gag att tac gat gag aac ggt gag ctg aat aat cgt gtt aat cgt gca			4032
Ser Ile Tyr Asp Glu Asn Gly Glu Leu Asn Asn Arg Val Asn Arg Ala			
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cag gtg cgc gaa gct ttt gtt gag cag atc agt cgc gct ggt ggt gtt			4080
Gln Val Arg Glu Ala Phe Val Glu Gln Ile Ser Arg Ala Gly Gly Val			
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atg gag att cct ttc cag tta cag ttg cgc aat ggt gca cag cta gaa			4128
Met Glu Ile Pro Phe Gln Leu Gln Leu Arg Asn Gly Ala Gln Leu Glu			
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gag tca cct aat aat cca gac atg tat cag ttg cca cta ctg agc ccg			4176
Glu Ser Pro Asn Asn Pro Asp Met Tyr Gln Leu Pro Leu Leu Ser Pro			
	1380	1385	1390
cat ttg cgc agt gat gag gat tta gcg gac ggt agt acc tct cga cat			4224
His Leu Arg Ser Asp Glu Asp Leu Ala Asp Gly Ser Thr Ser Arg His			
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gag tac acc acg cgg tat atg gct att ttt gat acg tgc tac aag ctg			4272
Glu Tyr Thr Thr Arg Tyr Met Ala Ile Phe Asp Thr Cys Tyr Lys Leu			
	1410	1415	1420

gca gaa gag caa gcc aag att gac gca ttg cgc cag gag gaa gcg cag 4320
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cac ggc acg ttg cct cgt gct gcg gaa aag cga ctg agc gag tca cag 4368
His Gly Thr Leu Pro Arg Ala Ala Glu Lys Arg Leu Ser Glu Ser Gln
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Ile Ala Asn Asp Ile Val Ala Ser Arg Ile Glu Thr Lys Asn Asn Val
1475 1480 1485

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Phe Lys Asp Gly Phe Met Ser Ala Arg Gln Ser His Ser Ala Thr Ala
1490 1495 1500

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Ser Ser Met Ala Arg Glu Leu Gly Val Leu Asp Asn Gly Tyr Ala Met
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Val Trp Arg Asp Pro Val Ile Arg Asp Gly Gly Val Arg Tyr Leu Arg
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Val Val Ile Asn Asp Asp Leu His Gly Val Ala Val Asn Pro Val Ser
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Val Lys Ser Phe Asp Gly Asp Phe Asp Gly Asp Ser Val Gly Leu Val
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ggc aat ctg ccg aaa aag gcg cat gag gag gca ttg tcc agg ctc aca 4800
Gly Asn Leu Pro Lys Lys Ala His Glu Glu Ala Leu Ser Arg Leu Thr
1585 1590 1595 1600

gtt gag gca aac atg ctt gat ctt ggt gat ggt aag cgt atg gag gac 4848
Val Glu Ala Asn Met Leu Asp Leu Gly Asp Gly Lys Arg Met Glu Asp
1605 1610 1615

ggc act atg ttt tat ggg cta act ctg cat gac agc ctc gat gta cag 4896
Gly Thr Met Phe Tyr Gly Leu Thr Leu His Asp Ser Leu Asp Val Gln
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gta gcg cag cac cat gat ccg gca atg gcc gag aac atg aag gtt att 4944
Val Ala Gln His His Asp Pro Ala Met Ala Glu Asn Met Lys Val Ile
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Val Ser Glu Leu Asn Arg Tyr Gln Arg Glu Tyr Glu Ala Gly Glu Ile
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agc cgc gaa gaa ttg cta gag gtc aac cgt gca cac atg gat gat ctc 5040
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Ile Met Phe Ala Ser Phe Asp Asp Ala Phe Ala Ala Asp Ala Glu Ala
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His Gly Cys Val His Arg Pro Gln Phe Ala Lys Val Thr Arg Arg Asn
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Ile Leu Asn Ser Pro Gln Tyr Thr Ala Ile Lys Ser Ser Tyr Asp Ala
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Leu Val Gln Gln Asp Leu Val Ala Gln Gln Gln Ala Gln Ala Leu
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Gln Gln Ala Ala Tyr Glu Gln Glu Gln Ala Ala Ile Phe Gln Ala Arg
 115 120 125

Asp Gln Ala Thr Phe Gln Ala Glu Gln Thr Leu Ala Gln Glu Ser Val
 130 135 140

Arg Gln Ser Glu Gly Val Gly Leu Pro Val Ile Asp Pro Met Glu Ser
 145 150 155 160

Tyr Phe Arg Glu Tyr Ala Phe Tyr Glu Gly Val Glu Met Phe Gly Thr
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Trp Gly Thr His Val Asp Ala Gly Val Ser Gln Phe Ser Thr Ser Asp
 180 185 190

Gly Arg Ala Ile Arg Ala Leu Val Asp Glu His Leu Ala Thr Tyr Glu
 195 200 205

Pro Val Glu Gln Arg Gly Ser Thr Gln Ala Phe Phe Ala Ser Val Asn
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Ala Ala Phe Ala Glu Val Ala Pro His Ala Ala Pro Met Phe Ser Ala
 225 230 235 240

Ile Ala Arg Glu Gly Glu Gly Ser Lys Gly Tyr Gln Ala Leu Arg His

[illegible]

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Leu Gly Asn Asn Ile Ala Leu Thr Arg Ala Arg Val Ala Glu Glu Leu
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Gly Val Glu Glu Leu Ile Ala Leu Ser Ala Gln Tyr Ala Asp Asp Pro
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Asp Phe Met Pro Ala Phe Ala Gly Glu Asp Glu Leu Met Ala Ile Lys
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Gln Asp Tyr Trp Ala Met Leu Arg Gly Glu Glu Thr Asp Leu Leu Asn
 645 650 655

Pro Gly Val Asn Arg Asp Asp Tyr Met Ala Ala Ile Arg Asp Gly Asp
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His Glu Gln Ile Ala Ala Met Thr Ser Ala Met Asn Ala Val Thr Val
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Glu Asp Arg Val Arg Gln His Ala Ala Leu Val Leu Asp Asp Tyr Val
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Gly Thr Val Glu Pro Asp Pro Val Thr Gly Leu Arg Phe Asn Pro Val
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Thr Val Ala Gln His Met Pro Ser Ala Lys Ser Leu Trp Ser Asn His
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Asp Asp Ile Ile Ala Ala Leu Arg Ala Thr Ser Ile Thr Gly Asp Glu
 740 745 750

Leu Arg Gly Asp Glu Phe Tyr Asn Asp Val Ile Asn Gln Gln Leu Leu
 755 760 765

Lys Phe Asn Pro Glu Thr Ala Gln Lys Met Val Asn Asn Pro Asp Leu
 770 775 780

Asp Pro Gln Leu Ala Arg Phe Gly Thr Val Ile Ala Glu Thr Ile Ser
 785 790 795 800

Arg Asn Gly Ala Asp Val Val Asp Ile Ala Val Asp Asp Asn Gly Val
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Val Arg Trp Thr Ala Gln Arg Arg Val Gly Ala Lys Asp Ser Arg Ala
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Val Asp Ser Lys Gly Gln Val Arg Gly Glu Arg Thr Arg His Val Gln
 835 840 845

Gly Glu Ile Gly Gln Ile Phe Thr Arg Gly Glu His Gly Glu Ile Val
 850 855 860

Thr Lys Phe Asn Gly Gly Glu Asn Tyr Met Phe Ala Pro Gly Tyr Thr
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Ala Ser Val Val Pro Gln Lys Pro Gly Glu Thr Lys Ser Leu Glu Glu
 885 890 895

Arg Thr Lys Leu Lys Gly Tyr Glu Gln Val Met Ser Glu Ala Leu Val
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 Tyr Arg Val Arg Glu Asp Leu Met Phe Thr Glu Arg Ser Arg Val Gly
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 Ala Thr Thr Ser Ile Asn Ser Ala Tyr Lys Arg Leu Tyr Asp Asn Arg
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 Phe Pro Val Asp Phe Phe Glu Arg Ser Ala Glu Gly Leu Ser Asp
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 Glu Trp Arg Ala Ala Leu Leu Glu Thr Ala Ser Leu Arg Val Arg Tyr
 965 970 975
 Asp Asn Ser Ile Arg Asp Gly Ala Asn Val Met Glu Asp Ile Arg Ala
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 Gln Gln Arg Gly Phe Asp Ala Arg Asn Asp Asn Ser Arg Asp Ala Leu
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 Lys Gly Phe Phe Asp Pro Met Met Thr Gly Met Ala Ala Asn Gln Gly
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 Lys Gly Val Thr Ala Leu Val Val Asp Pro Ala Met Ser Asp Ala Asp
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 Pro Asp Leu Glu Val Val Met Ser Pro Phe Ser Ala Ile Ser Arg Phe
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 Phe Arg Asn Asn Asp Gly Ser Thr Arg Val Gln Pro Gly Ala Ser Gly

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Val Tyr Asp Glu Glu Ala Val Arg Glu Gly Gln Gly Arg Lys Ala Ser 1250	1255	1260
Ser Gln Leu Ala Trp Val Leu Gln Ala Gln Glu Cys His Glu Ile Met 1265	1270	1275 1280
Glu His Phe Tyr Gly Asn Asn Val Ser Ala Leu Ala Asn Phe Gln Glu 1285	1290	1295
Tyr Leu Arg Val Thr Gly Leu Asp Val Thr Pro Tyr Gly Glu Leu Arg 1300	1305	1310
Glu Gly Phe Ser Glu Ser Asn Glu Gln Arg Asn Ile Ile Glu Met Pro 1315	1320	1325
Ser Ile Tyr Asp Glu Asn Gly Glu Leu Asn Asn Arg Val Asn Arg Ala 1330	1335	1340
Gln Val Arg Glu Ala Phe Val Glu Gln Ile Ser Arg Ala Gly Gly Val 1345	1350	1355 1360
Met Glu Ile Pro Phe Gln Leu Gln Leu Arg Asn Gly Ala Gln Leu Glu 1365	1370	1375
Glu Ser Pro Asn Asn Pro Asp Met Tyr Gln Leu Pro Leu Leu Ser Pro 1380	1385	1390
His Leu Arg Ser Asp Glu Asp Leu Ala Asp Gly Ser Thr Ser Arg His 1395	1400	1405
Glu Tyr Thr Thr Arg Tyr Met Ala Ile Phe Asp Thr Cys Tyr Lys Leu 1410	1415	1420
Ala Glu Glu Gln Ala Lys Ile Asp Ala Leu Arg Gln Glu Glu Ala Gln 1425	1430	1435 1440
His Gly Thr Leu Pro Arg Ala Ala Glu Lys Arg Leu Ser Glu Ser Gln 1445	1450	1455
Lys Phe Val Asp Gln Ala Gln Lys Lys Val Gln Ala Ser Phe Asp Gly 1460	1465	1470
Ile Ala Asn Asp Ile Val Ala Ser Arg Ile Glu Thr Lys Asn Asn Val 1475	1480	1485
Phe Lys Asp Gly Phe Met Ser Ala Arg Gln Ser His Ser Ala Thr Ala 1490	1495	1500
Val Trp Thr Gly Asp Pro Arg Leu Ser Val Asp Glu Val Ala Met Asn 1505	1510	1515 1520
Ser Ser Met Ala Arg Glu Leu Gly Val Leu Asp Asn Gly Tyr Ala Met 1525	1530	1535
Val Trp Arg Asp Pro Val Ile Arg Asp Gly Gly Val Arg Tyr Leu Arg 1540	1545	1550

Val Val Ile Asn Asp Asp Leu His Gly Val Ala Val Asn Pro Val Ser
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Val Lys Ser Phe Asp Gly Asp Phe Asp Gly Asp Ser Val Gly Leu Val
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Gly Asn Leu Pro Lys Lys Ala His Glu Glu Ala Leu Ser Arg Leu Thr
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Val Glu Ala Asn Met Leu Asp Leu Gly Asp Gly Lys Arg Met Glu Asp
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Gly Thr Met Phe Tyr Gly Leu Thr Leu His Asp Ser Leu Asp Val Gln
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Val Ala Gln His His Asp Pro Ala Met Ala Glu Asn Met Lys Val Ile
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Val Ser Glu Leu Asn Arg Tyr Gln Arg Glu Tyr Glu Ala Gly Glu Ile
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Val Val Thr Val Ala
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Gly Asn Glu Lys Asn Lys Ile Arg Glu Glu Arg Val Ala Arg Arg Ala
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Gln Ala Val Val Glu Ala Glu Ile Ser Leu Ala Ala Gln Ala Ser Glu
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Gln Val Arg Glu Gln Ala Glu Ala Pro Asp Val Asn Glu Gln Val Glu
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Glu Val Ser Val Glu Val Ser Ser Val Gln Ser Leu Thr Gln Pro Lys
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 Thr Leu Gly Gln Leu His Asp Pro Arg Lys Asn Val Met Ser Ser Ser
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 Glu Ser Glu Glu Pro Glu Thr Leu Arg Asp Val Leu Pro Arg Arg Lys
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ctt cac cca tct gag ata aca ccg agt tat gag gtt gct gat ggt gaa 499
 Leu His Pro Ser Glu Ile Thr Pro Ser Tyr Glu Val Ala Asp Gly Glu
 120 125 130

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 Gln Arg Ser Ile Phe Gly Glu Ser Ala Pro Ser Asp Phe Asp Asp Leu
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 Pro Ile Asp Val Ala Lys Lys Glu Arg Lys Ala Ala Glu Lys Lys Tyr
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 Ala Lys Pro Pro Lys Ser Asp Asn Pro Tyr Leu Ala Arg Asp Ala Lys
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 Asp Ala Ala Ala Arg Lys Arg Lys Ile Asn Ala Ala His Asp Asn Phe
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Met Thr Ala Thr Asp Val Ser Glu Ser Gly Leu Ala Ser Ala Lys Lys	
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Leu Leu Pro Asp Phe Asp Thr Arg Gly Arg Ser Ala Ser Arg Val Arg
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 Gln Val Trp Ala Met Asp Gln Ala Glu Lys Val Met Gln Arg Asp His
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 Pro Ala Ile Leu Asp Lys Phe Val Arg Lys His Gly Gln Thr Phe Gly
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 cag gat gcg gac gct ttt gtt aaa tcc ata act atg gaa aaa gac acg 2035
 Gln Asp Ala Asp Ala Phe Val Lys Ser Ile Thr Met Glu Lys Asp Thr
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 Ser Ser Glu Tyr Thr Asp Ala Met Val Arg Pro Gln Glu Asn Arg Gly
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 Ser Gly Arg Glu Leu Ala Ala Arg Arg Val Gln Ala Ala Gln Ile
 665 670 675
 aat cag gca gca cag ctg gat atg aat gtt cat gat ttc cgt gaa tcg 2179
 Asn Gln Ala Ala Gln Leu Asp Met Asn Val His Asp Phe Arg Glu Ser
 680 685 690
 aat ctg cca gag gaa cga ccc gcg aat cct tat gaa gcg tat gtt cgt 2227
 Asn Leu Pro Glu Glu Arg Pro Ala Asn Pro Tyr Glu Ala Tyr Val Arg
 695 700 705
 gag act gaa gcg aaa acc aat gat ccg cag tac ggt tat taatagaaaa 2276
 Glu Thr Glu Ala Lys Thr Asn Asp Pro Gln Tyr Gly Tyr
 710 715 720
 tgatagaaag aag 2289

<210> 14

<211> 722

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 14

Val Val Thr Val Ala Gly Asn Glu Lys Asn Lys Ile Arg Glu Glu Arg
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 Val Ala Arg Arg Ala Gln Ala Val Val Glu Ala Glu Ile Ser Leu Ala
 20 25 30
 Ala Gln Ala Ser Glu Gln Val Arg Glu Gln Ala Glu Ala Pro Asp Val
 35 40 45

Asn Glu Gln Val Glu Glu Val Ser Val Glu Val Ser Ser Val Gln Ser
 50 55 60
 Leu Thr Gln Pro Lys Thr Leu Gly Gln Leu His Asp Pro Arg Lys Asn
 65 70 75 80
 Val Met Ser Ser Ser Asp Leu Ala Ser Ile Ile Gly Val Glu Gln Gln
 85 90 95
 Pro Val Ala Tyr Glu Glu Ser Glu Glu Pro Glu Thr Leu Arg Asp Val
 100 105 110
 Leu Pro Arg Arg Lys Leu His Pro Ser Glu Ile Thr Pro Ser Tyr Glu
 115 120 125
 Val Ala Asp Gly Glu Gln Arg Ser Ile Phe Gly Glu Ser Ala Pro Ser
 130 135 140
 Asp Phe Asp Asp Leu Ser Asp Val Glu Glu Phe Asp Thr Ser His Trp
 145 150 155 160
 Val Arg Ala Gly Gln Asp Asp Arg Ser Asp Asp Asp Arg Leu Ala Asp
 165 170 175
 Glu Ala Gly Val Pro Arg Ser Gly Ala Gln Asp Val Ala Asp Asn Glu
 180 185 190
 Ala Asn Leu Ser Gly Val Asp Glu Gln Leu His Met Arg Glu Val His
 195 200 205
 Ala Gln Ser Phe Asp Pro Ile Asp Val Ala Lys Lys Glu Arg Lys Ala
 210 215 220
 Ala Glu Lys Lys Tyr Ala Lys Pro Pro Lys Ser Asp Asn Pro Tyr Leu
 225 230 235 240
 Ala Arg Asp Ala Lys Asp Ala Ala Ala Arg Lys Arg Lys Ile Asn Ala
 245 250 255
 Ala His Asp Asn Phe Ala Gln Glu Met Ala Gln Ala Ala Met Gly Pro
 260 265 270
 Leu Arg Lys Gly Val Asn Thr Gln Thr Val Met Ala Ala Cys Thr Thr
 275 280 285
 Ala Ala Val Met Trp Cys Met Ser Pro Arg Met Thr Gly Val Asn Val
 290 295 300
 Asp Met Lys Arg Lys Phe Asn Lys Asp Leu Glu Gln Ala Lys Asp Thr
 305 310 315 320
 Lys Leu Ser Lys Tyr Val Ser Lys Asp Phe Trp Lys Ser Lys Leu Thr
 325 330 335
 Arg Asp Lys Thr Glu Lys Glu Ala Lys Ser Leu Ser Asp Ala Phe Met
 340 345 350
 Gln Gln Lys Thr Ala Ile Ile Ser Asn Arg Glu Arg Ile Pro Met Ser
 355 360 365
 Val Ala Ser Ala Ala Gln Thr Val Val Arg Leu Ser Asp Gln Ala Tyr

370				375				380							
Glu	Ala	Met	Arg	Glu	Val	Asp	Thr	Asp	Gly	Gln	Ala	Ile	Val	Asp	Ala
385					390					395					400
Lys	Asp	Val	Ser	Ala	Gln	Val	Ala	Glu	Asp	Ile	Asp	Met	Val	Val	Lys
				405					410					415	
Gln	Gly	Glu	Glu	His	Gly	Leu	Lys	Ser	Lys	Asp	Ile	Tyr	Gly	Ala	Ala
		420						425					430		
Arg	Asp	Ile	Val	Gly	Arg	Arg	Met	Glu	Arg	Asp	Pro	Gly	Tyr	Ala	Ala
		435					440						445		
Arg	Phe	Asn	Glu	Thr	Ala	Phe	Gly	Thr	Val	Arg	Leu	Gly	Glu	Gln	Arg
	450					455					460				
Arg	Gly	Met	Val	Ile	Ser	Lys	Thr	Pro	Thr	Trp	Gln	Phe	Pro	Asp	Gly
465					470					475					480
Ala	Gly	Leu	Ser	Lys	Asn	Ala	Gly	Trp	Phe	Ser	Val	Arg	Glu	Pro	Met
				485						490				495	
Gly	Asn	Ala	Gln	Asn	Phe	Ala	Asp	Asn	Leu	Ala	Ala	Thr	Leu	Ala	Thr
			500						505				510		
Glu	Met	Arg	Val	Ala	Gly	Glu	Gln	Tyr	Gly	Ser	Asp	Gly	Val	Arg	Asp
		515					520						525		
Val	Val	Ala	Gly	Phe	Met	Thr	Ala	Thr	Asp	Val	Ser	Glu	Ser	Gly	Leu
	530					535					540				
Ala	Ser	Ala	Lys	Lys	Leu	Leu	Pro	Asp	Phe	Asp	Thr	Arg	Gly	Arg	Ser
545					550					555					560
Ala	Ser	Arg	Val	Arg	Gln	Ile	Ala	Met	Ala	Gln	Arg	Thr	Gln	Ala	Ala
				565					570					575	
Ile	Lys	Val	Leu	Gln	Asp	Asp	Gly	Asn	Gln	Thr	Ala	Met	Thr	Thr	Glu
		580						585					590		
Gln	Val	Lys	Glu	Val	Gln	Val	Trp	Ala	Met	Asp	Gln	Ala	Glu	Lys	Val
		595					600					605			
Met	Gln	Arg	Asp	His	Pro	Ala	Ile	Leu	Asp	Lys	Phe	Val	Arg	Lys	His
	610				615						620				
Gly	Gln	Thr	Phe	Gly	Gln	Asp	Ala	Asp	Ala	Phe	Val	Lys	Ser	Ile	Thr
625					630					635					640
Met	Glu	Lys	Asp	Thr	Ser	Ser	Glu	Tyr	Thr	Asp	Ala	Met	Val	Arg	Pro
			645						650				655		
Gln	Glu	Asn	Arg	Gly	Ser	Gly	Arg	Glu	Leu	Ala	Ala	Arg	Arg	Arg	Val
		660					665						670		
Gln	Ala	Ala	Gln	Ile	Asn	Gln	Ala	Ala	Gln	Leu	Asp	Met	Asn	Val	His
		675					680						685		
Asp	Phe	Arg	Glu	Ser	Asn	Leu	Pro	Glu	Glu	Arg	Pro	Ala	Asn	Pro	Tyr
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Glu Ala Tyr Val Arg Glu Thr Glu Ala Lys Thr Asn Asp Pro Gln Tyr
705 710 715 720

Gly Tyr

<210> 15
<211> 2046
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2023)
<223> FRXA01539

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taagacgttg gggcagctgc atgacccaag gaaaaatgtc atg agt agc agc gac 115
Met Ser Ser Ser Asp
1 5

tgt gct tct att att ggt gta gag caa cag cct gtt gct tat ggt gag 163
Leu Ala Ser Ile Ile Gly Val Glu Gln Gln Pro Val Ala Tyr Gly Glu
10 15 20

tct gag gaa cca gaa aca ctg cgt gat gtg ttg cct cgg cga aag ctt 211
Ser Glu Glu Pro Glu Thr Leu Arg Asp Val Leu Pro Arg Arg Lys Leu
25 30 35

cac cca tct gag ata aca ccg agt tat gag gtt gct gat ggt gaa cag 259
His Pro Ser Glu Ile Thr Pro Ser Tyr Glu Val Ala Asp Gly Glu Gln
40 45 50

cgc agc att ttt ggt gaa tca gct ccg tct gat ttt gat gac ctc agt 307
Arg Ser Ile Phe Gly Glu Ser Ala Pro Ser Asp Phe Asp Asp Leu Ser
55 60 65

gat gtc gaa gaa ttt gat acc agt cat tgg gtg cgt gct gga caa gat 355
Asp Val Glu Glu Phe Asp Thr Ser His Trp Val Arg Ala Gly Gln Asp
70 75 80 85

gat cgt agt gat gat gat cga ctc gct gat gag gct ggt gta ccg cct 403
Asp Arg Ser Asp Asp Asp Arg Leu Ala Asp Glu Ala Gly Val Pro Pro
90 95 100

agt ggc gca caa gat gta gct gat aat gag gct aat ctt tct ggt gtg 451
Ser Gly Ala Gln Asp Val Ala Asp Asn Glu Ala Asn Leu Ser Gly Val
105 110 115

gat gag cag ctg cac atg cgt gaa gtc cat gca cag agt ttt gac cct 499
Asp Glu Gln Leu His Met Arg Glu Val His Ala Gln Ser Phe Asp Pro
120 125 130

att gac gtt gcc aaa aag gaa cgc aaa gca cgc gaa aag aag tat gcc 547
Ile Asp Val Ala Lys Lys Glu Arg Lys Ala Ala Glu Lys Lys Tyr Ala
135 140 145

aag cca cca aaa agt gat aat ccg tac cta gca cgg gat gcc aaa gat	595
Lys Pro Pro Lys Ser Asp Asn Pro Tyr Leu Ala Arg Asp Ala Lys Asp	
150 155 160 165	
gca gct gct cgt aag cgg aag atc aat gca gct cat gat aat ttt gcc	643
Ala Ala Ala Arg Lys Arg Lys Ile Asn Ala Ala His Asp Asn Phe Ala	
170 175 180	
caa gag atg gca cag gct gcg atg gga cca ctg cgc aaa ggg gtc aac	691
Gln Glu Met Ala Gln Ala Ala Met Gly Pro Leu Arg Lys Gly Val Asn	
185 190 195	
act caa acg gtg atg gcc gcg tgt acg act gct gcg gtg atg tgg tgc	739
Thr Gln Thr Val Met Ala Ala Cys Thr Thr Ala Ala Val Met Trp Cys	
200 205 210	
atg agc cca cgt atg acc ggt gtg aac gtg gat atg aag cgc aag ttt	787
Met Ser Pro Arg Met Thr Gly Val Asn Val Asp Met Lys Arg Lys Phe	
215 220 225	
aac aag gat ctg gaa cag gct aaa gac act aag ttg tcg aag tat gtg	835
Asn Lys Asp Leu Glu Gln Ala Lys Asp Thr Lys Leu Ser Lys Tyr Val	
230 235 240 245	
tcc aaa gat ttt tgg aag tca aag ctg acg cgc gat aag acg gag aag	883
Ser Lys Asp Phe Trp Lys Ser Lys Leu Thr Arg Asp Lys Thr Lys	
250 255 260	
gaa gcg aag tcg ctc tct gat gcg ttc atg cag cag aaa aca gcg atc	931
Glu Ala Lys Ser Leu Ser Asp Ala Phe Met Gln Gln Lys Thr Ala Ile	
265 270 275	
atc agc aac cgt gaa cga atc ccc atg agt gtt gct tct gcc gcg cag	979
Ile Ser Asn Arg Glu Arg Ile Pro Met Ser Val Ala Ser Ala Ala Gln	
280 285 290	
acc gtg gtt cgg ttg tct gat caa gcg tat gag gcg atg cgt gaa gta	1027
Thr Val Val Arg Leu Ser Asp Gln Ala Tyr Glu Ala Met Arg Glu Val	
295 300 305	
gat acg gat ggt caa gcg ata gtg gat gcg aag gat gtc tct gca cag	1075
Asp Thr Asp Gly Gln Ala Ile Val Asp Ala Lys Asp Val Ser Ala Gln	
310 315 320 325	
gtg gca gaa gat att gac atg gtg gtc aag cag ggt gaa gag cat gcc	1123
Val Ala Glu Asp Ile Asp Met Val Val Lys Gln Gly Glu Glu His Gly	
330 335 340	
ctg aag tcg aag gat att tat ggc gct gcc cgc gat att gtg ggt cgt	1171
Leu Lys Ser Lys Asp Ile Tyr Gly Ala Ala Arg Asp Ile Val Gly Arg	
345 350 355	
gcg atg gag cgc gat cca ggc tat gct gcc cgg ttt aat gag acg gct	1219
Arg Met Glu Arg Asp Pro Gly Tyr Ala Ala Arg Phe Asn Glu Thr Ala	
360 365 370	
ttt gcc acc gtg cgc ctg ggt gaa caa cga cgt gcc atg gtg att tca	1267
Phe Gly Thr Val Arg Leu Gly Glu Gln Arg Arg Gly Met Val Ile Ser	
375 380 385	
aag acc ccg aca tgg caa ttc cct gat ggt gca ggt ttg agt aaa aac	1315

Lys Thr Pro Thr Trp Gln Phe Pro Asp Gly Ala Gly Leu Ser Lys Asn	
390 395 400	
gcc ggc tgg ttt agt gtt cgt gag ccg atg ggt aat gcg cag aac ttc	1363
Ala Gly Trp Phe Ser Val Arg Glu Pro Met Gly Asn Ala Gln Asn Phe	
410 415 420	
gct gac aac ctg gct gcg act ttg gcg aca gaa atg cgg gta gct ggt	1411
Ala Asp Asn Leu Ala Ala Thr Leu Ala Thr Glu Met Arg Val Ala Gly	
425 430 435	
gag cag tac ggt tcc gat gcg gtt cgt gat gta gtt gcc ggc ttc atg	1459
Glu Gln Tyr Gly Ser Asp Gly Val Arg Asp Val Ala Gly Phe Met	
440 445 450	
aca gcg act gat gtc tca gaa agt gcg ctc gcc tct gcg aag aaa ctg	1507
Thr Ala Thr Asp Val Ser Glu Ser Gly Leu Ala Ser Ala Lys Lys Leu	
455 460 465	
tta cct gac ttt gat aca cgt ggt cgc agt gct tct cgg gtg cgc cag	1555
Leu Pro Asp Phe Asp Thr Arg Gly Arg Ser Ala Ser Arg Val Arg Gln	
470 475 480 485	
att gct atg gca cag cgc aca cag gca gcg atc aag gtg ttg cag gat	1603
Ile Ala Met Ala Gln Arg Thr Gln Ala Ala Ile Lys Val Leu Gln Asp	
490 495 500	
gat ggt aat cag acc gcg atg acg act gag cag gtc aag gag gtt cag	1651
Asp Gly Asn Gln Thr Ala Met Thr Thr Glu Gln Val Lys Glu Val Gln	
505 510 515	
gta tgg gcg atg gat cag gct gag aag gtg atg cag cgt gat cat cca	1699
Val Trp Ala Ala Met Asp Gln Ala Glu Lys Val Met Gln Arg Asp His Pro	
520 525 530	
gcg att ctg gat aag ttt gtg cgc aaa cat ggg cag aca ttt ggg cag	1747
Ala Ile Leu Asp Lys Phe Val Arg Lys His Gly Gln Thr Phe Gly Gln	
535 540 545	
gat gcg gac gct ttt gtt aaa tcc ata act atg gaa aaa gac acg agc	1795
Asp Ala Asp Ala Phe Val Lys Ser Ile Thr Met Glu Lys Asp Thr Ser	
550 555 560 565	
agc gag tac act gat gct atg gtt cga cct caa gaa aat cgt gga tca	1843
Ser Glu Tyr Thr Asp Ala Met Val Arg Pro Gln Glu Asn Arg Gly Ser	
570 575 580	
ggt cga gaa ctg gca gct cgt cgt gta caa gca gcg caa atc aat	1891
Gly Arg Glu Leu Ala Ala Arg Arg Val Gln Ala Ala Gln Ile Asn	
585 590 595	
cag gca gca cag ctg gat atg aat gtt cat gat ttc cgt gaa tcg aat	1939
Gln Ala Ala Gln Leu Asp Met Asn Val His Asp Phe Arg Glu Ser Asn	
600 605 610	
ctg cca gag gaa cga ccc gcg aat cct tat gaa gcg tat gtt cgt gag	1987
Leu Pro Glu Glu Arg Pro Ala Asn Pro Tyr Glu Ala Tyr Val Arg Glu	
615 620 625	
act gaa gcg aaa acc aat gat ccg cag tac ggt tat taatagaaaa	2033
Thr Glu Ala Lys Thr Asn Asp Pro Gln Tyr Gly Tyr	

630

635

640

tgatagaaag aag

2046

<210> 16

<211> 641

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 16

Met Ser Ser Ser Asp Leu Ala Ser Ile Ile Gly Val Glu Gln Gln Pro
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Val Ala Tyr Gly Glu Ser Glu Glu Pro Glu Thr Leu Arg Asp Val Leu
 20 25 30

Pro Arg Arg Lys Leu His Pro Ser Glu Ile Thr Pro Ser Tyr Glu Val
 35 40 45

Ala Asp Gly Glu Gln Arg Ser Ile Phe Gly Glu Ser Ala Pro Ser Asp
 50 55 60

Phe Asp Asp Leu Ser Asp Val Glu Glu Phe Asp Thr Ser His Trp Val
 65 70 75 80

Arg Ala Gly Gln Asp Asp Arg Ser Asp Asp Arg Leu Ala Asp Glu
 85 90 95

Ala Gly Val Pro Pro Ser Gly Ala Gln Asp Val Ala Asp Asn Glu Ala
 100 105 110

Asn Leu Ser Gly Val Asp Glu Gln Leu His Met Arg Glu Val His Ala
 115 120 125

Gln Ser Phe Asp Pro Ile Asp Val Ala Lys Lys Glu Arg Lys Ala Ala
 130 135 140

Glu Lys Lys Tyr Ala Lys Pro Pro Lys Ser Asp Asn Pro Tyr Leu Ala
 145 150 155 160

Arg Asp Ala Lys Asp Ala Ala Ala Arg Lys Arg Lys Ile Asn Ala Ala
 165 170 175

His Asp Asn Phe Ala Gln Glu Met Ala Gln Ala Ala Met Gly Pro Leu
 180 185 190

Arg Lys Gly Val Asn Thr Gln Thr Val Met Ala Ala Cys Thr Thr Ala
 195 200 205

Ala Val Met Trp Cys Met Ser Pro Arg Met Thr Gly Val Asn Val Asp
 210 215 220

Met Lys Arg Lys Phe Asn Lys Asp Leu Glu Gln Ala Lys Asp Thr Lys
 225 230 235 240

Leu Ser Lys Tyr Val Ser Lys Asp Phe Trp Lys Ser Lys Leu Thr Arg
 245 250 255

Asp Lys Thr Glu Lys Glu Ala Lys Ser Leu Ser Asp Ala Phe Met Gln
 260 265 270

Gln Lys Thr Ala Ile Ile Ser Asn Arg Glu Arg Ile Pro Met Ser Val
 275 280 285
 Ala Ser Ala Ala Gln Thr Val Val Arg Leu Ser Asp Gln Ala Tyr Glu
 290 295 300
 Ala Met Arg Glu Val Asp Thr Asp Gly Gln Ala Ile Val Asp Ala Lys
 305 310 315 320
 Asp Val Ser Ala Gln Val Ala Glu Asp Ile Asp Met Val Val Lys Gln
 325 330 335
 Gly Glu Glu His Gly Leu Lys Ser Lys Asp Ile Tyr Gly Ala Ala Arg
 340 345 350
 Asp Ile Val Gly Arg Arg Met Glu Arg Asp Pro Gly Tyr Ala Ala Arg
 355 360 365
 Phe Asn Glu Thr Ala Phe Gly Thr Val Arg Leu Gly Glu Gln Arg Arg
 370 375 380
 Gly Met Val Ile Ser Lys Thr Pro Thr Trp Gln Phe Pro Asp Gly Ala
 385 390 395 400
 Gly Leu Ser Lys Asn Ala Gly Trp Phe Ser Val Arg Glu Pro Met Gly
 405 410 415
 Asn Ala Gln Asn Phe Ala Asp Asn Leu Ala Ala Thr Leu Ala Thr Glu
 420 425 430
 Met Arg Val Ala Gly Glu Gln Tyr Gly Ser Asp Gly Val Arg Asp Val
 435 440 445
 Val Ala Gly Phe Met Thr Ala Thr Asp Val Ser Glu Ser Gly Leu Ala
 450 455 460
 Ser Ala Lys Lys Leu Leu Pro Asp Phe Asp Thr Arg Gly Arg Ser Ala
 465 470 475 480
 Ser Arg Val Arg Gln Ile Ala Met Ala Gln Arg Thr Gln Ala Ala Ile
 485 490 495
 Lys Val Leu Gln Asp Asp Gly Asn Gln Thr Ala Met Thr Thr Glu Gln
 500 505 510
 Val Lys Glu Val Gln Val Trp Ala Met Asp Gln Ala Glu Lys Val Met
 515 520 525
 Gln Arg Asp His Pro Ala Ile Leu Asp Lys Phe Val Arg Lys His Gly
 530 535 540
 Gln Thr Phe Gly Gln Asp Ala Asp Ala Phe Val Lys Ser Ile Thr Met
 545 550 555 560
 Glu Lys Asp Thr Ser Ser Glu Tyr Thr Asp Ala Met Val Arg Pro Gln
 565 570 575
 Glu Asn Arg Gly Ser Gly Arg Glu Leu Ala Ala Arg Arg Arg Val Gln
 580 585 590

Ala Ala Gln Ile Asn Gln Ala Ala Gln Leu Asp Met Asn Val His Asp
 595 600
 Phe Arg Glu Ser Asn Leu Pro Glu Glu Arg Pro Ala Asn Pro Tyr Glu
 610 615 620
 Ala Tyr Val Arg Glu Thr Glu Ala Lys Thr Asn Asp Pro Gln Tyr Gly
 625 630 635 640

Tyr

<210> 17
 <211> 1095
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1072)
 <223> RXN01422

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 agttccccaa aaggtgcgag cgggaaaagg agaagcaaac atg gct cag cga aaa 115
 Met Ala Gln Arg Lys
 1 5
 ctg gcc tct gtg atc ggt gca gca ttg gca gca tct gct gta ctg gtt 163
 Leu Ala Ser Val Ile Gly Ala Ala Leu Ala Ala Ser Ala Val Leu Val
 10 15 20
 gga tta atg aca ccc gca aca gca caa agt agt ggc agc tca tca aca 211
 Gly Leu Met Thr Pro Ala Thr Ala Gln Ser Ser Gly Ser Ser Ser Thr
 25 30 35
 gac atc act cga gca ctc acc tca agt ggt ggt gtg gct gat agc cgt 259
 Asp Ile Thr Arg Ala Leu Thr Ser Ser Gly Gly Val Ala Asp Ser Arg
 40 45 50
 gct cct gaa ggt ggc gca aag gtc gtt gtt ttc ggt gac tcc cac acc 307
 Ala Pro Glu Gly Gly Ala Lys Val Val Val Phe Gly Asp Ser His Thr
 55 60 65
 tct ggc acc aat gct cca ttc cgt acc gat gag cgt ggc tgc ctc aag 355
 Ser Gly Thr Asn Ala Pro Phe Arg Thr Asp Glu Arg Gly Cys Leu Lys
 70 75 80 85
 ggt gca aac aac tgg gca gat cag ctg cag tct cag ctg gga ctt ggc 403
 Gly Ala Asn Asn Trp Ala Asp Gln Leu Gln Ser Gln Leu Gly Leu Gly
 90 95 100
 gcg gga gac ctc att gat gtc tcc tgc tcc ggt gca tgc atc aac tct 451
 Ala Gly Asp Leu Ile Asp Val Ser Cys Ser Gly Ala Ser Ile Asn Ser
 105 110 115
 gat gga ttc cac ttc tct gat gaa gtc cgc cat gct gaa gct cgt ggc 499
 Asp Gly Phe His Phe Ser Asp Glu Val Arg His Ala Glu Ala Arg Gly
 120 125 130

gca atc ggc cca aac acc acc gat att ttt gtt cag ttg ggc aag aat 547
 Ala Ile Gly Pro Asn Thr Asp Ile Phe Val Gln Leu Gly Lys Asn
 135 140 145

gat cag tgg ggc ctt tcc aat gtg aac ctt ctg cag tct gtt cag acc 595
 Asp Gln Trp Gly Leu Ser Asn Val Asn Leu Leu Gln Ser Val Gln Thr
 150 155 160 165

tgc ttg act gat gtg ttc gct ggt tgt ggc gat gct gcg gtt gct gct 643
 Cys Leu Thr Asp Val Phe Ala Gly Cys Gly Asp Ala Ala Val Ala Ala
 170 175 180

ggc aag atg cag gat cca aat gca gtt act gct gaa aac tat gca gag 691
 Gly Lys Met Gln Asp Pro Asn Ala Val Thr Ala Glu Asn Tyr Ala Glu
 185 190 195

cgc atg aag cca gtc att gac tac ttg aag tac tac gca cca aac gca 739
 Arg Met Lys Pro Val Ile Asp Tyr Leu Lys Tyr Tyr Ala Pro Asn Ala
 200 205 210

gag atc acc ttg gtt ggt tac cag gaa tac acc gct cgc agc gga agt 787
 Glu Ile Thr Leu Val Gly Tyr Gln Glu Tyr Thr Ala Arg Ser Gly Ser
 215 220 225

cag gta tgt gtt cgc ctt ggt gga acc cca ctg gtg aaa aat gat gca 835
 Gln Val Cys Val Arg Leu Gly Gly Thr Pro Leu Val Lys Asn Asp Ala
 230 235 240 245

cct gcg ctg gtt tgc ttc atg aac aag ttg gac atg gcg att gat ggt 883
 Pro Ala Leu Val Ser Phe Met Asn Lys Leu Asp Met Ala Ile Asp Gly
 250 255 260

gct gct gga atc ctc ggc gtc agc cac gtt gat ctg cgt agc gcg act 931
 Ala Ala Gly Ile Leu Gly Val Ser His Val Asp Leu Arg Ser Ala Thr
 265 270 275

gaa ggg cac gac agc tgc tcc aac gat cct tgg gtc aac ggt gtc ttt 979
 Glu Gly His Asp Ser Cys Ser Asn Asp Pro Trp Val Asn Gly Val Phe
 280 285 290

gat gca cgt gca gaa atc gtc ggc ggt ccg tgg cac cca tct gtt aag 1027
 Asp Ala Arg Ala Glu Ile Val Gly Gly Pro Trp His Pro Ser Val Lys
 295 300 305

gga gac tgc gtt act gca ggg atc ctg cga gat cga gta aac gcc 1072
 Gly Asp Ser Val Thr Ala Gly Ile Leu Arg Asp Arg Val Asn Ala
 310 315 320

taaagatgac gtcgaaaagc att 1095

<210> 18
 <211> 324
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 18
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Ser Ala Val Leu Val Gly Leu Met Thr Pro Ala Thr Ala Gln Ser Ser
 20 25 30
 Gly Ser Ser Ser Thr Asp Ile Thr Arg Ala Leu Thr Ser Ser Gly Gly
 35 40 45
 Val Ala Asp Ser Arg Ala Pro Glu Gly Gly Ala Lys Val Val Val Phe
 50 55 60
 Gly Asp Ser His Thr Ser Gly Thr Asn Ala Pro Phe Arg Thr Asp Glu
 65 70 75 80
 Arg Gly Cys Leu Lys Gly Ala Asn Asn Trp Ala Asp Gln Leu Gln Ser
 85 90 95
 Gln Leu Gly Leu Gly Ala Gly Asp Leu Ile Asp Val Ser Cys Ser Gly
 100 105 110
 Ala Ser Ile Asn Ser Asp Gly Phe His Phe Ser Asp Glu Val Arg His
 115 120 125
 Ala Glu Ala Arg Gly Ala Ile Gly Pro Asn Thr Thr Asp Ile Phe Val
 130 135 140
 Gln Leu Gly Lys Asn Asp Gln Trp Gly Leu Ser Asn Val Asn Leu Leu
 145 150 155 160
 Gln Ser Val Gln Thr Cys Leu Thr Asp Val Phe Ala Gly Cys Gly Asp
 165 170 175
 Ala Ala Val Ala Ala Gly Lys Met Gln Asp Pro Asn Ala Val Thr Ala
 180 185 190
 Glu Asn Tyr Ala Glu Arg Met Lys Pro Val Ile Asp Tyr Leu Lys Tyr
 195 200 205
 Tyr Ala Pro Asn Ala Glu Ile Thr Leu Val Gly Tyr Gln Glu Tyr Thr
 210 215 220
 Ala Arg Ser Gly Ser Gln Val Cys Val Arg Leu Gly Gly Thr Pro Leu
 225 230 235 240
 Val Lys Asn Asp Ala Pro Ala Leu Val Ser Phe Met Asn Lys Leu Asp
 245 250 255
 Met Ala Ile Asp Gly Ala Ala Gly Ile Leu Gly Val Ser His Val Asp
 260 265 270
 Leu Arg Ser Ala Thr Glu Gly His Asp Ser Cys Ser Asn Asp Pro Trp
 275 280 285
 Val Asn Gly Val Phe Asp Ala Arg Ala Glu Ile Val Gly Gly Pro Trp
 290 295 300
 His Pro Ser Val Lys Gly Asp Ser Val Thr Ala Gly Ile Leu Arg Asp
 305 310 315 320
 Arg Val Asn Ala

<210> 19
 <211> 806
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(783)
 <223> FRXA01422

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 Phe Gly Asp Ser His Thr Ser Gly Thr Asn Ala Pro Phe Arg Thr Asp
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 gag cgt ggc tgc ctc aag ggt gca aac aac tgg gca gat cag ctg cag 96
 Glu Arg Gly Cys Leu Lys Gly Ala Asn Trp Ala Asp Val Leu Gln
 20 25 30
 tct cag ctg gga ctt ggc gcg gga gac ctc att gat gtc tcc tgc tcc 144
 Ser Gln Leu Gly Leu Gly Ala Gly Asp Leu Ile Asp Val Ser Cys Ser
 35 40 45
 ggt gca tgc atc aac tct gat gga ttc cac ttc tct gat gaa gtc cgc 192
 Gly Ala Ser Ile Asn Ser Asp Gly Phe His Phe Ser Asp Glu Val Arg
 50 55 60
 cat gct gaa gct cgt ggc gca atc ggc cca aac acc acc gat att ttt 240
 His Ala Glu Ala Arg Gly Ala Ile Gly Pro Asn Thr Thr Asp Ile Phe
 65 70 75 80
 gtt cag ttg ggc aag aat gat cag tgg ggc ctt tcc aat gtg aac ctt 288
 Val Gln Leu Gly Lys Asn Asp Gln Trp Gly Leu Ser Asn Val Asn Leu
 85 90 95
 ctg cag tct gtt cag acc tgc ttg act gat gtg ttc gct ggt tgt ggc 336
 Leu Gln Ser Val Gln Thr Cys Leu Thr Asp Val Phe Ala Gly Cys Gly
 100 105 110
 gat gct gcg gtt gct gct ggc aag atg cag gat cca aat gca gtt act 384
 Asp Ala Ala Val Ala Ala Gly Lys Met Gln Asp Pro Asn Ala Val Thr
 115 120 125
 gct gaa aac tat gca gag cgc atg aag cca gtc att gac tac ttg aag 432
 Ala Glu Asn Tyr Ala Glu Arg Met Lys Pro Val Ile Asp Tyr Leu Lys
 130 135 140
 tac tac gca cca aac gca gag atc acc ttg gtt ggt tac cag gaa tac 480
 Tyr Tyr Ala Pro Asn Ala Glu Ile Thr Leu Val Gly Tyr Gln Glu Tyr
 145 150 155 160
 acc gct cgc agc gga agt cag gta tgt gtt cgc ctt ggt gga acc cca 528
 Thr Ala Arg Ser Gly Ser Gln Val Cys Val Arg Leu Gly Gly Thr Pro
 165 170 175
 ctg gtg aaa aat gat gca cct gcg ctg gtt tgc ttc atg aac aag ttg 576
 Leu Val Lys Asn Asp Ala Pro Ala Leu Val Ser Phe Met Asn Lys Leu
 180 185 190
 gac atg gcg att gat ggt gct gct gga atc ctc ggc gtc agc cac gtt 624
 Asp Met Ala Ile Asp Gly Ala Ala Gly Ile Leu Gly Val Ser His Val

195	200	205	
gat ctg cgt agc gcg act gaa ggg cac gac agc tgc tcc aac gat cct			672
Asp Leu Arg Ser Ala Thr Glu Gly His Asp Ser Cys Ser Asn Asp Pro			
210	215	220	
tgg gtc aac ggt gtc ttt gat gca cgt gca gaa atc gtc ggc ggt ccg			720
Trp Val Asn Gly Val Phe Asp Ala Arg Ala Glu Ile Val Gly Gly Pro			
225	230	235	240
tgg cac cca tct gtt aag gga gac tcg gtt act gca ggg atc ctg cga			768
Trp His Pro Ser Val Lys Gly Asp Ser Val Thr Ala Gly Ile Leu Arg			
245	250	255	
gat cga gta aac gcc taaagatgac gtcgaaaagc att			806
Asp Arg Val Asn Ala			
260			
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<211> 261			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 20			
Phe Gly Asp Ser His Thr Ser Gly Thr Asn Ala Pro Phe Arg Thr Asp			
1	5	10	15
Glu Arg Gly Cys Leu Lys Gly Ala Asn Asn Trp Ala Asp Gln Leu Gln			
20	25	30	
Ser Gln Leu Gly Leu Gly Ala Gly Asp Leu Ile Asp Val Ser Cys Ser			
35	40	45	
Gly Ala Ser Ile Asn Ser Asp Gly Phe His Phe Ser Asp Glu Val Arg			
50	55	60	
His Ala Glu Ala Arg Gly Ala Ile Gly Pro Asn Thr Thr Asp Ile Phe			
65	70	75	80
Val Gln Leu Gly Lys Asn Asp Gln Trp Gly Leu Ser Asn Val Asn Leu			
85	90	95	
Leu Gln Ser Val Gln Thr Cys Leu Thr Asp Val Phe Ala Gly Cys Gly			
100	105	110	
Asp Ala Ala Val Ala Ala Gly Lys Met Gln Asp Pro Asn Ala Val Thr			
115	120	125	
Ala Glu Asn Tyr Ala Glu Arg Met Lys Pro Val Ile Asp Tyr Leu Lys			
130	135	140	
Tyr Tyr Ala Pro Asn Ala Glu Ile Thr Leu Val Gly Tyr Gln Glu Tyr			
145	150	155	160
Thr Ala Arg Ser Gly Ser Gln Val Cys Val Arg Leu Gly Gly Thr Pro			
165	170	175	
Leu Val Lys Asn Asp Ala Pro Ala Leu Val Ser Phe Met Asn Lys Leu			
180	185	190	

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Asp Met Ala Ile Asp Gly Ala Ala Gly Ile Leu Gly Val Ser His Val
    195                      200                      205

Asp Leu Arg Ser Ala Thr Glu Gly His Asp Ser Cys Ser Asn Asp Pro
    210                      215                      220

Trp Val Asn Gly Val Phe Asp Ala Arg Ala Glu Ile Val Gly Gly Pro
    225                      230                      235                      240

Trp His Pro Ser Val Lys Gly Asp Ser Val Thr Ala Gly Ile Leu Arg
    245                      250                      255

Asp Arg Val Asn Ala
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<210> 21
<211> 771
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(748)
<223> RXN01403

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<400> 21
gtgcgtcgca tacggtgaat tatctttcgg cggatcggtt ccgcacggtg tcgagtttcg 60

tagagtttgc ggccgatcgc ggtattcagg aattcagcca ttg gtg cgc ggt cgg 115
                                Leu Val Arg Gly Arg
                                1                      5

ggc tat ttc aat cgc gtg gat att tat gag acc tcc acg caa cct gac 163
Gly Tyr Phe Asn Ala Val Asp Ile Tyr Glu Thr Ser Thr Gln Pro Asp
                                10                      15                      20

cag gaa ttt cct ttc gat ttt gac act ttt tca gcc gac ccc acg ccg 211
Gln Glu Phe Pro Phe Asp Phe Asp Thr Phe Ser Ala Asp Pro Thr Pro
                                25                      30                      35

ttt caa ctc tct cgc gtg cgt gcc gat acc ggc gag acc gtt ttt tgg 259
Phe Gln Leu Ser Ala Val Arg Ala Asp Thr Gly Glu Thr Val Phe Trp
                                40                      45                      50

ggc agg gaa gac acc ccg gat ttg agc gct ctg atg aag cgg gtt cgc 307
Gly Arg Glu Asp Thr Pro Asp Leu Ser Ala Leu Met Lys Arg Val Arg
                                55                      60                      65

gcg tcg tcg acc atg cct ggt ttc atg ccg atc acc tac atc gac ggc 355
Ala Ser Ser Thr Met Pro Gly Phe Met Pro Ile Thr Tyr Ile Asp Gly
                                70                      75                      80                      85

cat cca tat gtc gat ggc cgc gtc ggg gag acc ggc ggt ttg atg cta 403
His Pro Tyr Val Asp Gly Ala Val Gly Glu Thr Gly Gly Leu Met Leu
                                90                      95                      100

cag ccg gcc atc gat cgc gcc ttc acc cgc ttt ttc gtt atc gcc tcc 451
Gln Pro Ala Ile Asp Ala Gly Phe Thr Arg Phe Phe Val Ile Ala Ser
                                105                      110                      115

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cgt ccg cgc gat tat tgg cgc aag gag atc ggg cgc ccg ggt ttc atc 499
 Arg Pro Arg Asp Tyr Trp Arg Lys Glu Ile Gly Arg Pro Gly Phe Ile
 120 125 130

aaa gct gct tta cga cgt ttc ccc aca atc gcc gac ctc acc atc gcg 547
 Lys Ala Ala Leu Arg Arg Phe Pro Thr Ile Ala Asp Leu Thr Ile Ala
 135 140 145

cgt cct gca ctg tat aac tgg gta aag caa cag atc ctc gac cta gag 595
 Arg Pro Ala Leu Tyr Asn Ser Val Lys Gln Ile Leu Asp Leu Glu
 150 155 160 165

aaa caa ggc agc gcc tat gtg ttc ttt gcg gac aac atg aac atc cag 643
 Lys Gln Gly Ser Ala Tyr Val Phe Phe Ala Asp Asn Met Asn Ile Gln
 170 175 180

aac acg gaa atc aat ctg aag aaa ctc cgt gca tct ttc gat gca ggc 691
 Asn Thr Glu Ile Asn Leu Lys Lys Leu Arg Ala Ser Phe Asp Ala Gly
 185 190 195

atg cag cag acc cgc aaa gat tgg ccg gag atc atg agc ttc ctg aac 739
 Met Gln Gln Thr Arg Lys Asp Trp Pro Glu Ile Met Ser Phe Leu Asn
 200 205 210

caa acc aga taatgaaggt ttttagtcca act 771
 Gln Thr Arg
 215

<210> 22
 <211> 216
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 22
 Leu Val Arg Gly Arg Gly Tyr Phe Asn Ala Val Asp Ile Tyr Glu Thr
 1 5 10 15

Ser Thr Gln Pro Asp Gln Glu Phe Pro Phe Asp Phe Asp Thr Phe Ser
 20 25 30

Ala Asp Pro Thr Pro Phe Gln Leu Ser Ala Val Arg Ala Asp Thr Gly
 35 40 45

Glu Thr Val Phe Trp Gly Arg Glu Asp Thr Pro Asp Leu Ser Ala Leu
 50 55 60

Met Lys Arg Val Arg Ala Ser Ser Thr Met Pro Gly Phe Met Pro Ile
 65 70 75 80

Thr Tyr Ile Asp Gly His Pro Tyr Val Asp Gly Ala Val Gly Glu Thr
 85 90 95

Gly Gly Leu Met Leu Gln Pro Ala Ile Asp Ala Gly Phe Thr Arg Phe
 100 105 110

Phe Val Ile Ala Ser Arg Pro Arg Asp Tyr Trp Arg Lys Glu Ile Gly
 115 120 125

Arg Pro Gly Phe Ile Lys Ala Ala Leu Arg Arg Phe Pro Thr Ile Ala
 130 135 140

Asp Leu Thr Ile Ala Arg Pro Ala Leu Tyr Asn Ser Val Lys Gln Gln
145 150 155 160

Ile Leu Asp Leu Glu Lys Gln Gly Ser Ala Tyr Val Phe Phe Ala Asp
165 170 175

Asn Met Asn Ile Gln Asn Thr Glu Ile Asn Leu Lys Lys Leu Arg Ala
180 185 190

Ser Phe Asp Ala Gly Met Gln Gln Thr Arg Lys Asp Trp Pro Glu Ile
195 200 205

Met Ser Phe Leu Asn Gln Thr Arg
210 215

<210> 23

<211> 437

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(414)

<223> FRXA01403

<400> 23

cgc atc acc tac atc gac ggc cat cca tat gtc gat ggc gcg gtc ggg 48
Pro Ile Thr Tyr Ile Asp Gly His Pro Tyr Val Asp Gly Ala Val Gly
1 5 10 15

gag acc ggc ggt ttg atg cta cag ccg gcc atc gat gcg gcc ttc acc 96
Glu Thr Gly Gly Leu Met Leu Gln Pro Ala Ile Asp Ala Gly Phe Thr
20 25 30

cgc ttt ttc gtt atc gcc tcc cgt ccg cgc gat tat tgg cgc aag gag 144
Arg Phe Phe Val Ile Ala Ser Arg Pro Arg Asp Tyr Trp Arg Lys Glu
35 40 45

atc ggg cgc ccg ggt ttc atc aaa gct gct tta cga cgt ttc ccc aca 192
Ile Gly Arg Pro Gly Phe Ile Lys Ala Ala Leu Arg Arg Phe Pro Thr
50 55 60

atc gcc gac ctc acc atc gcg cgt cct gca ctg tat aac tcg gta aag 240
Ile Ala Asp Leu Thr Ile Ala Arg Pro Ala Leu Tyr Asn Ser Val Lys
65 70 75 80

caa cag atc ctc gac cta gag aaa caa gcc agc gcc tat gtg ttc ttt 288
Gln Gln Ile Leu Asp Leu Glu Lys Gln Gly Ser Ala Tyr Val Phe Phe
85 90 95

gcg gac aac atg aac atc cag aac acg gaa atc aat ctg aag aaa ctc 336
Ala Asp Asn Met Asn Ile Gln Asn Thr Glu Ile Asn Leu Lys Lys Leu
100 105 110

cgt gca tct ttc gat gca gcc atg cag cag acc cgc aaa gat tgg ccg 384
Arg Ala Ser Phe Asp Ala Gly Met Gln Gln Thr Arg Lys Asp Trp Pro
115 120 125

gag atc atg agc ttc ctg aac caa acc aga taatgaaggt ttttagtcca 434

Glu Ile Met Ser Phe Leu Asn Gln Thr Arg
130 135

act

437

<210> 24

<211> 138

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 24

Pro Ile Thr Tyr Ile Asp Gly His Pro Tyr Val Asp Gly Ala Val Gly
1 5 10 15

Glu Thr Gly Gly Leu Met Leu Gln Pro Ala Ile Asp Ala Gly Phe Thr
20 25 30

Arg Phe Phe Val Ile Ala Ser Arg Pro Arg Asp Tyr Trp Arg Lys Glu
35 40 45

Ile Gly Arg Pro Gly Phe Ile Lys Ala Ala Leu Arg Arg Phe Pro Thr
50 55 60

Ile Ala Asp Leu Thr Ile Ala Arg Pro Ala Leu Tyr Asn Ser Val Lys
65 70 75 80

Gln Gln Ile Leu Asp Leu Glu Lys Gln Gly Ser Ala Tyr Val Phe Phe
85 90 95

Ala Asp Asn Met Asn Ile Gln Asn Thr Glu Ile Asn Leu Lys Lys Leu
100 105 110

Arg Ala Ser Phe Asp Ala Gly Met Gln Gln Thr Arg Lys Asp Trp Pro
115 120 125

Glu Ile Met Ser Phe Leu Asn Gln Thr Arg
130 135

<210> 25

<211> 489

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(466)

<223> RXN01326

<400> 25

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gcaaacatct tttaacgctt ttggcccgta ttatggtggc atg gct ttc ccc gtg 115
Met Ala Phe Pro Val
1 5

aca gaa gac aaa atc ctg gca gct gag gaa acc ctt ggc agg cgc ctc 163
Thr Glu Asp Lys Ile Leu Ala Ala Glu Thr Leu Gly Arg Arg Leu
10 15 20

ccc gaa act ttg cgc gaa cga cta ctt caa aac aat ggt ggc gaa gtc 211
 Pro Glu Thr Leu Arg Glu Arg Leu Leu Gln Asn Asn Gly Gly Glu Val
 25 30 35

atc gac aat gaa aac aac gac tgg att ctc cat cca gtt cgt gat gac 259
 Ile Asp Asn Glu Asn Asn Asp Trp Ile Leu His Pro Val Arg Asp Asp
 40 45 50

agc gac cga aaa agg ctt gtc cga act gcc aac gac atc atc cgc gag 307
 Ser Asp Arg Lys Arg Leu Val Arg Thr Ala Asn Asp Ile Ile Arg Glu
 55 60 65

acc gaa tct gca cgt gaa tgg gac aat ttc ccc gaa aat gcg atc gca 355
 Thr Glu Ser Ala Arg Glu Trp Asp Asn Phe Pro Glu Asn Ala Ile Ala
 70 75 80 85

att gca aat gac gga acg ggc gac tta ata att ctg ctt ccc gac gat 403
 Ile Ala Asn Asp Gly Thr Gly Asp Leu Ile Ile Leu Leu Pro Asp Asp
 90 95 100

gat gct ttc tac atc tgg tgg cac gaa gat gaa ccc ctg atc gaa act 451
 Asp Ala Phe Tyr Ile Trp Ser His Glu Asp Glu Pro Leu Ile Glu Thr
 105 110 115

gaa ctt gag gat gcc taaaacagct ggacagaatt cga 489
 Glu Leu Glu Asp Ala
 120

<210> 26
 <211> 122
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 26
 Met Ala Phe Pro Val Thr Glu Asp Lys Ile Leu Ala Ala Glu Glu Thr
 1 5 10 15

Leu Gly Arg Arg Leu Pro Glu Thr Leu Arg Glu Arg Leu Leu Gln Asn
 20 25 30

Asn Gly Gly Glu Val Ile Asp Asn Glu Asn Asn Asp Trp Ile Leu His
 35 40 45

Pro Val Arg Asp Asp Ser Asp Arg Lys Arg Leu Val Arg Thr Ala Asn
 50 55 60

Asp Ile Ile Arg Glu Thr Glu Ser Ala Arg Glu Trp Asp Asn Phe Pro
 65 70 75 80

Glu Asn Ala Ile Ala Ile Ala Asn Asp Gly Thr Gly Asp Leu Ile Ile
 85 90 95

Leu Leu Pro Asp Asp Ala Phe Tyr Ile Trp Ser His Glu Asp Glu
 100 105 110

Pro Leu Ile Glu Thr Glu Leu Glu Asp Ala
 115 120

<210> 27

<211> 361
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (45)..(338)
 <223> FRXA01326

<400> 27
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 Leu Arg Glu Arg
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 cta ctt caa aac aat ggt ggc gaa gtc atc gac aat gaa aac aac gac 104
 Leu Leu Gln Asn Asn Gly Gly Glu Val Ile Asp Asn Glu Asn Asn Asp
 5 10 15 20
 tgg att ctc cat cca gtt cgt gat gac agc gac cga aaa agg ctt gtc 152
 Trp Ile Leu His Pro Val Arg Asp Asp Ser Asp Arg Lys Arg Leu Val
 25 30 35
 cga act gcc aac gac atc atc cgc gag acc gaa tct gca cgt gaa tgg 200
 Arg Thr Ala Asn Asp Ile Ile Arg Glu Thr Glu Ser Ala Arg Glu Trp
 40 45 50
 gac aat ttc ccc gaa aat gcg atc gca att gca aat gac gga acg ggc 248
 Asp Asn Phe Pro Glu Asn Ala Ile Ala Ile Ala Asn Asp Gly Thr Gly
 55 60 65
 gac tta ata att ctg ctt ccc gac gat gat gct ttc tac atc tgg tcg 296
 Asp Leu Ile Ile Leu Leu Pro Asp Asp Ala Phe Tyr Ile Trp Ser
 70 75 80
 cac gaa gat gaa ccc ctg atc gaa act gaa ctt gag gat gcc 338
 His Glu Asp Glu Pro Leu Ile Glu Thr Glu Leu Glu Asp Ala
 85 90 95
 taaaacagct ggacagaatt cga 361

<210> 28
 <211> 98
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 28
 Leu Arg Glu Arg Leu Leu Gln Asn Asn Gly Gly Glu Val Ile Asp Asn
 1 5 10 15
 Glu Asn Asn Asp Trp Ile Leu His Pro Val Arg Asp Asp Ser Asp Arg
 20 25 30
 Lys Arg Leu Val Arg Thr Ala Asn Asp Ile Ile Arg Glu Thr Glu Ser
 35 40 45
 Ala Arg Glu Trp Asp Asn Phe Pro Glu Asn Ala Ile Ala Ile Ala Asn
 50 55 60
 Asp Gly Thr Gly Asp Leu Ile Ile Leu Leu Pro Asp Asp Ala Phe
 65 70 75 80

Asp Ala

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<210> 29
<211> 648
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(625)  
<223> RXN01301
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cgcggtgcggg acgtgttcat ttctgtatag gaaaactacc ttg atc gtt gat acc 115
Leu Ile Val Asp Thr
1 5

cag ttt gag aag atc cct gct cac gac gtc gtg ggc atc cgg gta atc 163
Gln Phe Glu Lys Ile Pro Ala His Asp Val Val Gly Ile Arg Val Ile
10 15 20

ctt tcc tct gag gat ctc cct gag ctc ttt aaa cgc gcc tac gcg gaa 211
 Leu Ser Ser Glu Asp Leu Pro Glu Leu Phe Lys Arg Gly Tyr Ala Glu
 25 30 35

gta aag aaa ttc ctc cgc cta gaa ggc atc gaa cct aaa ggt cct gcc 259
Val Lys Lys Phe Leu Arg Leu Glu Gly Ile Glu Pro Lys Gly Pro Ala
40 45 50

cgc gcc tac tac ttt ggc gat gtc tct gac acc gta gac atc ctg att 307
Arg Ala Tyr Tyr Phe Gly Asp Val Ser Asp Thr Val Asp Ile Leu Ile
55 60 65

ggt ttc ccc gtc agc ccc gcg caa gca gaa tcc ctg cgc cgc ggc gca 355
Gly Phe Pro Val Ser Pro Ala Gln Ala Glu Ser Leu Arg Arg Gly Ala
70 75 80 85

ttg agc caa tcc ggt ggc gac atc gat gac gtt gtc ctc cac cac ttc 403
Leu Ser Gln Ser Gly Gly Asp Ile Asp Asp Val Val Leu His His Phe
90 95 100

cgc gac atg aaa acc atg cac agc cgc cac tcc ggc ccc ttc gat gga 451
Arg Asp Met Lys Thr Met His Ser Arg His Ser Gly Pro Phe Asp Gly
105 110 115

gtc gag cgc gtc tgg gac gaa atc ctc gat gaa gtc gaa gac ctc gga 499
Val Glu Arg Val Trp Asp Glu Ile Leu Asp Glu Val Glu Asp Leu Gly
120 125 130

tgc act ctg cca tcc agc agc atc ggt tgg gaa gaa tac atc gag ggc 547
Cys Thr Leu Pro Ser Ser Ser Ile Gly Trp Glu Glu Tyr Ile Glu Gly
135 140 145

cca gcc acc gct gat acc tgc gac caa ctg gcc tct gaa gtt tat gtt 595
 Pro Ala Thr Ala Asp Thr Cys Asp Gln Leu Ala Ser Glu Val Tyr Val
 150 155 160 165

cag gtg tgc caa gca ccg gtg aag tct gca taaagattca cccggaattt 645
 Gln Val Cys Gln Ala Pro Val Lys Ser Ala
 170 175

ccc 648

<210> 30

<211> 175

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 30

Leu Ile Val Asp Thr Gln Phe Glu Lys Ile Pro Ala His Asp Val Val
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Gly Ile Arg Val Ile Leu Ser Ser Glu Lys Asp Leu Pro Glu Leu Phe Lys
 20 25 30

Arg Gly Tyr Ala Glu Val Lys Lys Phe Leu Arg Leu Glu Gly Ile Glu
 35 40 45

Pro Lys Gly Pro Ala Arg Ala Tyr Tyr Phe Gly Asp Val Ser Asp Thr
 50 55 60

Val Asp Ile Leu Ile Gly Phe Pro Val Ser Pro Ala Gln Ala Glu Ser
 65 70 75 80

Leu Arg Arg Gly Ala Leu Ser Gln Ser Gly Gly Asp Ile Asp Asp Val
 85 90 95

Val Leu His His Phe Arg Asp Met Lys Thr Met His Ser Arg His Ser
 100 105 110

Gly Pro Phe Asp Gly Val Glu Arg Val Trp Asp Glu Ile Leu Asp Glu
 115 120 125

Val Glu Asp Leu Gly Cys Thr Leu Pro Ser Ser Ser Ile Gly Trp Glu
 130 135 140

Glu Tyr Ile Glu Gly Pro Ala Thr Ala Asp Thr Cys Asp Gln Leu Ala
 145 150 155 160

Ser Glu Val Tyr Val Gln Val Cys Gln Ala Pro Val Lys Ser Ala
 165 170 175

<210> 31

<211> 428

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(405)

<223> FRXA01301

<400> 31
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 Phe Leu Arg Leu Glu Gly Ile Glu Pro Lys Gly Pro Ala Arg Ala Tyr
 1 5 10 15

tac ttt ggc gat gtc tct gac acc gta gac atc ctg att ggt ttc ccc 96
 Tyr Phe Gly Asp Val Ser Asp Thr Val Asp Ile Leu Ile Gly Phe Pro
 20 25 30

gtc agc ccc gcg caa gca gaa tcc ctg cgc cgc ggc gca ttg agc caa 144
 Val Ser Pro Ala Gln Ala Glu Ser Leu Arg Arg Gly Ala Leu Ser Gln
 35 40 45

tcc ggt ggc gac atc gat gac gtt gtc ctc cac cac ttc cgc gac atg 192
 Ser Gly Gly Asp Ile Asp Val Val Leu His His Phe Arg Asp Met
 50 55 60

aaa acc atg cac agc cgc cac tcc ggc ccc ttc gat gga gtc gag cgc 240
 Lys Thr Met His Ser Glu His Ser Gly Pro Phe Asp Gly Val Glu Arg
 65 70 75 80

gtc tgg gac gaa atc ctc gat gaa gtc gaa gac ctc gga tgc act ctg 288
 Val Trp Asp Glu Ile Leu Asp Glu Val Glu Asp Leu Gly Cys Thr Leu
 85 90 95

cca tcc agc agc atc ggt tgg gaa gaa tac atc gag ggc cca gcc acc 336
 Pro Ser Ser Ser Ile Gly Trp Glu Glu Tyr Ile Glu Gly Pro Ala Thr
 100 105 110

gct gat acc tgc gac caa ctg gcc tct gaa gtt tat gtt cag gtg tgc 384
 Ala Asp Thr Cys Asp Gln Leu Ala Ser Glu Val Tyr Val Gln Val Cys
 115 120 125

caa gca ccg gtg aag tct gca taaagattca ccggaattt ccc 428
 Gln Ala Pro Val Lys Ser Ala
 130 135

<210> 32
 <211> 135
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 32
 Phe Leu Arg Leu Glu Gly Ile Glu Pro Lys Gly Pro Ala Arg Ala Tyr
 1 5 10 15

Tyr Phe Gly Asp Val Ser Asp Thr Val Asp Ile Leu Ile Gly Phe Pro
 20 25 30

Val Ser Pro Ala Gln Ala Glu Ser Leu Arg Arg Gly Ala Leu Ser Gln
 35 40 45

Ser Gly Gly Asp Ile Asp Val Val Leu His His Phe Arg Asp Met
 50 55 60

Lys Thr Met His Ser Arg His Ser Gly Pro Phe Asp Gly Val Glu Arg
 65 70 75 80

Val Trp Asp Glu Ile Leu Asp Glu Val Glu Asp Leu Gly Cys Thr Leu
 85 90 95

Pro Ser Ser Ser Ile Gly Trp Glu Glu Tyr Ile Glu Gly Pro Ala Thr
 100 105 110

Ala Asp Thr Cys Asp Gln Leu Ala Ser Glu Val Tyr Val Gln Val Cys
 115 120 125

Gln Ala Pro Val Lys Ser Ala
 130 135

<210> 33

<211> 567

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(544)

<223> RXN01276

<400> 33

tgcgtaaaac cctcatcacc atgctcgaga ccaccgcgat cgccttttcc gccatctcac 60

cagtgcaggc gcaaacctgt gacacagaca ctgacgcctc gtg tca tct gag ctg 115
 Val Ser Ser Glu Leu 5
 1

agc agc ggc aca agc tca gga agt tca gag gat tcc gaa gat tct gac 163
 Ser Ser Gly Thr Ser Ser Gly Ser Ser Glu Asp Ser Glu Asp Ser Asp 20
 10 15

atc tcc aac cgg gac atc atc ttc ggc atc gca gct atc gct gca gtc 211
 Ile Ser Asn Arg Asp Ile Ile Phe Gly Ile Ala Ala Ile Ala Ala Val 35
 25 30

ggc gga ctt atc gca agt ggt gtg cac tgg gca gta caa cag cgc atg 259
 Gly Gly Leu Ile Ala Ser Gly Val His Trp Ala Val Gln Gln Arg Met 50
 40 45 50

atc cca aat ccc ctc cca gga atc att cca aat ccc cct gca ctg gca 307
 Ile Pro Asn Pro Leu Pro Gly Ile Ile Pro Asn Pro Pro Ala Leu Ala 65
 55 60

cct cag gcg cct gcc cca gca cct gct ccc gct cct gcc cct cag gca 355
 Pro Gln Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Gln Ala 85
 70 75 80

gtc gcg ccc cag gtt gtc gct ccc cag gtt gtc gcg cct get cca gcc 403
 Val Ala Pro Gln Val Val Ala Pro Gln Val Val Ala Pro Ala Pro Ala 100
 90 95

cca gta cag acc aac cgc acc tac aaa aac tgc acc gaa gta tgg aac 451
 Pro Val Gln Thr Asn Arg Thr Tyr Lys Asn Cys Thr Glu Val Trp Asn 115
 105 110

gtc ctg gga agg tcc atc cgc caa agc gat cca gcc tac gcc aca cac 499
 Val Leu Gly Arg Ser Ile Arg Gln Ser Asp Pro Gly Tyr Gly Thr His 130
 120 125

ctc gac cgc gac cgc gac gcc atc gcc tgc gaa tca cgc cct agg 544

Leu Asp Arg Asp Arg Asp Gly Ile Gly Cys Glu Ser Arg Pro Arg
 135 140 145

tagtttgggt tttggggatc ttc

567

<210> 34

<211> 148

<212> PRT

<213> Corynebacterium glutamicum

<400> 34

Val Ser Ser Glu Leu Ser Ser Gly Thr Ser Ser Gly Ser Ser Glu Asp
 1 5 10 15

Ser Glu Asp Ser Asp Ile Ser Asn Arg Asp Ile Ile Phe Gly Ile Ala
 20 25 30

Ala Ile Ala Ala Val Gly Gly Leu Ile Ala Ser Gly Val His Trp Ala
 35 40 45

Val Gln Gln Arg Met Ile Pro Asn Pro Leu Pro Gly Ile Ile Pro Asn
 50 55 60

Pro Pro Ala Leu Ala Pro Gln Ala Pro Ala Pro Ala Pro Ala
 65 70 75 80

Pro Ala Pro Gln Ala Val Ala Pro Gln Val Val Ala Pro Gln Val Val
 85 90 95

Ala Pro Ala Pro Ala Pro Val Gln Thr Asn Arg Thr Tyr Lys Asn Cys
 100 105 110

Thr Glu Val Trp Asn Val Leu Gly Arg Ser Ile Arg Gln Ser Asp Pro
 115 120 125

Gly Tyr Gly Thr His Leu Asp Arg Asp Arg Asp Gly Ile Gly Cys Glu
 130 135 140

Ser Arg Pro Arg
 145

<210> 35

<211> 669

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(646)

<223> FRXA01276

<400> 35

ctagatgcc ggaaatagc atctcctata cacccaaaaa aaaggggagc gctgacagaa 60

aatagtaata attttgacag ctctgtgcaaa gatgattggc atg cgt aaa acc ctc 115
 Met Arg Lys Thr Leu
 1 5

atc acc atg ctc gcg acc acc gcg atc gcc ttt tcc gcc atc tca cca 163

Ile Thr Met Leu Ala Thr Thr Ala Ile Ala Phe Ser Ala Ile Ser Pro
 10 15 20
 gtg cag gcg caa acc gtg gac aca gac act gac gcc tcc gtg tca tct 211
 Val Gln Ala Gln Thr Val Asp Thr Asp Thr Asp Ala Ser Val Ser Ser
 25 30 35
 gag ctg agc agc ggc aca agc tca gga agt tca gag gat tcc gaa gat 259
 Glu Leu Ser Ser Gly Thr Ser Ser Gly Ser Ser Glu Asp Ser Glu Asp
 40 45 50
 tct gac atc tcc aac cgg gac atc atc ttc ggc atc gca gct atc gct 307
 Ser Asp Ile Ser Asn Arg Asp Ile Ile Phe Gly Ile Ala Ala Ile Ala
 55 60 65
 gca gtc ggc gga ctt atc gca ggt ggt gtg cac tgg gca gta caa cag 355
 Ala Val Gly Gly Leu Ile Ala Gly Gly Val His Trp Ala Val Gln Gln
 70 75 80 85
 cgc atg atc cca aat ccc ctc cca gga atc att cca aat ccc cct gca 403
 Arg Met Ile Pro Asn Pro Leu Pro Gly Ile Ile Pro Asn Pro Pro Ala
 90 95 100
 ctg gca cct cag gcg cct gcc cca gca cct gct ccc gct cct gcc cct 451
 Leu Ala Pro Gln Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro
 105 110 115
 cag gca gtc gcg ccc cag gtt gtc gct ccc cag gtt gtc gcg cct gct 499
 Gln Ala Val Ala Pro Gln Val Val Ala Pro Gln Val Val Ala Pro Ala
 120 125 130
 cca gcc cca gta cag acc aac cgc acc tac aaa aac tgc acc gaa gta 547
 Pro Ala Pro Val Gln Thr Asn Arg Thr Tyr Lys Asn Cys Thr Glu Val
 135 140 145
 tgg aac gtc ctg gga agg tcc atc cgc caa agc gat cca gcc tac gcc 595
 Trp Asn Val Leu Gly Arg Ser Ile Arg Gln Ser Asp Pro Gly Tyr Gly
 150 155 160 165
 aca cac ctc gac cgc gac cgc gac gcc atc gcc tgc gaa tca cgc cct 643
 Thr His Leu Asp Arg Asp Arg Asp Gly Ile Gly Cys Glu Ser Arg Pro
 170 175 180
 agg tagtttgggt ttggtgggac ttc 669
 Arg

<210> 36

<211> 182

<212> PRT

<213> Corynebacterium glutamicum

<400> 36

Met Arg Lys Thr Leu Ile Thr Met Leu Ala Thr Thr Ala Ile Ala Phe
 1 5 10 15

Ser Ala Ile Ser Pro Val Gln Ala Gln Thr Val Asp Thr Asp Thr Asp
 20 25 30

Ala Ser Val Ser Ser Glu Leu Ser Ser Gly Thr Ser Ser Gly Ser Ser

35 40 45
 Glu Asp Ser Glu Asp Ser Asp Ile Ser Asn Arg Asp Ile Ile Phe Gly
 50 55 60
 Ile Ala Ala Ile Ala Ala Val Gly Gly Leu Ile Ala Gly Gly Val His
 65 70 75 80
 Trp Ala Val Gln Gln Arg Met Ile Pro Asn Pro Leu Pro Gly Ile Ile
 85 90 95
 Pro Asn Pro Pro Ala Leu Ala Pro Gln Ala Pro Ala Pro Ala Pro Ala
 100 105 110
 Pro Ala Pro Ala Pro Gln Ala Val Ala Pro Gln Val Val Ala Pro Gln
 115 120 125
 Val Val Ala Pro Ala Pro Ala Pro Val Gln Thr Asn Arg Thr Tyr Lys
 130 135 140
 Asn Cys Thr Glu Val Trp Asn Val Leu Gly Arg Ser Ile Arg Gln Ser
 145 150 155 160
 Asp Pro Gly Tyr Gly Thr His Leu Asp Arg Asp Arg Asp Gly Ile Gly
 165 170 175
 Cys Glu Ser Arg Pro Arg
 180
 <210> 37
 <211> 366
 <212> DNA
 <213> *Corynebacterium glutamicum*
 <220>
 <221> CDS
 <222> (101)..(343)
 <223> RXN01231
 <400> 37
 tcctgggacg tcttccccga ggcgtgggag acattgaagg ttacctggg ctttcgtgcc 60
 ccaggcatcg agcacttcac ccccttatga cgccttgcaa atg ctg ggc tac acc 115
 Met Leu Gly Tyr Thr
 1 5
 ttc gtc atc ttt atc ctg gcg cgg ttt etc atc etc acc gga ata gcg 163
 Phe Val Ile Phe Ile Leu Ala Pro Phe Leu Ile Leu Thr Gly Ile Ala
 10 15 20
 atg gcc cgg gcc atc cgg tcc cgc ttc cgg tgg tac gtc aaa etc ttc 211
 Met Ala Pro Ala Ile Arg Ser Arg Phe Pro Trp Tyr Val Lys Leu Phe
 25 30 35
 ggc ggc cac cag ggt gca cgt tcc ctg cac ttc atc gcc atg gtg ttg 259
 Gly Gly His Gln Gly Ala Arg Ser Leu His Phe Ile Ala Met Val Leu
 40 45 50
 atg acg ggc ttt gtc atc atg cac gtc ggc ctg gtt ttt tgg tcc atg 307
 Met Thr Gly Phe Val Ile Met His Val Gly Leu Val Phe Trp Ser Met

55 60 65

gcg act aca aca tgg tcc aca tgg tct tgc gcg ata tgaacactga 353
 Ala Thr Thr Thr Trp Ser Thr Trp Ser Ser Ala Ile
 70 75 80

cogtgcggcg cag 366

<210> 38
 <211> 81
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 38
 Met Leu Gly Tyr Thr Phe Val Ile Phe Ile Leu Ala Pro Phe Leu Ile
 1 5 10 15
 Leu Thr Gly Ile Ala Met Ala Pro Ala Ile Arg Ser Arg Phe Pro Trp
 20 25 30
 Tyr Val Lys Leu Phe Gly Gly His Gln Gly Ala Arg Ser Leu His Phe
 35 40 45
 Ile Ala Met Val Leu Met Thr Gly Phe Val Ile Met His Val Gly Leu
 50 55 60
 Val Phe Trp Ser Met Ala Thr Thr Trp Ser Thr Trp Ser Ser Ala
 65 70 75 80
 Ile

<210> 39
 <211> 627
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(604)
 <223> FRXA01231

<400> 39
 cctgggacgt cttccccgag gcgtgggag acattgaagg ttacctggg ctttcgtgcc 60
 ccaggcatcg agcacttcac cccctatga cgccttgcaa atg ctg gcc tac acc 115
 Met Leu Gly Tyr Thr
 1 5
 ttc gtc atc ttt atc ctg gcg ccg ttt ctc atc ctc acc gga ata gcg 163
 Phe Val Ile Phe Ile Leu Ala Pro Phe Leu Ile Leu Thr Gly Ile Ala
 10 15 20
 atg gcc ccg gcc atc cgg tcc cgc ttc ccg tgg tac gtc aaa ctc ttc 211
 Met Ala Pro Ala Ile Arg Ser Arg Phe Pro Trp Tyr Val Lys Leu Phe
 25 30 35
 gcc gcc cac cag ggt gca cgt tcc ctg cac ttc atc gcc atg gtg ttg 259
 Gly Gly His Gln Gly Ala Arg Ser Leu His Phe Ile Ala Met Val Leu

40	45	50	
atg acg ggc ttt gtc atc atg cac ngf cgg cct ggt ttt ttg gtc cat			307
Met Thr Gly Phe Val Ile Met His Xaa Arg Pro Gly Phe Leu Val His			
55	60	65	
ggc gac tac aac atg gtc cac atg gtc ttc ggc gat atg aac act gac			355
Gly Asp Tyr Asn Met Val His Met Val Phe Gly Asp Met Asn Thr Asp			
70	75	80	85
cgt gcg gcg cag gcc tac atc atc atc gtc atc acc acc atc gtc ant ggt			403
Arg Ala Ala Gln Ala Tyr Ile Ile Val Ile Thr Thr Ile Val Xaa Gly			
90	95	100	
ggt gtt ktt ctg rat cgg gct cag tat att kgt mrc tgg ctk acc grg			451
Gly Val Xaa Leu Xaa Xaa Ala Gln Tyr Ile Xaa Xaa Trp Xaa Thr Xaa			
105	110	115	
mcc gcg ccm wgc ggt tya cgg cca gcw tca tck gag wtm gdw cgc aaa			499
Xaa Ala Xaa Xaa Gly Xaa Pro Pro Xaa Ser Xaa Glu Xaa Xaa Arg Lys			
120	125	130	
atc ttt nct caw cgg gct gcg tcc cgg gat gag cga gan nan cac			547
Ile Phe Xaa Xaa Pro Ala Ala Ser Pro Asp Glu Gln Ala Xaa Xaa His			
135	140	145	
cta cac gga caa gga cat ctc gca gtt cca ctg gac caa tgg cct gcc			595
Leu His Gly Gln Gly His Leu Ala Val Pro Leu Asp Gln Trp Pro Ala			
150	155	160	165
gcc gac cga tgatgaatcc cccgagtggg tcg			627
Ala Asp Arg			
<210> 40			
<211> 168			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 40			
Met Leu Gly Tyr Thr Phe Val Ile Phe Ile Leu Ala Pro Phe Leu Ile			
1	5	10	15
Leu Thr Gly Ile Ala Met Ala Pro Ala Ile Arg Ser Arg Phe Pro Trp			
20	25	30	
Tyr Val Lys Leu Phe Gly Gly His Gln Gly Ala Arg Ser Leu His Phe			
35	40	45	
Ile Ala Met Val Leu Met Thr Gly Phe Val Ile Met His Xaa Arg Pro			
50	55	60	
Gly Phe Leu Val His Gly Asp Tyr Asn Met Val His Met Val Phe Gly			
65	70	75	80
Asp Met Asn Thr Asp Arg Ala Ala Gln Ala Tyr Ile Ile Val Ile Thr			
85	90	95	
Thr Ile Val Xaa Gly Gly Val Xaa Leu Xaa Xaa Ala Gln Tyr Ile Xaa			
100	105	110	

Xaa Trp Xaa Thr Xaa Xaa Ala Xaa Xaa Gly Xaa Pro Pro Xaa Ser Xaa
 115 120 125

Glu Xaa Xaa Arg Lys Ile Phe Xaa Xaa Pro Ala Ala Ser Pro Asp Glu
 130 135 140

Gln Ala Xaa Xaa His Leu His Gly Gln Gly His Leu Ala Val Pro Leu
 145 150 155 160

Asp Gln Trp Pro Ala Ala Asp Arg
 165

<210> 41
 <211> 954
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(931)
 <223> RXN01210

<400> 41
 ttctgctgcaa aaccgcgcac cttggaatcc gtattcatgg acatgcgctc actcgagaac 60

acctcgctgc aaaccgccta gaatctttaa ggagaccaca atg acc acg tca cac 115
 Met Thr Thr Ser His
 1 5

acc gcc cgc ggg ctg caa cat gca acc ccg gag cgc cgc aag act tca 163
 Thr Ala Arg Gly Leu Gln His Ala Thr Pro Glu Arg Arg Lys Thr Ser
 10 15 20

ttt ttc aaa acc tct ctg ttt aag gcc gaa tgg ctc cag ttc cgc aga 211
 Phe Phe Lys Thr Ser Leu Phe Lys Ala Glu Trp Leu Gln Phe Arg Arg
 25 30 35

aat aaa acc ctg ttg ttc atg gcc acc gta ttc cca gtc gga atc cct 259
 Asn Lys Thr Leu Leu Phe Met Ala Thr Val Phe Pro Val Gly Ile Pro
 40 45 50

ttg ttg ctc ttt ctc atc gga aat ggt ggg gca gca gag tcc gcg aac 307
 Leu Leu Leu Phe Leu Ile Gly Asn Gly Gly Ala Ala Glu Ser Ala Asn
 55 60 65

tcc ttc gac tac ttc gtc atg tac acc ctg cta ttt gtg cag ttc tac 355
 Ser Phe Asp Tyr Phe Val Met Tyr Thr Leu Leu Phe Val Gln Phe Tyr
 70 75 80 85

acg gtg ctg tcc atg gca acc acc cgc cgt gat gaa cgt gtg ctg aaa 403
 Thr Val Leu Ser Met Ala Thr Thr Arg Arg Asp Glu Arg Val Leu Lys
 90 95 100

agg ctg cgc acg gga gaa gcc cgc gac atc gat atc atc ggt gcc atc 451
 Arg Leu Arg Thr Gly Glu Ala Arg Asp Ile Asp Ile Ile Gly Ala Ile
 105 110 115

tgt ttc ccc gcc gcg ctc ctc aca ctg atc ttc acc gtg gtg atc att 499
 Cys Phe Pro Gly Ala Leu Leu Thr Leu Ile Phe Thr Val Val Ile Ile

120	125	130	
cca ttg ctc atg gtt ttg gga gct ccc gcg ccc atc aac ctt gtg ccc			547
Pro Leu Leu Met Val Leu Gly Ala Pro Ala Pro Ile Asn Leu Val Pro			
135	140	145	
att gtg ttt gcc gta ctg atc gga cta ctt ctt tgt agt gct ctt gcc			595
Ile Val Phe Ala Val Leu Ile Gly Leu Leu Leu Cys Ser Ala Leu Ala			
150	155	160	165
ttg atg acc agc ggt ttc acc cga aac gcc gaa gcc gca cag atg acc			643
Leu Met Thr Ser Gly Phe Thr Arg Asn Ala Glu Ala Ala Gln Met Thr			
170	175	180	
tcc atg ccc gtg ttc atg ctt gcg atg ggt gga ctt gga tca atc cgc			691
Ser Met Pro Val Phe Met Leu Ala Met Gly Gly Leu Gly Ser Ile Arg			
185	190	195	
ttc gta ttc ggc gac agc att gtg gct gat atc ttg gcc tac acc cca			739
Phe Val Phe Gly Asp Ser Ile Val Ala Asp Ile Leu Ala Tyr Thr Pro			
200	205	210	
ttc gcc gcg atc agt gac ctt gtc caa atc ggc tgg gct ggc gcc acc			787
Phe Ala Ala Ile Ser Asp Leu Val Gln Ile Gly Trp Ala Gly Ala Thr			
215	220	225	
ttc gcc gac agc gtt ggt gga gta gag gca gca aac ttc gct gga att			835
Phe Ala Asp Ser Val Gly Gly Val Glu Ala Ala Asn Phe Ala Gly Ile			
230	235	240	245
ttc caa gac atg ctc ata cca ctt gga att ctg gca gcg tgg aca gct			883
Phe Gln Asp Met Leu Ile Pro Leu Gly Ile Leu Ala Ala Trp Thr Ala			
250	255	260	
gca gcg gtg tgg gcg gcg aac cgc tac atg cgc tgg gac tgc tac cgc			931
Ala Ala Val Trp Ala Ala Asn Arg Tyr Met Arg Trp Asp Ser Tyr Arg			
265	270	275	
taagcctgca gccgacggga tta			954

<210> 42

<211> 277

<212> PRT

<213> Corynebacterium glutamicum

<400> 42

Met Thr Thr Ser His Thr Ala Arg Gly Leu Gln His Ala Thr Pro Glu
1 5 10 15

Arg Arg Lys Thr Ser Phe Phe Lys Thr Ser Leu Phe Lys Ala Glu Trp
20 25 30

Leu Gln Phe Arg Arg Asn Lys Thr Leu Leu Phe Met Ala Thr Val Phe
35 40 45

Pro Val Gly Ile Pro Leu Leu Phe Leu Ile Gly Asn Gly Gly Ala
50 55 60

Ala Glu Ser Ala Asn Ser Phe Asp Tyr Phe Val Met Tyr Thr Leu Leu
65 70 75 80

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Phe Val Gln Phe Tyr Thr Val Leu Ser Met Ala Thr Thr Arg Arg Asp
      85                      90                      95

Glu Arg Val Leu Lys Arg Leu Arg Thr Gly Glu Ala Arg Asp Ile Asp
      100                      105                      110

Ile Ile Gly Ala Ile Cys Phe Pro Gly Ala Leu Leu Thr Leu Ile Phe
      115                      120                      125

Thr Val Val Ile Ile Pro Leu Leu Met Val Leu Gly Ala Pro Ala Pro
      130                      135                      140

Ile Asn Leu Val Pro Ile Val Phe Ala Val Leu Ile Gly Leu Leu Leu
      145                      150                      155                      160

Cys Ser Ala Leu Ala Leu Met Thr Ser Gly Phe Thr Arg Asn Ala Glu
      165                      170                      175

Ala Ala Gln Met Thr Ser Met Pro Val Phe Met Leu Ala Met Gly Gly
      180                      185                      190

Leu Gly Ser Ile Arg Phe Val Phe Gly Asp Ser Ile Val Ala Asp Ile
      195                      200                      205

Leu Ala Tyr Thr Pro Phe Ala Ala Ile Ser Asp Leu Val Gln Ile Gly
      210                      215                      220

Trp Ala Gly Ala Thr Phe Ala Asp Ser Val Gly Gly Val Glu Ala Ala
      225                      230                      235                      240

Asn Phe Ala Gly Ile Phe Gln Asp Met Leu Ile Pro Leu Gly Ile Leu
      245                      250                      255

Ala Ala Trp Thr Ala Ala Ala Val Trp Ala Ala Asn Arg Tyr Met Arg
      260                      265                      270

Trp Asp Ser Tyr Arg
      275

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<210> 43
<211> 716
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (1)..(693)
<223> FRXA01210

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<400> 43
gta ttc cca gtc gga atc cct ttg ttg ctc ttt ctc atc gga aat ggt 48
Val Phe Pro Val Gly Ile Pro Leu Leu Leu Phe Leu Ile Gly Asn Gly
      1          5          10          15

ggg gca gca gag tcc gcg aac tcc ttc gac tac ttc gtc atg tac acc 96
Gly Ala Ala Glu Ser Ala Asn Ser Phe Asp Tyr Phe Val Met Tyr Thr
      20          25          30

ctg cta ttt gtg cag ttc tac acg gtg ctg tcc atg gca acc acc cgc 144

```

```

Leu Leu Phe Val Gln Phe Tyr Thr Val Leu Ser Met Ala Thr Thr Arg
      35                      40                      45

cgt gat gaa cgt gtg ctg aaa agg ctg cgc acg gga gaa gcc cgc gac 192
Arg Asp Glu Arg Val Leu Lys Arg Leu Arg Thr Gly Glu Ala Arg Asp
      50                      55                      60

atc gat atc atc ggt gcc atc tgt ttc ccc gcc gcg ctc ctc aca ctg 240
Ile Asp Ile Ile Gly Ala Ile Cys Phe Pro Gly Ala Leu Leu Thr Leu
      65                      70                      75                      80

atc ttc acc gtg gtg atc att cca ttg ctc atg gtt ttg gga gct ccc 288
Ile Phe Thr Val Val Ile Ile Pro Leu Leu Met Val Leu Gly Ala Pro
      85                      90                      95

gcg ccc atc aac ctt gtg ccc att gtg ttt gcc gta ctg atc gga cta 336
Ala Pro Ile Asn Leu Val Pro Ile Val Phe Ala Val Leu Ile Gly Leu
      100                     105                     110

ctt ctt tgt agt gct ctt gcc ttg atg acc agc ggt ttc acc cga aac 384
Leu Leu Cys Ser Ala Leu Ala Leu Met Thr Ser Gly Phe Thr Arg Asn
      115                     120                     125

gcc gaa gcc gca cag atg acc tcc atg ccc gtg ttc atg ctt gcg atg 432
Ala Glu Ala Ala Gln Met Thr Ser Met Pro Val Phe Met Leu Ala Met
      130                     135                     140

ggt gga ctt gga tca atc cgc ttc gta ttc gcc gac agc att gtg gct 480
Gly Gly Leu Gly Ser Ile Arg Phe Val Phe Gly Asp Ser Ile Val Ala
      145                     150                     155                     160

gat atc ttg gcc tac acc cca ttc gcc gcg atc agt gac ctt gtc caa 528
Asp Ile Leu Ala Tyr Thr Pro Phe Ala Ala Ile Ser Asp Leu Val Gln
      165                     170                     175

atc gcc tgg gct gcc gcc acc ttc gcc gac agc gtt ggt gga gta gag 576
Ile Gly Trp Ala Gly Ala Thr Phe Ala Asp Ser Val Gly Gly Val Glu
      180                     185                     190

gca gca aac ttc gct gga att ttc caa gac atg ctc ata cca ctt gga 624
Ala Ala Asn Phe Ala Gly Ile Phe Gln Asp Met Leu Ile Pro Leu Gly
      195                     200                     205

att ctg gca gcg tgg aca gct gca gcg gtg tgg gcg gcg aac cgc tac 672
Ile Leu Ala Ala Trp Thr Ala Ala Ala Val Trp Ala Ala Asn Arg Tyr
      210                     215                     220

atg cgc tgg gac tcg tac cgc taagcctgca gccgacggga tta 716
Met Arg Trp Asp Ser Tyr Arg
      225                     230

```

<210> 44

<211> 231

<212> PRT

<213> Corynebacterium glutamicum

<400> 44

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Val Phe Pro Val Gly Ile Pro Leu Leu Leu Phe Leu Ile Gly Asn Gly
  1                      5                      10                     15

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[illegible]

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<220>
<221> CDS
<222> (101)..(400)
<223> RXN01206
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400> 45
ccgtgccagt gatgaaaagc cggcgagccg ccaaacttga ttaagtgtatt gtcactttgg 60
attgtcatat tgggcgaata aaccggtagg attcccccttc gtg agc gcc gaa aat 115
Val Ser Ala Glu Asn
1 5
acc gag aac aca gat tcc cca ttt gaa atc tcc gag ttt gat gat cac 163

```

Thr Glu Asn Thr Asp Ser Pro Phe Glu Ile Ser Glu Phe Asp Asp His
                10                15                20

cga cgc ccc ctc cag cgg gcc ctc aaa ttc ggt tcc atc gcc cta att 211
Arg Arg Pro Leu Gln Arg Ala Leu Lys Phe Gly Ser Ile Ala Leu Ile
                25                30                35

gtc ttc acc ctg atc tcc cta gcg atc tgg ggt gca act cgt ggc gta 259
Val Phe Thr Leu Ile Ser Leu Ala Ile Trp Gly Ala Thr Arg Gly Val
                40                45                50

ccc ggc gta tca gca gtt gtt atc ggc gca gca gtt ggc gca ggc ttt 307
Pro Gly Val Ser Ala Val Val Ile Gly Ala Ala Val Gly Ala Gly Phe
                55                60                65

gtc ctc tta acg gct ctc agc gtc ctg ttt aca act aat tcc aac gtc 355
Val Leu Leu Thr Ala Leu Ser Val Leu Phe Thr Thr Asn Ser Asn Val
                70                75                80                85

acc acc acc ggt gcg gtg gtg ctc ggt ggc tgg ctg ctg aag atc 400
Thr Thr Thr Gly Ala Val Val Leu Gly Gly Trp Leu Leu Lys Ile
                90                95                100

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<210> 46

<211> 100

<212> PRT

<213> Corynebacterium glutamicum

<400> 46

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Val Ser Ala Glu Asn Thr Glu Asn Thr Asp Ser Pro Phe Glu Ile Ser
    1                5                10                15

Glu Phe Asp Asp His Arg Arg Pro Leu Gln Arg Ala Leu Lys Phe Gly
    20                25                30

Ser Ile Ala Leu Ile Val Phe Thr Leu Ile Ser Leu Ala Ile Trp Gly
    35                40                45

Ala Thr Arg Gly Val Pro Gly Val Ser Ala Val Val Ile Gly Ala Ala
    50                55                60

Val Gly Ala Gly Phe Val Leu Leu Thr Ala Leu Ser Val Leu Phe Thr
    65                70                75                80

Thr Asn Ser Asn Val Thr Thr Thr Gly Ala Val Val Leu Gly Gly Trp
    85                90                95

Leu Leu Lys Ile
    100

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<210> 47

<211> 361

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(361)

<223> FRXA01206

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<400> 47
ccgtgccagt gatgaaaagc cggcgagccg ccaaacttga ttaagtgatt gtcactttgg 60

attgtcatat tgggcgaata aaccggtagg attccccctc gtg agc gcc gaa aat 115
                                   Val Ser Ala Glu Asn
                                   1           5

acc gag aac aca gat tcc cca ttt gaa atc tcc gag ttt gat gat cac 163
Thr Glu Asn Thr Asp Ser Pro Phe Glu Ile Ser Glu Phe Asp Asp His
                10                15                20

cga cgc ccc ctc cag cgg gcc ctc aaa ttc ggt tcc atc gcc cta att 211
Arg Arg Pro Leu Gln Arg Ala Leu Lys Phe Gly Ser Ile Ala Leu Ile
                25                30                35

gtc ttc acc ctg atc tcc cta gcg atc tgg ggt gca act cgt ggc gta 259
Val Phe Thr Leu Ile Ser Leu Ala Ile Trp Gly Ala Thr Arg Gly Val
                40                45                50

ccc ggc gta tca gca gtt gtt atc ggc gca gca gtt ggc gca ggc ttt 307
Pro Gly Val Ser Ala Val Val Ile Gly Ala Ala Val Gly Ala Gly Phe
                55                60                65

gtc ctc tta acg gct ctc agc gtc ctg ttt aca act aat tcc aac gtc 355
Val Leu Leu Thr Ala Leu Ser Val Leu Phe Thr Thr Asn Ser Asn Val
                70                75                80                85

acc acc 361
Thr Thr

#
<210> 48
<211> 87
<212> PRT
<213> Corynebacterium glutamicum

<400> 48
Val Ser Ala Glu Asn Thr Glu Asn Thr Asp Ser Pro Phe Glu Ile Ser
1           5           10           15

Glu Phe Asp Asp His Arg Arg Pro Leu Gln Arg Ala Leu Lys Phe Gly
20                25                30

Ser Ile Ala Leu Ile Val Phe Thr Leu Ile Ser Leu Ala Ile Trp Gly
35                40                45

Ala Thr Arg Gly Val Pro Gly Val Ser Ala Val Val Ile Gly Ala Ala
50                55                60

Val Gly Ala Gly Phe Val Leu Leu Thr Ala Leu Ser Val Leu Phe Thr
65                70                75                80

Thr Asn Ser Asn Val Thr Thr
85

<210> 49
<211> 1209
<212> DNA

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<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}..(1186)

<223> RXN01121

<400> 49

aaagatttac tgcgtacaac tctaaccaac aatattggca atgggttggt ccactcttagc 60

gctttacctg tgaactctgc agagcggtagc gcttaagcta atg aat ccc gaa ttt 115
 Met Asn Pro Glu Phe
 1 5

att cac ggc gca acc gaa att gaa acc aca aac agg ggc ctt cgc ccg 163
 Ile His Gly Ala Thr Glu Ile Glu Thr Thr Asn Arg Gly Leu Arg Pro
 10 15 20

cat cga ctc agc aaa gaa ata gta gaa cgc tac tgt gat ccc cag ttt 211
 His Arg Leu Ser Lys Glu Ile Val Glu Arg Tyr Cys Asp Pro Gln Phe
 25 30 35

agc gcg atg gaa cgc caa cca tcg ggc gtg cgc gtt gtg tgt cgc acc 259
 Ser Ala Met Glu Arg Gln Pro Ser Gly Val Arg Val Val Cys Arg Thr
 40 45 50

acc gcc acc tcc gtc acg ctg acc acg tat tcc acg cgg gtg gtg tac 307
 Thr Ala Thr Ser Val Thr Thr Thr Tyr Ser Thr Arg Val Val Tyr
 55 60 65

ctc gat tcc ggc cgg ccg gcc gcc aag att gat gtg ctt atc gac gcc 355
 Leu Asp Ser Gly Arg Pro Gly Gly Lys Ile Asp Val Leu Ile Asp Gly
 70 75 80 85

gcc ccc aca tct tcc acg cca act tcc ggg gcc gag acc acg gaa gtc 403
 Ala Pro Thr Ser Ser Thr Pro Thr Ser Gly Gly Glu Thr Thr Glu Val
 90 95 100

aat ttc atc acc gcc gcc acg gaa cgg cgc ctg aaa gat ccg cag gtg 451
 Asn Phe Ile Thr Gly Ala Thr Glu Arg Arg Leu Lys Asp Pro Gln Val
 105 110 115

ctc aca gtg gat gga ctt tca gag cag gaa aag gtg gtg gag ttc tgg 499
 Leu Thr Val Asp Gly Leu Ser Glu Gln Glu Lys Val Val Glu Phe Trp
 120 125 130

ctg cct cac aat gaa gaa att gaa gtg atc tcc ctt aaa gcc aac gca 547
 Leu Pro His Asn Glu Glu Ile Glu Val Ile Ser Leu Lys Ala Asn Ala
 135 140 145

gct tta aac act gtc gaa gac acc cgt ccc gtg tgg atc aat tac gcc 595
 Ala Leu Asn Thr Val Glu Asp Thr Arg Pro Val Trp Ile Asn Tyr Gly
 150 155 160 165

agc tcc att agc cac ggt tcg gtt gcc act gcc cca acc aaa att tgg 643
 Ser Ser Ile Ser His Gly Ser Val Ala Thr Ala Pro Thr Lys Ile Trp
 170 175 180

cca gcc att gtt gcc cag tcc aaa aac tac aac ctg cgt aac ttc ggt 691
 Pro Ala Ile Val Ala Gln Ser Lys Asn Tyr Asn Leu Arg Asn Phe Gly
 185 190 195


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ttt ggt ggc agc gcc atg ttg gat cct ttt atg gcg agg cta atc agg 739
Phe Gly Gly Ser Ala Met Leu Asp Pro Phe Met Ala Arg Leu Ile Arg
      200                205                210

gat act cca gct gat ctg atc acc ttg gaa att ggc atc aat att gtc 787
Asp Thr Pro Ala Asp Leu Ile Thr Leu Glu Ile Gly Ile Asn Ile Val
      215                220                225

aat ggt gat gtg atg cgt cgc cgc gga cta gag gct gct gtg gat ggg 835
Asn Gly Asp Val Met Arg Arg Arg Gly Leu Glu Ala Ala Val Asp Gly
      230                235                240                245

ttc atc aat acc atc cgc gat ggc cac ccc acc acg ccg atc aag att 883
Phe Ile Asn Thr Ile Arg Asp Gly His Pro Thr Thr Pro Ile Lys Ile
      250                255                260

gtg tgc ccg ttc tac tgc ccc att cat gag aaa act cca gga ccc ggc 931
Val Ser Pro Phe Tyr Cys Pro Ile His Glu Lys Thr Pro Gly Pro Gly
      265                270                275

gcg ttt gat acc tca tgc ttt ggc agt ggt cag att agg ttc atc gcc 979
Ala Phe Asp Thr Ser Ser Phe Gly Ser Gly Gln Ile Arg Phe Ile Ala
      280                285                290

act ggt gaa cct gat gag cat ggt cga ctg acg ctg gag atg gtg cgt 1027
Thr Gly Glu Pro Asp Glu His Gly Arg Leu Thr Leu Glu Met Val Arg
      295                300                305

gag gtg ttg gag ggg ttc gtc gaa aag caa aaa gac ccg cac ctg acc 1075
Glu Val Leu Glu Gly Phe Val Glu Lys Gln Lys Asp Pro His Leu Thr
      310                315                320                325

tac gtc gat ggt cgc agc ctt tat cag gcc agc gat cgc ccg ttg ctg 1123
Tyr Val Asp Gly Ala Ser Leu Tyr Gln Ala Ser Asp Ala Pro Leu Leu
      330                335                340

gat aat ttg cac cca gac gag gcg tgc cac gcc tta att gcg cag cgt 1171
Asp Asn Leu His Pro Asp Glu Ala Ser His Ala Leu Ile Ala Gln Arg
      345                350                355

ttg ctt aag caa ctt tgaaatcgcc ttccgtgatt tgc 1209
Leu Leu Lys Gln Leu
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<210> 50
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<212> PRT
<213> Corynebacterium glutamicum

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Met Asn Pro Glu Phe Ile His Gly Ala Thr Glu Ile Glu Thr Thr Asn
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Arg Gly Leu Arg Pro His Arg Leu Ser Lys Glu Ile Val Glu Arg Tyr
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Cys Asp Pro Gln Phe Ser Ala Met Glu Arg Gln Pro Ser Gly Val Arg
      35                40                45

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Val Val Cys Arg Thr Thr Ala Thr Ser Val Thr Leu Thr Thr Tyr Ser
 50 55 60
 Thr Arg Val Val Tyr Leu Asp Ser Gly Arg Pro Gly Gly Lys Ile Asp
 65 70 75 80
 Val Leu Ile Asp Gly Ala Pro Thr Ser Ser Thr Pro Thr Ser Gly Gly
 85 90 95
 Glu Thr Thr Glu Val Asn Phe Ile Thr Gly Ala Thr Glu Arg Arg Leu
 100 105 110
 Lys Asp Pro Gln Val Leu Thr Val Asp Gly Leu Ser Glu Gln Glu Lys
 115 120 125
 Val Val Glu Phe Trp Leu Pro His Asn Glu Glu Ile Glu Val Ile Ser
 130 135 140
 Leu Lys Ala Asn Ala Leu Asn Thr Val Glu Asp Thr Arg Pro Val
 145 150 155 160
 Trp Ile Asn Tyr Gly Ser Ser Ile Ser His Gly Ser Val Ala Thr Ala
 165 170 175
 Pro Thr Lys Ile Trp Pro Ala Ile Val Ala Gln Ser Lys Asn Tyr Asn
 180 185 190
 Leu Arg Asn Phe Gly Phe Gly Gly Ser Ala Met Leu Asp Pro Phe Met
 195 200 205
 Ala Arg Leu Ile Arg Asp Thr Pro Ala Asp Leu Ile Thr Leu Glu Ile
 210 215 220
 Gly Ile Asn Ile Val Asn Gly Asp Val Met Arg Arg Arg Gly Leu Glu
 225 230 235 240
 Ala Ala Val Asp Gly Phe Ile Asn Thr Ile Arg Asp Gly His Pro Thr
 245 250 255
 Thr Pro Ile Lys Ile Val Ser Pro Phe Tyr Cys Pro Ile His Glu Lys
 260 265 270
 Thr Pro Gly Pro Gly Ala Phe Asp Thr Ser Ser Phe Gly Ser Gly Gln
 275 280 285
 Ile Arg Phe Ile Ala Thr Gly Glu Pro Asp Glu His Gly Arg Leu Thr
 290 295 300
 Leu Glu Met Val Arg Glu Val Leu Glu Gly Phe Val Glu Lys Gln Lys
 305 310 315 320
 Asp Pro His Leu Thr Tyr Val Asp Gly Ala Ser Leu Tyr Gln Ala Ser
 325 330 335
 Asp Ala Pro Leu Leu Asp Asn Leu His Pro Asp Glu Ala Ser His Ala
 340 345 350
 Leu Ile Ala Gln Arg Leu Leu Lys Gln Leu
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<222> (101)..(778)
<223> FRXA01121
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ttt ggt ggc agc gcc atg ttg gat cct ttt atg gcg agg cta atc agg 739
 Phe Gly Gly Ser Ala Met Leu Asp Pro Phe Met Ala Arg Leu Ile Arg
 200 205 210

gat act cca gct gat ctg atc acc ttg gaa att ggc atc 778
 Asp Thr Pro Ala Asp Leu Ile Thr Leu Glu Ile Gly Ile
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<210> 52

<211> 226

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 52

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Arg Gly Leu Arg Pro His Arg Leu Ser Lys Glu Ile Val Glu Arg Tyr
 20 25 30

Cys Asp Pro Gln Phe Ser Ala Met Glu Arg Gln Pro Ser Gly Val Arg
 35 40 45

Val Val Cys Arg Thr Thr Ala Thr Ser Val Thr Leu Thr Thr Tyr Ser
 50 55 60

Thr Arg Val Val Tyr Leu Asp Ser Gly Arg Pro Gly Gly Lys Ile Asp
 65 70 75 80

Val Leu Ile Asp Gly Ala Pro Thr Ser Ser Thr Pro Thr Ser Gly Gly
 85 90 95

Glu Thr Thr Glu Val Asn Phe Ile Thr Gly Ala Thr Glu Arg Arg Leu
 100 105 110

Lys Asp Pro Gln Val Leu Thr Val Asp Gly Leu Ser Glu Gln Glu Lys
 115 120 125

Val Val Glu Phe Trp Leu Pro His Asn Glu Glu Ile Glu Val Ile Ser
 130 135 140

Leu Lys Ala Asn Ala Ala Leu Asn Thr Val Glu Asp Thr Arg Pro Val
 145 150 155 160

Trp Ile Asn Tyr Gly Ser Ser Ile Ser His Gly Ser Val Ala Thr Ala
 165 170 175

Pro Thr Lys Ile Trp Pro Ala Ile Val Ala Gln Ser Lys Asn Tyr Asn
 180 185 190

Leu Arg Asn Phe Gly Phe Gly Gly Ser Ala Met Leu Asp Pro Phe Met
 195 200 205

Ala Arg Leu Ile Arg Asp Thr Pro Ala Asp Leu Ile Thr Leu Glu Ile
 210 215 220

Gly Ile
225

<210> 53

<211> 902

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(879)

<223> RXN01085

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Arg Lys Arg Gly Glu Gly Leu Asp Pro Asn Ser Pro Glu Ala Ile Glu

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10

15

cag gcg aag aag aaa ggg gaa cgg aag gct cgt aat gag cgt tgc cgc 96

Gln Ala Lys Lys Lys Gly Glu Arg Lys Ala Arg Asn Glu Arg Cys Arg

20

25

30

aaa aac ttc aaa ggt ggt ggc acc aaa gat ctt aag cag act gat cgg 144

Lys Asn Phe Lys Gly Gly Gly Thr Lys Asp Leu Lys Gln Thr Asp Arg

35

40

45

acc ttt gat cag ctg cga aaa cag cgg gtg acg gat aaa gcc cgc aac 192

Thr Phe Asp Gln Leu Arg Lys Gln Arg Val Thr Asp Lys Ala Arg Asn

50

55

60

cgt gac gta cac aat gag cag caa ctg gca cgc ggt gaa atc gga gaa 240

Arg Asp Val His Asn Glu Gln Gln Leu Ala Arg Gly Glu Ile Gly Glu

65

70

75

80

atg cgc tca ccg atg tgg gtt gag gtg ggt gct cgc att ctg ggc gtg 288

Met Arg Ser Pro Met Trp Val Glu Val Gly Ala Ala Ile Leu Gly Val

85

90

95

ttt gtc ctg gtt gtg atg tgg ctg gcc tgg ggc ggt atc ggg ctg ctg 336

Phe Val Leu Val Val Met Trp Leu Ala Trp Gly Gly Ile Gly Leu Leu

100

105

110

atc cag acc atg atg aat act ggc tca cct aat gac aaa gag ctt ttt 384

Ile Gln Thr Met Met Asn Thr Gly Ser Pro Asn Asp Lys Glu Leu Phe

115

120

125

gat gag ctt ggt gtg aga ccc tat tat gtt gct gtc gaa cag caa atc 432

Asp Glu Leu Gly Val Arg Pro Tyr Tyr Val Ala Val Glu Gln Gln Ile

130

135

140

ggc acc agt agt gct cac acc acg tgc tac caa ccg ctt gat gaa ttt 480

Gly Thr Ser Ser Ala His Thr Thr Cys Tyr Gln Pro Leu Asp Glu Phe

145

150

155

160

ggc aat aat ttt ggc gac tgt acg cgt agc gtg cct aaa gag cca gtg 528

Gly Asn Asn Phe Gly Asp Cys Thr Arg Ser Val Pro Lys Glu Pro Val

165

170

175

tgg tac gcc gat tat gta gct agt gtg ttc gca gaa cat ggc ttt gat 576

Trp Tyr Ala Asp Tyr Val Ala Ser Val Phe Ala Glu His Gly Phe Asp

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	Ala Pro Glu Pro Ile Asp Asn Ser Val Gly Ser Trp Leu Phe Gly			
	195	200	205	
	cat gtg ggc att att cgg gtg acg ttt gtg att gcg gtt gca gcg ggt			672
	His Val Gly Ile Ile Arg Val Thr Phe Val Ile Ala Val Ala Ala Gly			
	210	215	220	
	gtg tat gcg atg tca cgc gca gca atg atg cgt cag cta gaa aca caa			720
	Val Tyr Ala Met Ser Arg Ala Ala Met Met Arg Gln Leu Glu Thr Gln			
	225	230	235	240
	aac gtc gct gtg gac acc acc gat att aac cag cac acc aat gac gca			768
	Asn Val Ala Val Asp Thr Thr Asp Ile Asn Gln His Thr Asn Asp Ala			
	245	250	255	
	cgt ttg gcg att cgg cag gag att gtg cgc gat ttg agt ctg ttc ccc			816
	Arg Leu Ala Ile Pro Gln Glu Ile Val Arg Asp Leu Ser Leu Phe Pro			
	260	265	270	
	gat gtc ggt gca cac ttc acc agt cca gcc ctc aag cat gat ttc cca			864
	Asp Val Gly Ala His Phe Thr Ser Pro Ala Leu Lys His Asp Phe Pro			
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	Cys Asp Ala Val Glu			
	290			
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	<213> <i>Corynebacterium glutamicum</i>			
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	Gln Ala Lys Lys Lys Gly Glu Arg Lys Ala Arg Asn Glu Arg Cys Arg			
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	Lys Asn Phe Lys Gly Gly Gly Thr Lys Asp Leu Lys Gln Thr Asp Arg			
	35	40	45	
	Thr Phe Asp Gln Leu Arg Lys Gln Arg Val Thr Asp Lys Ala Arg Asn			
	50	55	60	
	Arg Asp Val His Asn Glu Gln Gln Leu Ala Arg Gly Glu Ile Gly Glu			
	65	70	75	80
	Met Arg Ser Pro Met Trp Val Glu Val Gly Ala Ala Ile Leu Gly Val			
	85	90	95	
	Phe Val Leu Val Val Met Trp Leu Ala Trp Gly Gly Ile Gly Leu Leu			
	100	105	110	
	Ile Gln Thr Met Met Asn Thr Gly Ser Pro Asn Asp Lys Glu Leu Phe			
	115	120	125	

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Asp Glu Leu Gly Val Arg Pro Tyr Tyr Val Ala Val Glu Gln Gln Ile
130                      135                      140

Gly Thr Ser Ser Ala His Thr Thr Cys Tyr Gln Pro Leu Asp Glu Phe
145                      150                      155                      160

Gly Asn Asn Phe Gly Asp Cys Thr Arg Ser Val Pro Lys Glu Pro Val
165                      170                      175

Trp Tyr Ala Asp Tyr Val Ala Ser Val Phe Ala Glu His Gly Phe Asp
180                      185                      190

Ala Pro Glu Pro Ile Asp Asn Ser Val Gly Ser Trp Leu Leu Phe Gly
195                      200                      205

His Val Gly Ile Ile Arg Val Thr Phe Val Ile Ala Val Ala Ala Gly
210                      215                      220

Val Tyr Ala Met Ser Arg Ala Ala Met Met Arg Gln Leu Glu Thr Gln
225                      230                      235                      240

Asn Val Ala Val Asp Thr Thr Asp Ile Asn Gln His Thr Asn Asp Ala
245                      250                      255

Arg Leu Ala Ile Pro Gln Glu Ile Val Arg Asp Leu Ser Leu Phe Pro
260                      265                      270

Asp Val Gly Ala His Phe Thr Ser Pro Ala Leu Lys His Asp Phe Pro
275                      280                      285

Cys Asp Ala Val Glu
290

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<210> 55
<211> 1057
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(1057)
<223> FRXA01085

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gcgactgat cggacctttg atcagctgcg aaaacagcgg gtg acg gat aaa gcc 115
                               Val Thr Asp Lys Ala
                               1                      5

cgc aac cgt gac gta cac aat gag cag caa ctg gca cgc ggt gaa atc 163
Arg Asn Arg Asp Val His Asn Glu Gln Gln Leu Ala Arg Gly Glu Ile
                               10                      15                      20

gga gaa atg cgc tca ccg atg tgg gtt gag gtg ggt gct gcg att ctg 211
Gly Glu Met Arg Ser Pro Met Trp Val Glu Val Gly Ala Ala Ile Leu
                               25                      30                      35

ggc gtg ttt gtc ctg gtt gtg atg tgg ctg gcc tgg ggc ggt atc ggg 259
Gly Val Phe Val Leu Val Val Met Trp Leu Ala Trp Gly Gly Ile Gly

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	40	45	50	
	ctg ctg atc cag acc atg atg aat act ggc tca cct aat gac aaa gag			307
	Leu Leu Ile Gln Thr Met Met Asn Thr Gly Ser Pro Asn Asp Lys Glu			
	55	60	65	
	ctt ttt gat gag ctt ggt gtg aga ccc tat tat gtt gct gtc gaa cag			355
	Leu Phe Asp Glu Leu Gly Val Arg Pro Tyr Tyr Val Ala Val Glu Gln			
	70	75	80	85
	caa atc ggc acc agt agt gct cac acc acg tgc tac caa cag ctt gat			403
	Gln Ile Gly Thr Ser Ser Ala His Thr Thr Cys Tyr Gln Pro Leu Asp			
	90	95	100	
	gaa ttt ggc aat aat ttt ggc gac tgt acg cgt agc gtg cct aaa gag			451
	Glu Phe Gly Asn Asn Phe Gly Asp Cys Thr Arg Ser Val Pro Lys Glu			
	105	110	115	
	cca gtg tgg tac gcc gat tat gta gct agt gtg ttc gca gaa cat ggc			499
	Pro Val Trp Tyr Ala Asp Tyr Val Ala Ser Val Phe Ala Glu His Gly			
	120	125	130	
	ttt gat gca cca gaa cct att gat aat tgc gtg ggt agc tgg ctg tta			547
	Phe Asp Ala Pro Glu Pro Ile Asp Asn Ser Val Gly Ser Trp Leu Leu			
	135	140	145	
	ttt ggt cat gtg ggc att att cgg gtg acg ttt gtg att gcg gtt gca			595
	Phe Gly His Val Gly Ile Ile Arg Val Thr Phe Val Ile Ala Val Ala			
	150	155	160	165
	gcg ggt gtg tat gcg atg tca cgc gca gca atg atg cgt cag cta gaa			643
	Ala Gly Val Tyr Ala Met Ser Arg Ala Ala Met Met Arg Gln Leu Glu			
	170	175	180	
	aca caa aac gtc gct gtg gac acc acc gat att aac cag cac acc aat			691
	Thr Gln Asn Val Ala Val Asp Thr Thr Asp Ile Asn Gln His Thr Asn			
	185	190	195	
	gac gca cgt ttg gcg att ccg cag gag att gtg cgc gat ttg agt ctg			739
	Asp Ala Arg Leu Ala Ile Pro Gln Glu Ile Val Arg Asp Leu Ser Leu			
	200	205	210	
	ttc ccc gat gtc ggt gca cac tca cca gtc cag ccc tca agc atg att			787
	Phe Pro Asp Val Gly Ala His Ser Pro Val Gln Pro Ser Ser Met Ile			
	215	220	225	
	tcc cat gtg atg ctg tgc aat aag ggc ttg aaa aag gtg gat gta acg			835
	Ser His Val Met Leu Ser Asn Lys Gly Leu Lys Lys Val Asp Val Thr			
	230	235	240	245
	cag ttt gca cag gag aca att atc gac aat gac act ggt gaa att gtc			883
	Gln Phe Ala Gln Thr Thr Ile Ile Asp Asn Asp Thr Gly Glu Ile Val			
	250	255	260	
	tct gaa aag ggt gaa gtg ctc tat gac ggt gca gga caa cag atc aca			931
	Ser Glu Lys Gly Glu Val Leu Tyr Asp Gly Ala Gly Gln Pro Ile Thr			
	265	270	275	
	aag agc ttg ccg atg att gac aac gaa ttt agc cat gcg att ttt gac			979
	Lys Ser Leu Pro Met Ile Asp Asn Glu Phe Ser His Ala Ile Phe Asp			
	280	285	290	

aaa tca gat gtc cgg aat ctt ccc gag ctg cga cgg ttc ttt aat cca 1027
 Lys Ser Asp Val Pro Asn Leu Pro Glu Leu Arg Arg Phe Phe Asn Pro
 295 300 305

gca aag att gag tgg aat cct ggt ggt agt 1057
 Ala Lys Ile Glu Trp Asn Pro Gly Gly Ser
 310 315

<210> 56

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 56

Val Thr Asp Lys Ala Arg Asn Arg Asp Val His Asn Glu Gln Gln Leu
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Ala Arg Gly Glu Ile Gly Glu Met Arg Ser Pro Met Trp Val Glu Val
 20 25 30

Gly Ala Ala Ile Leu Gly Val Phe Val Leu Val Val Met Trp Leu Ala
 35 40 45

Trp Gly Gly Ile Gly Leu Leu Ile Gln Thr Met Met Asn Thr Gly Ser
 50 55 60

Pro Asn Asp Lys Glu Leu Phe Asp Glu Leu Gly Val Arg Pro Tyr Tyr
 65 70 75 80

Val Ala Val Glu Gln Ile Gly Thr Ser Ser Ala His Thr Thr Cys
 85 90 95

Tyr Gln Pro Leu Asp Glu Phe Gly Asn Asn Phe Gly Asp Cys Thr Arg
 100 105 110

Ser Val Pro Lys Glu Pro Val Trp Tyr Ala Asp Tyr Val Ala Ser Val
 115 120 125

Phe Ala Glu His Gly Phe Asp Ala Pro Glu Pro Ile Asp Asn Ser Val
 130 135 140

Gly Ser Trp Leu Leu Phe Gly His Val Gly Ile Ile Arg Val Thr Phe
 145 150 155 160

Val Ile Ala Val Ala Ala Gly Val Tyr Ala Met Ser Arg Ala Ala Met
 165 170 175

Met Arg Gln Leu Glu Thr Gln Asn Val Ala Val Asp Thr Thr Asp Ile
 180 185 190

Asn Gln His Thr Asn Asp Ala Arg Leu Ala Ile Pro Gln Glu Ile Val
 195 200 205

Arg Asp Leu Ser Leu Phe Pro Asp Val Gly Ala His Ser Pro Val Gln
 210 215 220

Pro Ser Ser Met Ile Ser His Val Met Leu Ser Asn Lys Gly Leu Lys
 225 230 235 240

Lys Val Asp Val Thr Gln Phe Ala Gln Glu Thr Ile Ile Asp Asn Asp
 245 250 255
 Thr Gly Glu Ile Val Ser Glu Lys Gly Glu Val Leu Tyr Asp Gly Ala
 260 265 270
 Gly Gln Pro Ile Thr Lys Ser Leu Pro Met Ile Asp Asn Glu Phe Ser
 275 280 285
 His Ala Ile Phe Asp Lys Ser Asp Val Pro Asn Leu Pro Glu Leu Arg
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 Arg Phe Phe Asn Pro Ala Lys Ile Glu Trp Asn Pro Gly Gly Ser
 305 310 315

<210> 57

<211> 1824

<212> DNA

<213> *Corynebacterium glutamicum*

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<221> CDS

<222> (101)..(1801)

<223> RXN00022

<400> 57

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 Met Ser Ala Pro Thr
 1 5
 atc tac ccc ggc acc aaa aca tct att gat cgg atc acc atg gat gac 163
 Ile Tyr Pro Gly Thr Lys Thr Ser Ile Asp Pro Ile Thr Met Asp Asp
 10 15 20
 gct cgc atc atc ttt ttc gat att gag tcg etc cac aat att ttc acg 211
 Ala Arg Ile Ile Phe Phe Asp Ile Glu Ser Leu His Asn Ile Phe Thr
 25 30 35
 gta gca acc tac gat tct ctg tcc cac cac gtc gat gtc ttt tac ctg 259
 Val Ala Thr Tyr Asp Ser Leu Ser His His Val Asp Val Phe Tyr Leu
 40 45 50
 etc gat cac aca acc agc cct cag atc acg gtg ctg ccg cac tca atg 307
 Leu Asp His Thr Thr Ser Pro Gln Ile Thr Val Leu Pro His Ser Met
 55 60 65
 gat tat ttc gat caa acg cgc agc gat gct gtt atg gct gcc atc att 355
 Asp Tyr Phe Asp Gln Thr Arg Ser Asp Ala Val Met Ala Ala Ile Ile
 70 75 80 85
 gag caa aac cct cgc ttc gca gaa att aaa ggc tca ccc att aca acc 403
 Glu Gln Asn Pro Ala Phe Ala Glu Ile Lys Gly Ser Pro Ile Thr Thr
 90 95 100
 gca gat gta gcc etc cac aat etc ggt gac acc aac gcc aac cga cgc 451
 Ala Asp Val Ala Leu His Asn Leu Gly Asp Thr Asn Ala Asn Arg Arg
 105 110 115

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Trp	Gln	Ser	Asn	Val	Leu	Leu	Ala	Arg	Leu	Leu	Gly	Gly	Ile	Ser	Val		
120																125	
cgc	gga	gag	gta	cct	gag	cac	cag	agc	cac	aac	cat	ctc	gcc	aag	cag	547	
Arg	Gly	Glu	Val	Pro	Glu	His	Gln	Ser	His	Asn	His	Leu	Ala	Lys	Gln		
135																140	145
ttt	gcc	gag	gca	acc	ttg	gtc	acc	agg	gac	ttc	gat	gtg	aat	tat	gat	595	
Phe	Ala	Glu	Ala	Thr	Leu	Val	Thr	Arg	Asp	Phe	Asp	Val	Asn	Tyr	Asp		
150																155	160
cca	aca	agc	gct	cac	cct	ttt	act	gct	ggc	ttc	aac	tcg	atc	aac	tat	643	
Pro	Thr	Ser	Ala	His	Pro	Phe	Thr	Ala	Gly	Phe	Asn	Ser	Ile	Asn	Tyr		
170																175	180
gac	acc	acc	ttg	ctc	agc	ctg	tac	ttc	gca	atg	ttg	acc	tca	aat	atc	691	
Asp	Thr	Thr	Leu	Leu	Ser	Leu	Tyr	Phe	Ala	Met	Leu	Thr	Ser	Asn	Ile		
185																190	195
gga	agt	aca	ccg	acg	tat	ttc	ccg	gtg	atc	acc	gca	cag	gaa	ctt	cgt	739	
Gly	Ser	Thr	Pro	Thr	Tyr	Phe	Pro	Val	Ile	Thr	Ala	Gln	Glu	Leu	Arg		
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gcg	cat	aac	gac	aag	ctc	ttt	agc	cct	gag	ttc	atc	aaa	aac	atg	cca	787	
Ala	His	Asn	Asp	Lys	Leu	Phe	Ser	Pro	Glu	Phe	Ile	Lys	Asn	Met	Pro		
215																220	225
aag	tat	ctc	tggt	gat	cgc	gac	agc	ggt	gct	gga	ctc	aga	gct	gca	tcg	835	
Leu	Tyr	Leu	Trp	Asp	Arg	Asp	Ser	Gly	Ala	Gly	Leu	Arg	Ala	Ala	Ser		
230																235	240
ggt	ttc	cgc	aac	gcc	atg	ctc	aaa	tcg	ggt	cgc	cac	att	gat	att	caa	883	
Gly	Phe	Arg	Asn	Ala	Met	Leu	Lys	Ser	Gly	Arg	His	Ile	Asp	Ile	Gln		
250																255	260
cgc	ctc	aat	gaa	aaa	cag	ctc	ttt	gtt	gga	ctc	aag	cgc	ctg	ctt	ggt	931	
Arg	Leu	Asn	Glu	Lys	Gln	Leu	Phe	Val	Gly	Leu	Lys	Arg	Leu	Leu	Gly		
265																270	275
ctc	ctc	ggt	cac	cag	att	ctc	gaa	tct	gat	cgt	ctc	tct	ggt	gat	gat	979	
Leu	Leu	Gly	His	Gln	Ile	Leu	Glu	Ser	Asp	Arg	Leu	Ser	Gly	Asp	Asp		
280																285	290
gcc	cat	gtt	gat	act	aac	gag	gat	gta	ctt	gat	ctc	att	gcc	tac	aac	1027	
Ala	His	Val	Asp	Thr	Asn	Glu	Asp	Val	Leu	Asp	Leu	Ile	Ala	Tyr	Asn		
295																300	305
gtc	tca	gac	gtg	gtg	ggc	acc	aga	ctg	ctc	gct	gag	gac	ccg	gtg	tac	1075	
Val	Ser	Asp	Val	Val	Gly	His	Arg	Leu	Leu	Ala	Glu	Asp	Pro	Val	Tyr		
310																315	320
tcc	ggc	tct	ttc	gat	ctg	cgg	gca	ggt	cta	ctg	agc	acc	tac	cca	gag	1123	
Ser	Gly	Ser	Phe	Asp	Leu	Arg	Ala	Gly	Leu	Leu	Ser	Thr	Tyr	Pro	Glu		
330																335	340
act	gtt	ttt	gat	cat	gat	ggt	act	ttc	cgt	cag	cca	tcc	acg	cag	atg	1171	
Thr	Val	Phe	Asp	His	Asp	Gly	Thr	Phe	Arg	Gln	Pro	Ser	Thr	Gln	Met		
345																350	355
cgt	aaa	gat	cgc	cta	acg	att	aat	acc	tca	tca	gct	cag	ttc	gca	cgc	1219	
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Arg	Lys	Asp	Arg	Leu	Thr	Ile	Asn	Thr	Ser	Ser	Ala	Gln	Phe	Ala	Ala		
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cgt	att	ttg	gcg	cca	tat	cgc	cca	ctc	cgc	gat	gtc	cct	gat	gcg	att	1267	
Arg	Ile	Leu	Ala	Pro	Tyr	Arg	Pro	Leu	Arg	Asp	Val	Pro	Asp	Ala	Ile		
	375					380					385						
ggc	gac	atg	ccg	gtg	gtg	tct	tac	ttg	tac	ccg	gat	gca	gca	gtc	gcc	1315	
Gly	Asp	Met	Pro	Val	Val	Ser	Tyr	Leu	Tyr	Pro	Asp	Ala	Ala	Val	Ala		
	390				395					400				405			
gaa	gca	aca	ggg	caa	aaa	caa	gtc	aac	gtg	ctt	gat	gag	tca	aag	aag	1363	
Glu	Ala	Thr	Gly	Gln	Lys	Gln	Val	Asn	Val	Leu	Asp	Glu	Ser	Lys	Lys		
			410					415						420			
ttc	ttc	tat	gac	aac	atc	acc	gac	ccg	gaa	gca	cgt	gct	gcc	ttt	gat	1411	
Phe	Phe	Tyr	Asp	Asn	Ile	Thr	Asp	Pro	Glu	Ala	Arg	Ala	Ala	Phe	Asp		
			425					430						435			
gag	gtc	ttt	gct	ttt	tac	gct	gat	att	gag	ggg	cgc	aac	ttc	aac	agt	1459	
Glu	Val	Phe	Ala	Phe	Tyr	Ala	Asp	Ile	Glu	Gly	Arg	Asn	Phe	Asn	Ser		
		440				445						450					
cac	aat	gag	gct	att	gat	acc	cag	att	aac	caa	tta	cgt	gct	tat	ctc	1507	
His	Asn	Glu	Ala	Ile	Asp	Thr	Gln	Ile	Asn	Gln	Leu	Arg	Ala	Tyr	Leu		
		455				460					465						
aac	cag	gtt	gtc	gca	ttc	gat	gca	gct	ggg	tat	gcg	ctc	tat	gat	gta	1555	
Asn	Gln	Val	Val	Ala	Phe	Asp	Ala	Ala	Gly	Tyr	Ala	Leu	Tyr	Asp	Val		
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cgt	aca	cgt	ttt	gag	cag	atc	ttc	ccc	aag	gat	cgc	agc	tac	atc	aac	1603	
Arg	Thr	Arg	Phe	Glu	Gln	Ile	Phe	Pro	Lys	Asp	Arg	Ser	Tyr	Ile	Asn		
			490					495						500			
gat	gct	acg	gat	atg	acc	cct	cgc	gca	gta	tcg	agc	ttt	gac	gat	ctg	1651	
Asp	Ala	Thr	Asp	Met	Thr	Pro	Arg	Ala	Val	Ser	Ser	Phe	Asp	Asp	Leu		
			505					510					515				
gtt	gca	ctc	tgt	gat	gat	att	cgc	ggg	gta	ctt	gat	cga	ggg	tta	gag	1699	
Val	Ala	Leu	Cys	Asp	Asp	Ile	Arg	Gly	Val	Leu	Asp	Arg	Gly	Leu	Glu		
		520					525						530				
atc	tca	tct	ccg	aat	cat	cat	gag	atg	gtg	gat	gct	atg	cgc	aag	cag	1747	
Ile	Ser	Ser	Pro	Asn	His	His	Glu	Met	Val	Asp	Ala	Met	Arg	Lys	Gln		
		535				540				545							
ctg	cac	tat	att	cag	gca	ttt	tac	cgt	gcc	tggt	gac	cca	tca	acg	ccg	1795	
Leu	His	Tyr	Ile	Gln	Ala	Phe	Tyr	Arg	Ala	Trp	Asp	Pro	Ser	Thr	Pro		
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Leu	Gln																

<210> 58

<211> 567

<212> PRT

<213> Corynebacterium glutamicum

<400> 58

Met Ser Ala Pro Thr Ile Tyr Pro Gly Thr Lys Thr Ser Ile Asp Pro
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 20 25 30

His Asn Ile Phe Thr Val Ala Thr Tyr Asp Ser Leu Ser His His Val
 35 40 45

Asp Val Phe Tyr Leu Leu Asp His Thr Thr Ser Pro Gln Ile Thr Val
 50 55 60

Leu Pro His Ser Met Asp Tyr Phe Asp Gln Thr Arg Ser Asp Ala Val
 65 70 75 80

Met Ala Ala Ile Ile Glu Gln Asn Pro Ala Phe Ala Glu Ile Lys Gly
 85 90 95

Ser Pro Ile Thr Thr Ala Asp Val Ala Leu His Asn Leu Gly Asp Thr
 100 105 110

Asn Ala Asn Arg Arg Trp Gln Ser Asn Val Leu Leu Ala Arg Leu Leu
 115 120 125

Gly Gly Ile Ser Val Arg Gly Glu Val Pro Glu His Gln Ser His Asn
 130 135 140

His Leu Ala Lys Gln Phe Ala Glu Ala Thr Leu Val Thr Arg Asp Phe
 145 150 155 160

Asp Val Asn Tyr Asp Pro Thr Ser Ala His Pro Phe Thr Ala Gly Phe
 165 170 175

Asn Ser Ile Asn Tyr Asp Thr Thr Leu Leu Ser Leu Tyr Phe Ala Met
 180 185 190

Leu Thr Ser Asn Ile Gly Ser Thr Pro Thr Tyr Phe Pro Val Ile Thr
 195 200 205

Ala Gln Glu Leu Arg Ala His Asn Asp Lys Leu Phe Ser Pro Glu Phe
 210 215 220

Ile Lys Asn Met Pro Lys Tyr Leu Trp Asp Arg Asp Ser Gly Ala Gly
 225 230 235 240

Leu Arg Ala Ala Ser Gly Phe Arg Asn Ala Met Leu Lys Ser Gly Arg
 245 250 255

His Ile Asp Ile Gln Arg Leu Asn Glu Lys Gln Leu Phe Val Gly Leu
 260 265 270

Lys Arg Leu Leu Gly Leu Leu Gly His Gln Ile Leu Glu Ser Asp Arg
 275 280 285

Leu Ser Gly Asp Asp Ala His Val Asp Thr Asn Glu Asp Val Leu Asp
 290 295 300

Leu Ile Ala Tyr Asn Val Ser Asp Val Val Gly Thr Arg Leu Leu Ala
 305 310 315 320

THE UNIVERSITY OF CHICAGO

<211> 835

<213> Cor

<221> CDS

<222> (101) .. (835)

<223> FRXA00022

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				Met	Ser	Ala	Pro	Thr	5							
atc	tac	ccc	ggc	acc	aaa	aca	tct	att	gat	ccg	atc	acc	atg	gat	gac	163
Ile	Tyr	Pro	Gly	Thr	Lys	Thr	Ser	Ile	Asp	Pro	Ile	Thr	Met	Asp	Asp	20
gct	cgc	atc	atc	ttt	ttc	gat	att	gag	tcg	ctc	cac	aat	att	ttc	acg	211
Ala	Arg	Ile	Ile	Phe	Phe	Asp	Ile	Glu	Ser	Leu	His	Asn	Ile	Phe	Thr	35
gta	gca	acc	tac	gat	tct	ctg	tcc	cac	cac	gtc	gat	gtc	ttt	tac	ctg	259
Val	Ala	Thr	Tyr	Asp	Ser	Leu	Ser	His	His	Val	Asp	Val	Phe	Tyr	Leu	40
ctc	gat	cac	aca	acc	agc	cct	cag	atc	acg	gtg	ctg	ccg	cac	tca	atg	307
Leu	Asp	His	Thr	Thr	Ser	Pro	Gln	Ile	Thr	Val	Leu	Pro	His	Ser	Met	60
gat	tat	ttc	gat	caa	acg	cgc	agc	gat	gct	gtt	atg	gct	gcc	atc	att	355
Asp	Tyr	Phe	Asp	Gln	Thr	Arg	Ser	Asp	Ala	Val	Met	Ala	Ala	Ile	Ile	75
gag	caa	aac	cct	gcg	ttc	gca	gaa	att	aaa	ggc	tca	ccc	att	aca	acc	403
Glu	Gln	Asn	Pro	Ala	Phe	Ala	Glu	Ile	Lys	Gly	Ser	Pro	Ile	Thr	Thr	90
gca	gat	gta	gcc	ctc	cac	aat	ctc	ggt	gac	acc	aac	gcc	aac	cga	cgc	451
Ala	Asp	Val	Ala	Leu	His	Asn	Leu	Gly	Asp	Thr	Asn	Ala	Asn	Arg	Arg	105
tgg	cag	tct	aac	gtg	ctg	ctt	gcc	cgg	cta	ctc	ggg	ggt	att	agt	gtg	499
Trp	Gln	Ser	Asn	Val	Leu	Leu	Ala	Arg	Leu	Leu	Gly	Gly	Ile	Ser	Val	120
cgc	gga	gag	gta	cct	gag	cac	cag	agc	cac	aac	cat	ctc	gcc	aag	cag	547
Arg	Gly	Glu	Val	Pro	Glu	His	Gln	Ser	His	Asn	His	Leu	Ala	Lys	Gln	135
ttt	gcc	gag	gca	acc	ttg	gtc	acc	agg	gac	ttc	gat	gtg	aat	tat	gat	595
Phe	Ala	Glu	Ala	Thr	Leu	Val	Thr	Arg	Asp	Phe	Asp	Val	Asn	Tyr	Asp	150
cca	aca	agc	gct	cac	cct	ttt	act	gct	ggc	ttc	aac	tcg	atc	aac	tat	643
Pro	Thr	Ser	Ala	His	Pro	Phe	Thr	Ala	Gly	Phe	Asn	Ser	Ile	Asn	Tyr	170
gac	acc	acc	ttg	ctc	agc	ctg	tac	ttc	gca	atg	ttg	acc	tca	aat	atc	691
Asp	Thr	Thr	Leu	Leu	Ser	Leu	Tyr	Phe	Ala	Met	Leu	Thr	Ser	Asn	Ile	185
gga	agt	aca	ccg	acg	tat	ttc	ccg	gtg	atc	acc	gca	caa	gaa	ctt	cgt	739
Gly	Ser	Thr	Pro	Thr	Tyr	Phe	Pro	Val	Ile	Thr	Ala	Gln	Glu	Leu	Arg	200
gcg	cat	aac	gac	aag	ctc	ttt	agc	cct	gag	ttc	atc	aaa	aac	atg	cca	787
Ala	His	Asn	Asp	Lys	Leu	Phe	Ser	Pro	Glu	Phe	Ile	Lys	Asn	Met	Pro	215

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<210> 60

<211> 245

<212> PRT

<213> *Corynebacterium glutamicum*

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Met Ser Ala Pro Thr Ile Tyr Pro Gly Thr Lys Thr Ser Ile Asp Pro
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Ile Thr Met Asp Asp Ala Arg Ile Ile Phe Phe Asp Ile Glu Ser Leu
 20 25 30

His Asn Ile Phe Thr Val Ala Thr Tyr Asp Ser Leu Ser His His Val
 35 40 45

Asp Val Phe Tyr Leu Leu Asp His Thr Thr Ser Pro Gln Ile Thr Val
 50 55 60

Leu Pro His Ser Met Asp Tyr Phe Asp Gln Thr Arg Ser Asp Ala Val
 65 70 75 80

Met Ala Ala Ile Ile Glu Gln Asn Pro Ala Phe Ala Glu Ile Lys Gly
 85 90 95

Ser Pro Ile Thr Thr Ala Asp Val Ala Leu His Asn Leu Gly Asp Thr
 100 105 110

Asn Ala Asn Arg Arg Trp Gln Ser Asn Val Leu Leu Ala Arg Leu Leu
 115 120 125

Gly Gly Ile Ser Val Arg Gly Glu Val Pro Glu His Gln Ser His Asn
 130 135 140

His Leu Ala Lys Gln Phe Ala Glu Ala Thr Leu Val Thr Arg Asp Phe
 145 150 155 160

Asp Val Asn Tyr Asp Pro Thr Ser Ala His Pro Phe Thr Ala Gly Phe
 165 170 175

Asn Ser Ile Asn Tyr Asp Thr Thr Leu Leu Ser Leu Tyr Phe Ala Met
 180 185 190

Leu Thr Ser Asn Ile Gly Ser Thr Pro Thr Tyr Phe Pro Val Ile Thr
 195 200 205

Ala Gln Glu Leu Arg Ala His Asn Asp Lys Leu Phe Ser Pro Glu Phe
 210 215 220

Ile Lys Asn Met Pro Lys Tyr Phe Trp Asp Arg Asp Ser Gly Ala Gly
 225 230 235 240

Leu Arg Ala Ala Ser
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<210> 61

<211> 939

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(939)

<223> FRXA01921

<400> 61

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His	Ile	Asp	Ile	Gln	Arg	Leu	Asn	Glu	Lys	Gln	Leu	Phe	Val	Gly	Leu	
1				5					10				15			

aag	cg	ctg	ctt	ggt	ctc	ctc	ggt	cac	cag	att	ctc	gaa	tct	gat	cgt	96
Lys	Arg	Leu	Leu	Gly	Leu	Leu	Gly	His	Gln	Ile	Leu	Glu	Ser	Asp	Arg	
		20					25					30				

ctc	tct	ggt	gat	gat	gcc	cat	gtt	gat	act	aac	gag	gat	gta	ctt	gat	144
Leu	Ser	Gly	Asp	Asp	Ala	His	Val	Asp	Thr	Asn	Glu	Asp	Val	Leu	Asp	
		35					40					45				

ctc	att	gcc	tac	aac	gtc	tca	gac	gtg	gtg	ggc	acc	aga	ctg	ctc	gct	192
Leu	Ile	Ala	Tyr	Asn	Val	Ser	Asp	Val	Val	Gly	Thr	Arg	Leu	Leu	Ala	
	50					55				60						

gag	gac	ccg	gtg	tac	tcc	ggc	tct	ttc	gat	ctg	cgg	gca	ggt	cta	ctg	240
Glu	Asp	Pro	Val	Tyr	Ser	Gly	Ser	Phe	Asp	Leu	Arg	Ala	Gly	Leu	Leu	
65					70				75					80		

agc	acc	tac	cca	gag	act	gtt	ttt	gat	cat	gat	ggt	act	ttc	cgt	cag	288
Ser	Thr	Tyr	Pro	Glu	Thr	Val	Phe	Asp	His	Asp	Gly	Thr	Phe	Arg	Gln	
			85						90				95			

cca	tcc	acg	cag	atg	cgt	aaa	gat	cg	cta	acg	att	aat	acc	tca	tca	336
Pro	Ser	Thr	Gln	Met	Arg	Lys	Asp	Arg	Leu	Thr	Ile	Asn	Thr	Ser	Ser	
			100					105					110			

gct	cag	ttc	gca	gcg	cgt	att	ttg	gcg	cca	tat	cgc	cca	ctc	cgc	gat	384
Ala	Gln	Phe	Ala	Ala	Arg	Ile	Leu	Ala	Pro	Tyr	Arg	Pro	Leu	Arg	Asp	
	115						120					125				

gtc	cct	gat	gcg	att	ggc	gac	atg	ccg	gtg	gtg	tct	tac	ttg	tac	ccg	432
Val	Pro	Asp	Ala	Ile	Gly	Asp	Met	Pro	Val	Val	Ser	Tyr	Leu	Tyr	Pro	
	130				135						140					

gat	gca	gca	gtc	gcc	gaa	gca	aca	ggt	caa	aaa	caa	gtc	aac	gtg	ctt	480
Asp	Ala	Ala	Val	Ala	Glu	Ala	Thr	Gly	Gln	Lys	Gln	Val	Asn	Val	Leu	
145				150					155					160		

gat	gag	tca	aag	aag	ttc	ttc	tat	gac	aac	atc	acc	gac	ccg	gaa	gca	528
Asp	Glu	Ser	Lys	Lys	Phe	Phe	Tyr	Asp	Asn	Ile	Thr	Asp	Pro	Glu	Ala	
			165						170					175		

cgt	gct	gcc	ttt	gat	gag	gtc	ttt	gct	ttt	tac	gct	gat	att	gag	ggt	576
Arg	Ala	Ala	Phe	Asp	Glu	Val	Phe	Ala	Phe	Tyr	Ala	Asp	Ile	Glu	Gly	
		180					185					190				

cgc	aac	ttc	aac	agt	cac	aat	gag	gct	att	gat	acc	cag	att	aac	caa	624
Arg	Asn	Phe	Asn	Ser	His	Asn	Glu	Ala	Ile	Asp	Thr	Gln	Ile	Asn	Gln	
	195					200						205				

tta cgt gct tat ctc aac cag gtt gtc gca ttc gat gca gct ggg tat 672
 Leu Arg Ala Tyr Leu Asn Gln Val Val Ala Phe Asp Ala Ala Gly Tyr
 210 215 220

gcg ctc tat gat gta cgt aca cgt ttt gag cag atc ttc ccc aag gat 720
 Ala Leu Tyr Asp Val Arg Thr Arg Phe Glu Gln Ile Phe Pro Lys Asp
 225 230 235 240

cgc agc tac atc aac gat gct acg gat atg acc cct cgc gca gta tcg 768
 Arg Ser Tyr Ile Asn Asp Ala Thr Asp Met Thr Pro Arg Ala Val Ser
 245 250 255

agc ttt gac gat ctg gtt gca ctc tgt gat gat att cgc ggt gta ctt 816
 Ser Phe Asp Asp Leu Val Ala Leu Cys Asp Asp Ile Arg Gly Val Leu
 260 265 270

gat cga ggt tta gag atc tca tct ccg aat cat cat gag atg gtg gat 864
 Asp Arg Gly Leu Glu Ile Ser Ser Pro Asn His His Glu Met Val Asp
 275 280 285

gct atg cgc aag cag ctg cac tat att cag gca ttt acc gtg cct ggg 912
 Ala Met Arg Lys Gln Leu His Tyr Ile Gln Ala Phe Thr Val Pro Gly
 290 295 300

acc cat caa cgc cgc ttc aat gac gct 939
 Thr His Gln Arg Arg Phe Asn Asp Ala
 305 310

<210> 62
 <211> 313
 <212> PRT
 <213> *Corynebacterium glutamicum*

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Lys Arg Leu Leu Gly Leu Leu Gly His Gln Ile Leu Glu Ser Asp Arg
 20 25 30

Leu Ser Gly Asp Asp Ala His Val Asp Thr Asn Glu Asp Val Leu Asp
 35 40 45

Leu Ile Ala Tyr Asn Val Ser Asp Val Val Gly Thr Arg Leu Leu Ala
 50 55 60

Glu Asp Pro Val Tyr Ser Gly Ser Phe Asp Leu Arg Ala Gly Leu Leu
 65 70 75 80

Ser Thr Tyr Pro Glu Thr Val Phe Asp His Asp Gly Thr Phe Arg Gln
 85 90 95

Pro Ser Thr Gln Met Arg Lys Asp Arg Leu Thr Ile Asn Thr Ser Ser
 100 105 110

Ala Gln Phe Ala Ala Arg Ile Leu Ala Pro Tyr Arg Pro Leu Arg Asp
 115 120 125

Val Pro Asp Ala Ile Gly Asp Met Pro Val Val Ser Tyr Leu Tyr Pro

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 Leu Ala Phe Leu Ala Gly Gly Ile Ala Phe Glu Ala Phe Gln Ile Ser
 40 45 50

 gga cta tcg gat act gtc cgt aca aca atc gcg gtt ttt atc att gcg 307
 Gly Leu Ser Asp Thr Val Arg Thr Thr Ile Ala Val Phe Ile Ile Ala
 55 60 65

 gtt ggc atg atc att gcc gct ggt gct gcg gtg agg tgg atg aat gtg 355
 Val Gly Met Ile Ile Ala Ala Gly Ala Ala Val Arg Trp Met Asn Val
 70 75 80 85

 gag cgt gca atg cgt aaa cag aag cca ctt ccc gta cct gcg att att 403
 Glu Arg Ala Met Arg Lys Gln Lys Pro Leu Pro Val Pro Ala Ile Ile
 90 95 100

 ccg ttt ctg tct att gcg gct ttg gtg gcc tct gcg gct gtc ttg gtt 451
 Pro Phe Leu Ser Ile Ala Ala Leu Val Ala Ser Ala Ala Val Leu Val
 105 110 115

 ctg att att gtt cag tagctatgcg cattcatgag gat 489
 Leu Ile Ile Val Gln
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<210> 64

<211> 122

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 64

Val Asp Glu Arg Ser Arg Phe Ala Arg Ser Val Phe Pro Asp Gly Glu
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 20 25 30

 Trp Thr Arg Thr Ser Leu Ala Phe Leu Ala Gly Gly Ile Ala Phe Glu
 35 40 45

 Ala Phe Gln Ile Ser Gly Leu Ser Asp Thr Val Arg Thr Thr Ile Ala
 50 55 60

 Val Phe Ile Ile Ala Val Gly Met Ile Ile Ala Ala Gly Ala Ala Val
 65 70 75 80

 Arg Trp Met Asn Val Glu Arg Ala Met Arg Lys Gln Lys Pro Leu Pro
 85 90 95

 Val Pro Ala Ile Ile Pro Phe Leu Ser Ile Ala Ala Leu Val Ala Ser
 100 105 110

 Ala Ala Val Leu Val Leu Ile Ile Val Gln
 115 120

<210> 65

<211> 489

<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (101)..(466)

<223> FRXA00027

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 Val Asp Glu Arg Ser
 1 5

cgg ttt gcg cgc agc gtt ttc ccg gac ggt gaa gaa cca gat cca cgt 163
 Arg Phe Ala Arg Ser Val Phe Pro Asp Gly Glu Glu Pro Asp Pro Arg
 10 15 20

ttc act ttg gcc aat gag cgc acg ttt cta gca tgg acg cgt acg tct 211
 Phe Thr Leu Ala Asn Glu Arg Thr Phe Leu Ala Trp Thr Arg Thr Ser
 25 30 35

ttg gcg ttt ctt gcc ggt ggt att gct ttt gag gcg ttc cag atc agt 259
 Leu Ala Phe Leu Ala Gly Gly Ile Ala Phe Glu Ala Phe Gln Ile Ser
 40 45 50

gga cta tcg gat act gtc cgt aca aca atc gcg gtt ttt atc att gcg 307
 Gly Leu Ser Asp Thr Val Arg Thr Thr Ile Ala Val Phe Ile Ile Ala
 55 60 65

gtt gcc atg atc att gcc gct ggt gct gcg gtg agg tgg atg aat gtg 355
 Val Gly Met Ile Ile Ala Ala Gly Ala Ala Val Arg Trp Met Asn Val
 70 75 80 85

gag cgt gca atg cgt aaa cag aag cca ctt ccc gta cct gcg att att 403
 Glu Arg Ala Met Arg Lys Gln Lys Pro Leu Pro Val Pro Ala Ile Ile
 90 95 100

ccg ttt ctg tct att gcg gct ttg gtg gcc tct gcg gct gtc ttg gtt 451
 Pro Phe Leu Ser Ile Ala Ala Leu Val Ala Ser Ala Ala Val Leu Val
 105 110 115

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 Leu Ile Ile Val Gln
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<210> 66

<211> 122

<212> PRT

<213> Corynebacterium glutamicum

<400> 66

Val Asp Glu Arg Ser Arg Phe Ala Arg Ser Val Phe Pro Asp Gly Glu
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Glu Pro Asp Pro Arg Phe Thr Leu Ala Asn Glu Arg Thr Phe Leu Ala
 20 25 30

Trp Thr Arg Thr Ser Leu Ala Phe Leu Ala Gly Gly Ile Ala Phe Glu
 35 40 45

Ala Phe Gln Ile Ser Gly Leu Ser Asp Thr Val Arg Thr Thr Ile Ala

66
122
PRT
Corynebacterium glutamicum
66
122
PRT
Corynebacterium glutamicum

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50              55              60
Val Phe Ile Ile Ala Val Gly Met Ile Ile Ala Ala Gly Ala Ala Val
65              70              75              80
Arg Trp Met Asn Val Glu Arg Ala Met Arg Lys Gln Lys Pro Leu Pro
85              90              95
Val Pro Ala Ile Ile Pro Phe Leu Ser Ile Ala Ala Leu Val Ala Ser
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Ala Ala Val Leu Val Leu Ile Ile Val Gln
115             120

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<210> 67
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<212> DNA
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<222> (101)..(2047)
<223> RXN00028

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Met Thr Leu Thr Ala
1 5
tct tcc ttg gag gcc ggg aaa atg tct ttt agt ggc ggg tat atc gtg 163
Ser Ser Leu Glu Ala Gly Lys Met Ser Phe Ser Gly Gly Tyr Ile Val
10 15 20
ggc gag acg atg atc ttc ctc gtc gat ccc gat gaa gtc gag ata cga 211
Gly Glu Thr Met Ile Phe Leu Val Asp Pro Asp Glu Val Glu Ile Arg
25 30 35
cgc agc cct aac agc ctc cac gtc ctg cgt aac ggt agc gat att ctg 259
Arg Ser Pro Asn Ser Leu His Val Leu Arg Asn Gly Ser Asp Ile Leu
40 45 50
cgc cgc aac gag cat cat tgc tgg gta ttt gag aat ttc aat aaa ccc 307
Arg Arg Asn Glu His His Cys Trp Val Phe Glu Asn Phe Asn Lys Pro
55 60 65
att gac cca cct gtt cga ttg ggt cct cgg gat atc atc tgc ccg agc 355
Ile Asp Pro Pro Val Arg Leu Gly Pro Arg Asp Ile Ile Cys Pro Ser
70 75 80 85
gcc ttg gcc tgg gtt ctt caa cag cat tcc atc tcc cgg tcc tta tcc 403
Ala Leu Ala Trp Val Leu Gln Gln His Ser Ile Ser Arg Ser Leu Ser
90 95 100
cac cac ctt cac cgc gat aag atc act cgc gga gag att gct gga cgc 451
His His Leu His Ala Asp Lys Ile Thr Ala Gly Glu Ile Ala Gly Arg
105 110 115
ccc acc tgg atc ctc cgt gag gaa cct act tca gga ggg cag gac cca 499

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Pro	Thr	Trp	Ile	Leu	Arg	Glu	Glu	Pro	Thr	Ser	Gly	Gly	Gln	Asp	Pro	
		120					125					130				
agt	cga	ttg	gtc	agt	ctt	gaa	atc	gac	cag	gaa	cac	ggg	gtc	atc	ctt	547
Ser	Arg	Leu	Val	Ser	Leu	Glu	Ile	Asp	Gln	Glu	His	Gly	Val	Ile	Leu	
		135				140					145					
gca	gtg	gag	act	gga	caa	gaa	cga	ctc	gaa	gcc	acg	gag	att	tct	ttt	595
Ala	Val	Glu	Thr	Gly	Gln	Glu	Arg	Leu	Glu	Ala	Thr	Glu	Ile	Ser	Phe	
		150			155					160					165	
cct	gac	act	ctt	cct	aat	cct	tcc	tgg	gac	gga	gcc	tgg	gaa	cca	ttc	643
Pro	Asp	Thr	Leu	Pro	Asn	Pro	Ser	Trp	Asp	Gly	Ala	Trp	Glu	Pro	Phe	
				170					175					180		
cat	tat	cca	gat	tgg	aca	cca	cac	act	gcc	cct	gat	gtt	gct	gaa	ata	691
His	Tyr	Pro	Asp	Ser	Thr	Pro	His	Thr	Ala	Pro	Asp	Val	Ala	Glu	Ile	
			185					190					195			
ccc	ggg	tac	att	cag	tca	ctg	cgg	cgg	cag	tct	gaa	gat	cct	cgc	aga	739
Pro	Gly	Tyr	Ile	Gln	Ser	Leu	Pro	Pro	Gln	Ser	Glu	Asp	Pro	Arg	Arg	
		200					205					210				
cta	cga	gtc	ttc	gtc	aat	gag	ata	gca	ctc	gaa	ggg	gat	ttc	cct	gac	787
Leu	Arg	Val	Phe	Val	Asn	Glu	Ile	Ala	Leu	Glu	Gly	Asp	Phe	Pro	Asp	
		215				220					225					
tac	cgt	caa	gga	caa	tct	gtg	cga	ctt	act	ttg	gga	att	agc	tcc	tcc	835
Tyr	Arg	Gln	Gly	Gln	Ser	Val	Arg	Leu	Thr	Leu	Gly	Ile	Ser	Ser	Ser	
		230			235					240				245		
cct	gtg	cca	ctc	gaa	gga	atg	aca	acc	aga	cgc	cgg	ggc	cgg	gta	cgc	883
Pro	Val	Pro	Leu	Glu	Gly	Met	Thr	Thr	Arg	Arg	Arg	Gly	Arg	Val	Arg	
				250				255						260		
aac	ctt	ggg	gaa	gaa	gct	agt	cca	ggc	gat	gac	ggg	atg	ccc	cag	tgg	931
Asn	Leu	Gly	Glu	Glu	Ala	Ser	Pro	Gly	Asp	Asp	Gly	Met	Pro	Gln	Trp	
			265				270						275			
cca	atc	ctg	ctc	act	ggg	gat	ggg	tgg	acg	gcg	ctg	gcc	tac	act	ccc	979
Pro	Ile	Leu	Leu	Thr	Gly	Asp	Gly	Trp	Thr	Ala	Leu	Ala	Tyr	Thr	Pro	
		280				285						290				
atc	cca	aaa	cgt	gga	gat	gca	gag	atc	cag	ggg	tgg	ttt	tat	tat	tcc	1027
Ile	Pro	Lys	Arg	Gly	Asp	Ala	Glu	Ile	Gln	Gly	Trp	Phe	Tyr	Tyr	Ser	
		295				300					305					
gcc	tac	gga	att	gtt	gat	gtt	ccc	aca	gat	cta	cgg	gta	gag	cgt	att	1075
Ala	Tyr	Gly	Ile	Val	Asp	Val	Pro	Thr	Asp	Leu	Arg	Val	Glu	Arg	Ile	
		310			315					320				325		
ttc	gct	ggg	atc	ggc	aca	agt	ggc	acc	aac	gag	cgt	ttg	tgg	cag	gag	1123
Phe	Ala	Gly	Ile	Gly	Thr	Ser	Gly	Thr	Asn	Glu	Arg	Leu	Trp	Gln	Glu	
				330				335						340		
ata	gac	aat	act	tct	tgg	gct	tat	cac	tgg	gaa	gat	tgg	tgg	atc	cgc	1171
Ile	Asp	Asn	Thr	Ser	Ser	Ala	Tyr	His	Ser	Glu	Asp	Trp	Trp	Ile	Arg	
			345				350						355			
gat	gtc	gtt	tta	gac	gtc	acg	ttg	gat	gga	gct	gtt	cgg	cct	cgg	ctt	1219
Asp	Val	Val	Leu	Asp	Val	Thr	Leu	Asp	Gly	Ala	Val	Pro	Pro	Pro	Leu	

360	365	370	
aga cgt gac gtc ttc act gct gtc gat cct att gtg gcg ggt gac aaa Arg Arg Asp Val Phe Thr Ala Val Asp Pro Ile Val Ala Gly Asp Lys 375 380 385			1267
ttg tgg ctg tgt gac gtg cac ttt ccg gta gcc cgc tgc tgg gag acc Leu Trp Leu Cys Asp Val His Phe Pro Val Ala Arg Cys Trp Glu Thr 390 395 400 405			1315
acg acc ggc cga tac ttg ggg cag act tta gtc cca gca cca ctg cga Thr Thr Gly Arg Tyr Leu Leu Gly Gln Thr Leu Val Pro Ala Pro Leu Arg 410 415 420			1363
gat cga tcg tac gtc ctt gag ctg cac agc gac caa caa tta gga gcc Asp Arg Ser Tyr Val Leu Glu Leu His Ser Asp Gln Gln Leu Gly Ala 425 430 435			1411
gta gcg gca agt ggg aag agt ggt tgg att ctc aca cct ggt caa gca Val Ala Ala Ser Gly Lys Ser Gly Trp Ile Leu Thr Pro Gly Gln Ala 440 445 450			1459
gta gcc act aaa gct cct gat tgg act cct ccc acc cgg gca acc gat Val Ala Thr Lys Ala Pro Asp Trp Thr Pro Pro Thr Arg Ala Thr Asp 455 460 465			1507
ctg cct cag gtc ccc tcc ccc tgg gag atc gtc gct gtc cgt ggc caa Leu Pro Gln Val Pro Ser Pro Trp Glu Ile Val Ala Val Arg Gly Gln 470 475 480 485			1555
ggt ctg ttt gag ctg cag gtg gaa act agt aga cgc acc gcc ctc ggt Gly Leu Phe Glu Leu Gln Val Glu Thr Ser Arg Arg Thr Ala Leu Gly 490 495 500			1603
cga gtt aat gcg acc ggt ggc gtc gac atc ggt gaa ctc ccg ccc aac Arg Val Asn Ala Thr Gly Gly Val Asp Ile Gly Glu Leu Pro Pro Asn 505 510 515			1651
ggc tat acc atc agt tct gtg gtt cag atc ggt gat gaa tac atc gtg Gly Tyr Thr Ile Ser Ser Val Val Gln Ile Gly Asp Glu Tyr Ile Val 520 525 530			1699
ggc agg tgg gta gag gaa tac cgg ctc aac tcc aaa ctg gag gtc att Gly Arg Trp Val Glu Glu Tyr Arg Leu Asn Ser Lys Leu Glu Val Ile 535 540 545			1747
tct acc aaa gag cta gat atc tcc gca tcc gga tgg aaq agc aag ggg Ser Thr Lys Glu Leu Asp Ile Ser Ala Ser Gly Trp Lys Ser Lys Gly 550 555 560 565			1795
acg gtt gct tat ctg tcg gaa gac act cac ata tgt ttc ttc gac cag Thr Val Ala Tyr Leu Ser Glu Asp Thr His Ile Cys Phe Phe Asp Gln 570 575 580			1843
gtc agc ggg gcc gag ctt ccc agc ctg ggt atc gcc gag gga cac cag Val Ser Gly Ala Glu Leu Pro Ser Leu Gly Ile Ala Glu Gly His Gln 585 590 595			1891
ggc gag gtt atg tca gca act tct tca gag agc atc gtg ctt atc tac Gly Glu Val Met Ser Ala Thr Ser Ser Glu Ser Ile Val Leu Ile Tyr 600 605 610			1939

cgg cgc aac ccg aac aat tca atg tgg att gtc ccg act tcc gtt gcc 1987
 Arg Arg Asn Pro Asn Asn Ser Met Ser Ile Val Pro Thr Ser Val Ala
 615 620 625
 acc tat gac aat ggc acc tgg acg act atg ccg cta cag gaa gct cca 2035
 Thr Tyr Asp Asn Gly Thr Trp Thr Thr Met Pro Leu Gln Glu Ala Pro
 630 635 640 645
 gcg gaa ctg tcc taaactgtct atagactgct gag 2070
 Ala Glu Leu Ser

<210> 68

<211> 649

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 68

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 20 25 30
 Glu Val Glu Ile Arg Arg Ser Pro Asn Ser Leu His Val Leu Arg Asn
 35 40 45
 Gly Ser Asp Ile Leu Arg Arg Asn Glu His His Cys Trp Val Phe Glu
 50 55 60
 Asn Phe Asn Lys Pro Ile Asp Pro Pro Val Arg Leu Gly Pro Arg Asp
 65 70 75 80
 Ile Ile Cys Pro Ser Ala Leu Ala Trp Val Leu Gln Gln His Ser Ile
 85 90 95
 Ser Arg Ser Leu Ser His His Leu His Ala Asp Lys Ile Thr Ala Gly
 100 105 110
 Glu Ile Ala Gly Arg Pro Thr Trp Ile Leu Arg Glu Glu Pro Thr Ser
 115 120 125
 Gly Gly Gln Asp Pro Ser Arg Leu Val Ser Leu Glu Ile Asp Gln Glu
 130 135 140
 His Gly Val Ile Leu Ala Val Glu Thr Gly Gln Glu Arg Leu Glu Ala
 145 150 155 160
 Thr Glu Ile Ser Phe Pro Asp Thr Leu Pro Asn Pro Ser Trp Asp Gly
 165 170 175
 Ala Trp Glu Pro Phe His Tyr Pro Asp Ser Thr Pro His Thr Ala Pro
 180 185 190
 Asp Val Ala Glu Ile Pro Gly Tyr Ile Gln Ser Leu Pro Pro Gln Ser
 195 200 205
 Glu Asp Pro Arg Arg Leu Arg Val Phe Val Asn Glu Ile Ala Leu Glu
 210 215 220

Gly Asp Phe Pro Asp Tyr Arg Gln Gly Gln Ser Val Arg Leu Thr Leu
 225 230 235 240
 Gly Ile Ser Ser Ser Pro Val Pro Leu Glu Gly Met Thr Thr Arg Arg
 245 250 255
 Arg Gly Arg Val Arg Asn Leu Gly Glu Glu Ala Ser Pro Gly Asp Asp
 260 265 270
 Gly Met Pro Gln Trp Pro Ile Leu Leu Thr Gly Asp Gly Trp Thr Ala
 275 280 285
 Leu Ala Tyr Thr Pro Ile Pro Lys Arg Gly Asp Ala Glu Ile Gln Gly
 290 295 300
 Trp Phe Tyr Tyr Ser Ala Tyr Gly Ile Val Asp Val Pro Thr Asp Leu
 305 310 315 320
 Arg Val Glu Arg Ile Phe Ala Gly Ile Gly Thr Ser Gly Thr Asn Glu
 325 330 335
 Arg Leu Trp Gln Glu Ile Asp Asn Thr Ser Ser Ala Tyr His Ser Glu
 340 345 350
 Asp Trp Trp Ile Arg Asp Val Val Leu Asp Val Thr Leu Asp Gly Ala
 355 360 365
 Val Pro Pro Pro Leu Arg Arg Asp Val Phe Thr Ala Val Asp Pro Ile
 370 375 380
 Val Ala Gly Asp Lys Leu Trp Leu Cys Asp Val His Phe Pro Val Ala
 385 390 395 400
 Arg Cys Trp Glu Thr Thr Thr Gly Arg Tyr Leu Gly Gln Thr Leu Val
 405 410 415
 Pro Ala Pro Leu Arg Asp Arg Ser Tyr Val Leu Glu Leu His Ser Asp
 420 425 430
 Gln Gln Leu Gly Ala Val Ala Ala Ser Gly Lys Ser Gly Trp Ile Leu
 435 440 445
 Thr Pro Gly Gln Ala Val Ala Thr Lys Ala Pro Asp Trp Thr Pro Pro
 450 455 460
 Thr Arg Ala Thr Asp Leu Pro Gln Val Pro Ser Pro Trp Glu Ile Val
 465 470 475 480
 Ala Val Arg Gly Gln Gly Leu Phe Glu Leu Gln Val Glu Thr Ser Arg
 485 490 495
 Arg Thr Ala Leu Gly Arg Val Asn Ala Thr Gly Gly Val Asp Ile Gly
 500 505 510
 Glu Leu Pro Pro Asn Gly Tyr Thr Ile Ser Ser Val Val Gln Ile Gly
 515 520 525
 Asp Glu Tyr Ile Val Gly Arg Trp Val Glu Glu Tyr Arg Leu Asn Ser
 530 535 540

Lys Leu Glu Val Ile Ser Thr Lys Glu Leu Asp Ile Ser Ala Ser Gly
 545 550 555 560
 Trp Lys Ser Lys Gly Thr Val Ala Tyr Leu Ser Glu Asp Thr His Ile
 565 570 575
 Cys Phe Phe Asp Gln Val Ser Gly Ala Glu Leu Pro Ser Leu Gly Ile
 580 585 590
 Ala Glu Gly His Gln Gly Glu Val Met Ser Ala Thr Ser Ser Glu Ser
 595 600 605
 Ile Val Leu Ile Tyr Arg Arg Asn Pro Asn Asn Ser Met Ser Ile Val
 610 615 620
 Pro Thr Ser Val Ala Thr Tyr Asp Asn Gly Thr Trp Thr Thr Met Pro
 625 630 635 640
 Leu Gln Glu Ala Pro Ala Glu Leu Ser
 645

<210> 69

<211> 2070

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2047)

<223> FRXA00028

<400> 69

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 Met Thr Leu Thr Ala
 1 5

 tct tcc ttg gag gcc ggg aaa atg tct ttt agt ggc ggg tat atc gtg 163
 Ser Ser Leu Glu Ala Gly Lys Met Ser Phe Ser Gly Gly Tyr Ile Val
 10 15 20

 ggc gag acg atg atc ttc ctc gtc gat ccc gat gaa gtc gag ata cga 211
 Gly Glu Thr Met Ile Phe Leu Val Asp Pro Asp Glu Val Glu Ile Arg
 25 30 35

 cgc agc cct aac agc ctc cac gtc ctg cgt aac ggt agc gat att ctg 259
 Arg Ser Pro Asn Ser Leu His Val Leu Arg Asn Gly Ser Asp Ile Leu
 40 45 50

 cgc cgc aac gag cat cat tgc tgg gta ttt gag aat ttc aat aaa ccc 307
 Arg Arg Asn Glu His His Cys Trp Val Phe Glu Asn Phe Asn Lys Pro
 55 60 65

 att gac cca cct gtt cga ttg ggt cct cgg gat atc atc tgc ccg agc 355
 Ile Asp Pro Pro Val Arg Leu Gly Pro Arg Asp Ile Ile Cys Pro Ser
 70 75 80 85

 gcc ttg gcc tgg gtt ctt caa cag cat tcc atc tcc cgg tcc tta tcc 403
 Ala Leu Ala Trp Val Leu Gln Gln His Ser Ile Ser Arg Ser Leu Ser

	90	95	100	
	cac cac ctt	cac gcg gat aag atc act gcg gga gag att gct gga cgc	451	
	His His Leu	His Ala Asp Lys Ile Thr Ala Gly Glu Ile Ala Gly Arg		
	105	110	115	
	ccc acc tgg atc ctc cgt gag gaa cct act tca gga ggg cag gac cca	499		
	Pro Thr Trp	Ile Leu Arg Glu Glu Pro Thr Ser Gly Glu Gln Asp Pro		
	120	125	130	
	agt cga ttg gtc agt ctt gaa atc gac cag gaa cac ggt gtc atc ctt	547		
	Ser Arg Leu Val Ser Leu	Glu Ile Asp Gln Glu His Gly Val Ile Leu		
	135	140	145	
	gca gtg gag act gga caa gaa cga ctc gaa gcc acg gag att tct ttt	595		
	Ala Val Glu Thr Gly Gln Glu Arg Leu Glu Ala Thr Glu Ile Ser Phe			
	150	155	160	165
	cct gac act ctt cct aat cct tcc tgg gac gga gcc tgg gaa cca ttc	643		
	Pro Asp Thr Leu Pro Asn Pro Ser Trp Asp Gly Ala Trp Glu Pro Phe			
	170	175	180	
	cat tat cca gat tgc aca cca cac act gcc cct gat gtt gct gaa ata	691		
	His Tyr Pro Asp Ser Thr Pro His Thr Ala Pro Asp Val Ala Glu Ile			
	185	190	195	
	ccc ggt tac att cag tca ctg ccg ccg cag tct gaa gat cct cgc aga	739		
	Pro Gly Tyr Ile Gln Ser Leu Pro Pro Gln Ser Glu Asp Pro Arg Arg			
	200	205	210	
	cta cga gtc ttc gtc aat gag ata gca ctc gaa ggt gat ttc cct gac	787		
	Leu Arg Val Phe Val Asn Glu Ile Ala Leu Glu Gly Asp Phe Pro Asp			
	215	220	225	
	tac cgt caa gga caa tct gtg cga ctt act ttg gga att agc tcc tcc	835		
	Tyr Arg Gln Gly Gln Ser Val Arg Leu Thr Leu Gly Ile Ser Ser Ser			
	230	235	240	245
	cct gtg cca ctc gaa gga atg aca acc aga cgc cgg gcc cgg gta cgc	883		
	Pro Val Pro Leu Glu Gly Met Thr Thr Arg Arg Gly Arg Val Arg			
	250	255	260	
	aac ctt ggg gaa gaa gct agt cca gcc gat gac ggt atg ccc cag tgg	931		
	Asn Leu Gly Glu Glu Ala Ser Pro Gly Asp Asp Gly Met Pro Gln Trp			
	265	270	275	
	cca atc ctg ctc act ggt gat ggg tgg acg gcg ctg gcc tac act ccc	979		
	Pro Ile Leu Leu Thr Gly Asp Glu Trp Thr Ala Leu Ala Tyr Thr Pro			
	280	285	290	
	atc cca aaa cgt gga gat gca gag atc cag ggg tgg ttt tat tat tcc	1027		
	Ile Pro Lys Arg Gly Asp Ala Glu Ile Gln Gly Trp Phe Tyr Tyr Ser			
	295	300	305	
	gcc tac gga att gtt gat gtt ccc aca gat cta cgg gta gag cgt att	1075		
	Ala Tyr Gly Ile Val Asp Val Pro Thr Asp Leu Arg Val Glu Arg Ile			
	310	315	320	325
	ttc gct ggt atc gcc aca agt gcc acc aac gag cgt ttg tgg cag gag	1123		
	Phe Ala Gly Ile Gly Thr Ser Gly Thr Asn Glu Arg Leu Trp Gln Glu			
	330	335	340	

ata gac aat act tct tcg gct tat cac tcg gaa gat tgg tgg atc cgc Ile Asp Asn Thr Ser Ser Ala Tyr His Ser Glu Asp Trp Trp Ile Arg 345 350 355	1171
gat gtc gtt tta gac gtc acg ttg gat gga gct gtt ccg cct ccg ctt Asp Val Val Leu Asp Val Thr Leu Asp Gly Ala Val Pro Pro Pro Leu 360 365 370	1219
aga cgt gac gtc ttc act gct gtc gat cct att gtg gcg ggt gac aaa Arg Arg Asp Val Phe Thr Ala Val Asp Pro Ile Val Ala Gly Asp Lys 375 380 385	1267
ttg tgg ctg tgt gac gtg cac ttt ccg gta gcc cgc tgc tgg gag acc Leu Trp Leu Cys Asp Val His Phe Pro Val Ala Arg Cys Trp Glu Thr 390 395 400 405	1315
acg acc ggc cga tac ttg ggg cag act tta ktc cca gca cca ctg cga Thr Thr Gly Arg Tyr Leu Gly Gln Thr Leu Xaa Pro Ala Pro Leu Arg 410 415 420	1363
gat cga tcg tac gtc ctt gag ctg cac agc gac caa caa tta gga gcc Asp Arg Ser Tyr Val Leu Glu Leu His Ser Asp Gln Gln Leu Gly Ala 425 430 435	1411
gta gcg gca agt ggg aag agt ggt tgg att ctc aca cct ggt caa gca Val Ala Ala Ser Gly Lys Ser Gly Trp Ile Leu Thr Pro Gly Gln Ala 440 445 450	1459
gta gcc act aaa gct cct gat tgg act cct ccc acc cgg gca acc gat Val Ala Thr Lys Ala Pro Asp Trp Thr Pro Pro Thr Arg Ala Thr Asp 455 460 465	1507
ctg cct cag gtc ccc tcc ccc tgg gag atc gtc gct gtc cgt ggc caa Leu Pro Gln Val Pro Ser Pro Trp Glu Ile Val Ala Val Arg Gly Gln 470 475 480 485	1555
ggt ctg ttt gag ctg cag gtg gaa act agt aga cgc acc gcc ctc ggt Gly Leu Phe Glu Leu Gln Val Glu Thr Ser Arg Arg Thr Ala Leu Gly 490 495 500	1603
cga gtt aat gcg acc ggt ggc gtc gac atc ggt gaa ctc ccg ccc aac Arg Val Asn Ala Thr Gly Gly Val Asp Ile Gly Glu Leu Pro Pro Asn 505 510 515	1651
ggc tat acc atc agt tct gtg gtt cag atc ggt gat gaa tac atc gtg Gly Tyr Thr Ile Ser Ser Val Val Gln Ile Gly Asp Glu Tyr Ile Val 520 525 530	1699
ggc agg tgg gta gag gaa tac cgg ctc aac tcc aaa ctg gag gtc att Gly Arg Trp Val Glu Glu Tyr Arg Leu Asn Ser Lys Leu Glu Val Ile 535 540 545	1747
tct acc aaa gag cta gat atc tcc gca tcc gga tgg aag agc aag ggg Ser Thr Lys Glu Leu Asp Ile Ser Ala Ser Gly Trp Lys Ser Lys Gly 550 555 560 565	1795
acg gtt gct tat ctg tcg gaa gac act cac ata tgt ttc ttc gac cag Thr Val Ala Tyr Leu Ser Glu Asp Thr His Ile Cys Phe Phe Asp Gln 570 575 580	1843

gtc agc ggg gcc gag ctt ccc agc ctg ggt atc gcc gag gga cac cag 1891
 Val Ser Gly Ala Glu Leu Pro Ser Leu Gly Ile Ala Glu Gly His Gln
 585 590 595

ggc gag gtt atg tca gca act tct tca gag agc atc gtg ctt atc tac 1939
 Gly Glu Val Met Ser Ala Thr Ser Ser Glu Ser Ile Val Leu Ile Tyr
 600 605 610

cgg cgc aac ccg aac aat tca atg tcg att gtc ccg act tcc gtt gcc 1987
 Arg Arg Asn Pro Asn Asn Ser Met Ser Ile Val Pro Thr Ser Val Ala
 615 620 625

acc tat gac aat ggc acc tgg acg act atg ccg cta cag gaa gct cca 2035
 Thr Tyr Asp Asn Gly Thr Trp Thr Thr Met Pro Leu Gln Glu Ala Pro
 630 635 640 645

gcg gaa ctg tcc taaactgctc atagactgct gag 2070
 Ala Glu Leu Ser

<210> 70

<211> 649

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 70

Met Thr Leu Thr Ala Ser Ser Leu Glu Ala Gly Lys Met Ser Phe Ser
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 20 25 30

Glu Val Glu Ile Arg Arg Ser Pro Asn Ser Leu His Val Leu Arg Asn
 35 40 45

Gly Ser Asp Ile Leu Arg Arg Asn Glu His His Cys Trp Val Phe Glu
 50 55 60

Asn Phe Asn Lys Pro Ile Asp Pro Pro Val Arg Leu Gly Pro Arg Asp
 65 70 75 80

Ile Ile Cys Pro Ser Ala Leu Ala Trp Val Leu Gln Gln His Ser Ile
 85 90 95

Ser Arg Ser Leu Ser His His Leu His Ala Asp Lys Ile Thr Ala Gly
 100 105 110

Glu Ile Ala Gly Arg Pro Thr Trp Ile Leu Arg Glu Glu Pro Thr Ser
 115 120 125

Gly Gly Gln Asp Pro Ser Arg Leu Val Ser Leu Glu Ile Asp Gln Glu
 130 135 140

His Gly Val Ile Leu Ala Val Glu Thr Gly Gln Glu Arg Leu Glu Ala
 145 150 155 160

Thr Glu Ile Ser Phe Pro Asp Thr Leu Pro Asn Pro Ser Trp Asp Gly
 165 170 175

Ala Trp Glu Pro Phe His Tyr Pro Asp Ser Thr Pro His Thr Ala Pro

[illegible]

Glu Leu Pro Pro Asn Gly Tyr Thr Ile Ser Ser Val Val Gln Ile Gly
515 520 525

Asp Glu Tyr Ile Val Gly Arg Trp Val Glu Glu Tyr Arg Leu Asn Ser
530 535 540

Lys Leu Glu Val Ile Ser Thr Lys Glu Leu Asp Ile Ser Ala Ser Gly
545 550 555 560

Trp Lys Ser Lys Gly Thr Val Ala Tyr Leu Ser Glu Asp Thr His Ile
565 570 575

Cys Phe Phe Asp Gln Val Ser Gly Ala Glu Leu Pro Ser Leu Gly Ile
580 585 590

Ala Glu Gly His Gln Gly Glu Val Met Ser Ala Thr Ser Ser Glu Ser
595 600 605

Ile Val Leu Ile Tyr Arg Arg Asn Pro Asn Asn Ser Met Ser Ile Val
610 615 620

Pro Thr Ser Val Ala Thr Tyr Asp Asn Gly Thr Trp Thr Thr Met Pro
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Leu Gln Glu Ala Pro Ala Glu Leu Ser
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<210> 71

<211> 1458

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1435)

<223> RXN00033

<400> 71

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Met Ser Val Gln Gln
1 5

agc ggg ttg ctc gaa cgt ctc ggc att ccc cga ccc ttg att ttc gga 163
Ser Gly Leu Leu Glu Arg Leu Gly Ile Pro Arg Pro Leu Ile Phe Gly
10 15 20

ttt atc ggc ctc acc atc ttc atg atc ggt gac ggt gtc gaa acc aac 211
Phe Ile Gly Leu Thr Ile Phe Met Ile Gly Asp Gly Val Glu Thr Asn
25 30 35

att ttg gaa cct ttc ctc agt tcc gaa cat ggt ttc agc gtt tcc ctc 259
Ile Leu Glu Pro Phe Leu Ser Ser Glu His Gly Phe Ser Val Ser Leu
40 45 50

gcg gga acc ctg gtg act gtt tac ggt gtt gcc gtg gcg atc gca gca 307
Ala Gly Thr Leu Val Thr Val Tyr Gly Val Ala Val Ala Ile Ala Ala
55 60 65

ttc ttc gcg gcg gca ctt tcg gac ctg tgg ggt cca cga aaa gtg atg 355
 Phe Phe Ala Ala Ala Leu Ser Asp Leu Trp Gly Pro Arg Lys Val Met
 70 75 80 85

atc ctc ggt gct tca atc tgg atc gtc ttt gag ctg atc ttc ctc acc 403
 Ile Leu Gly Ala Ser Ile Trp Ile Val Phe Glu Leu Ile Phe Leu Thr
 90 95 100

gtg gca ctg acc acc gac cat act tgg ttg atc ttc ctt gct tat ggt 451
 Val Ala Leu Thr Thr Asp His Thr Trp Leu Ile Phe Leu Ala Tyr Gly
 105 110 115

ctc cgc ggc ttt ggt tat cca ttc ttc gcc tac gga ttc ttg gtg tgg 499
 Leu Arg Gly Phe Gly Tyr Pro Phe Phe Ala Tyr Gly Phe Leu Val Trp
 120 125 130

atc acc gca act gcc tca cct aag caa ttg ggt acc ggt gtg ggt tgg 547
 Ile Thr Ala Thr Ala Ser Pro Lys Gln Leu Gly Thr Gly Val Gly Trp
 135 140 145

ttc tac gtt gcc ttc tct gca ggt ctt cct acc ttg ggt gcg ctg gtt 595
 Phe Tyr Val Ala Phe Ser Ala Gly Leu Pro Thr Leu Gly Ala Leu Val
 150 155 160 165

gcc acc att tcc atg cag tac gtg aac ttg acc ttc tat gaa acg ttg 643
 Ala Thr Ile Ser Met Gln Tyr Val Asn Leu Thr Phe Tyr Glu Thr Leu
 170 175 180

tgg gtt tcc ctc gtg ctg gtg gtc atc gga tcg ctc atc gca ctg ctg 691
 Trp Val Ser Leu Val Leu Val Ile Gly Ser Leu Ile Ala Leu Leu
 185 190 195

gga gtg aag gaa cgt cgc gga cgc cac cca ctg gtt gcc aac ccc gac 739
 Gly Val Lys Glu Arg Arg Gly Arg His Pro Leu Val Ala Asn Pro Asp
 200 205 210

gat gtg aag caa aca ctt ggc cag gcc ttc aaa ctt ctg cgc aat gat 787
 Asp Val Lys Gln Thr Leu Gly Gln Gly Phe Lys Leu Leu Arg Asn Asp
 215 220 225

cga cgt gca cgt ttt gtc acc tac atc cgc acc atc aac tcc att ccg 835
 Arg Arg Ala Arg Phe Val Thr Tyr Ile Arg Thr Ile Asn Ser Ile Pro
 230 235 240 245

acc tac gcg atg gct gtg ttc ttc cca tca ttt ttc act gac gat ctg 883
 Thr Tyr Ala Met Ala Val Phe Phe Pro Ser Phe Phe Thr Asp Asp Leu
 250 255 260

aag tgg cag cta agc tgg ttc ctc atc ctc acc act gta att tac gca 931
 Lys Trp Gln Leu Ser Trp Phe Leu Ile Leu Thr Thr Val Ile Tyr Ala
 265 270 275

gtc aac ctg ccg ttc aat cct ttc ttc ggt agc ttc ggc gac cgc cac 979
 Val Asn Leu Pro Phe Asn Pro Phe Phe Gly Ser Phe Gly Asp Arg His
 280 285 290

ggt tgg gca cga act gtg ttc tgg ggc gga tca atc ggt ggc gca gtc 1027
 Gly Trp Ala Arg Thr Val Phe Trp Gly Gly Ser Ile Gly Gly Ala Val
 295 300 305

acc ctc gcg ttg gtt tac ttc att ccg atg ttc ggc gtt cag gct ggc 1075
 Thr Leu Ala Leu Val Tyr Phe Ile Pro Met Phe Gly Val Gln Ala Gly
 310 315 320 325

atg tcc aac ggt gtc gtt ttc gga atc acc atc gca gcc ggc gca ctc 1123
 Met Ser Asn Gly Val Val Phe Gly Ile Thr Ile Ala Ala Gly Ala Leu
 330 335 340

ttt ggt gtg tcc ctc gcg ggc ttc gtg cca ctt tcc gca atc gct gtc 1171
 Phe Gly Val Ser Leu Ala Gly Phe Val Pro Leu Ser Ala Ile Ala Val
 345 350 355

tcc ctt gat ccc aag cac ccc ggc gca gcg atg gcc aca tac aac ctc 1219
 Ser Leu Asp Pro Lys His Pro Gly Ala Ala Met Ala Thr Tyr Asn Leu
 360 365 370

ggc gtt ggt ggc gct gta gct gtg gga ccg ctc ctg gtt gca gtc ttc 1267
 Gly Val Gly Gly Ala Val Ala Val Gly Pro Leu Leu Val Ala Val Phe
 375 380 385

cac cca ctg att ggt cca acc gga ttg atc ctg gtc atg atc gcc ctc 1315
 His Pro Leu Ile Gly Pro Thr Gly Leu Ile Leu Val Met Ile Ala Leu
 390 395 400 405

tac ctg ctc tcc ggt tgg atg act ctt caa ctt cgc ggc acc caa cca 1363
 Tyr Leu Leu Ser Gly Trp Met Thr Leu Gln Leu Arg Gly Thr Gln Pro
 410 415 420

gga ttc gac gga gtg cca gca ctt gct gaa gac gcc cac atc gaa gac 1411
 Gly Phe Asp Gly Val Pro Ala Leu Ala Glu Asp Ala His Ile Glu Asp
 425 430 435

ctt gca gat gta aac gca aac gcc taactgtttt tcgagctaaa ccc 1458
 Leu Ala Asp Val Asn Ala Asn Ala
 440 445

<210> 72

<211> 445

<212> PRT

<213> Corynebacterium glutamicum

<400> 72

Met Ser Val Gln Gln Ser Gly Leu Leu Glu Arg Leu Gly Ile Pro Arg
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Pro Leu Ile Phe Gly Phe Ile Gly Leu Thr Ile Phe Met Ile Gly Asp
 20 25 30

Gly Val Glu Thr Asn Ile Leu Glu Pro Phe Leu Ser Ser Glu His Gly
 35 40 45

Phe Ser Val Ser Leu Ala Gly Thr Leu Val Thr Val Tyr Gly Val Ala
 50 55 60

Val Ala Ile Ala Ala Phe Phe Ala Ala Ala Leu Ser Asp Leu Trp Gly
 65 70 75 80

Pro Arg Lys Val Met Ile Leu Gly Ala Ser Ile Trp Ile Val Phe Glu
 85 90 95

Leu Ile Phe Leu Thr Val Ala Leu Thr Thr Asp His Thr Trp Leu Ile
 100 105 110
 Phe Leu Ala Tyr Gly Leu Arg Gly Phe Gly Tyr Pro Phe Phe Ala Tyr
 115 120 125
 Gly Phe Leu Val Trp Ile Thr Ala Thr Ala Ser Pro Lys Gln Leu Gly
 130 135 140
 Thr Gly Val Gly Trp Phe Tyr Val Ala Phe Ser Ala Gly Leu Pro Thr
 145 150 155 160
 Leu Gly Ala Leu Val Ala Thr Ile Ser Met Gln Tyr Val Asn Leu Thr
 165 170 175
 Phe Tyr Glu Thr Leu Trp Val Ser Leu Val Leu Val Val Ile Gly Ser
 180 185 190
 Leu Ile Ala Leu Leu Gly Val Lys Glu Arg Arg Gly Arg His Pro Leu
 195 200 205
 Val Ala Asn Pro Asp Asp Val Lys Gln Thr Leu Gly Gln Gly Phe Lys
 210 215 220
 Leu Leu Arg Asn Asp Arg Arg Ala Arg Phe Val Thr Tyr Ile Arg Thr
 225 230 235
 Ile Asn Ser Ile Pro Thr Tyr Ala Met Ala Val Phe Phe Pro Ser Phe
 245 250 255
 Phe Thr Asp Asp Leu Lys Trp Gln Leu Ser Trp Phe Leu Ile Leu Thr
 260 265 270
 Thr Val Ile Tyr Ala Val Asn Leu Pro Phe Asn Pro Phe Phe Gly Ser
 275 280 285
 Phe Gly Asp Arg His Gly Trp Ala Arg Thr Val Phe Trp Gly Gly Ser
 290 295 300
 Ile Gly Gly Ala Val Thr Leu Ala Leu Val Tyr Phe Ile Pro Met Phe
 305 310 315 320
 Gly Val Gln Ala Gly Met Ser Asn Gly Val Val Phe Gly Ile Thr Ile
 325 330 335
 Ala Ala Gly Ala Leu Phe Gly Val Ser Leu Ala Gly Phe Val Pro Leu
 340 345 350
 Ser Ala Ile Ala Val Ser Leu Asp Pro Lys His Pro Gly Ala Ala Met
 355 360 365
 Ala Thr Tyr Asn Leu Gly Val Gly Gly Ala Val Ala Val Gly Pro Leu
 370 375 380
 Leu Val Ala Val Phe His Pro Leu Ile Gly Pro Thr Gly Leu Ile Leu
 385 390 395 400
 Val Met Ile Ala Leu Tyr Leu Leu Ser Gly Trp Met Thr Leu Gln Leu
 405 410 415
 Arg Gly Thr Gln Pro Gly Phe Asp Gly Val Pro Ala Leu Ala Glu Asp

420

425

430

Ala His Ile Glu Asp Leu Ala Asp Val Asn Ala Asn Ala
 435 440 445

<210> 73

<211> 873

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}..(850)

<223> RXN00056

<400> 73

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taatcgcggt tcaggacacc tacatgatca ggagctcttt ttg tta aac aga gtc 115
 Leu Leu Asn Arg Val
 1 5

agt cgt att gca ggc gct tct gca atc aca cta tgc atc ggc tta acc 163
 Ser Arg Ile Ala Gly Ala Ser Ala Ile Thr Leu Cys Ile Gly Leu Thr
 10 15 20

aca ata cta agc cct act tcc act gca caa agc ctc gaa cag atc acc 211
 Thr Ile Leu Ser Pro Thr Ser Thr Ala Gln Ser Leu Glu Gln Ile Thr
 25 30 35

cct tta cct gaa tct gca atc gac ctc aac gcc gag att cac gta aac 259
 Pro Leu Pro Glu Ser Ala Ile Asp Leu Asn Ala Glu Ile His Val Asn
 40 45 50

aca agc gac att tca gct gaa cag atc ctt ggt gct caa gat gaa atc 307
 Thr Ser Asp Ile Ser Ala Glu Gln Ile Leu Gly Ala Gln Asp Glu Ile
 55 60 65

aca act atg tac gat tct cat gac ccc tac gag tac ttc gat acc ctc 355
 Thr Thr Met Tyr Asp Ser His Asp Pro Tyr Glu Tyr Phe Asp Thr Leu
 70 75 80 85

acc gac atc gaa cag cgt tca ata ata gca gcg ctt aaa cgg gat ccg 403
 Thr Asp Ile Glu Gln Arg Ser Ile Ile Ala Ala Leu Lys Arg Asp Pro
 90 95 100

agt tca ctc caa caa cgc caa gaa acc cgt ctc gcg gca cag tcc gac 451
 Ser Ser Leu Gln Gln Arg Gln Glu Thr Arg Leu Ala Ala Gln Ser Asp
 105 110 115

ccc tac aaa att tac ata tca ggc ctc gaa atg ctt tca tgc atc aat 499
 Pro Tyr Lys Ile Tyr Ile Ser Gly Leu Glu Met Leu Ser Cys Ile Asn
 120 125 130

cta gtt gat gtt gta tca tgc ggg att gca aac caa gca gca acc aaa 547
 Leu Val Asp Val Val Ser Cys Gly Ile Ala Asn Gln Ala Ala Thr Lys
 135 140 145

gca aat aat gag gct gtc gca cga tac cca ggc gat tcc ctt cgc aac 595
 Ala Asn Asn Glu Ala Val Ala Arg Tyr Pro Gly Asp Ser Leu Arg Asn

150	155	160	165	
ggc aaa ggc gat gca ttt cgg cat tgc tca tgg aac gct ctg atg acg Gly Lys Gly Asp Ala Phe Arg His Cys Ser Trp Asn Ala Leu Met Thr	170	175	180	643
ata cga atc ggg agc aat gga gct gaa aga att gca aca aac cac gag Ile Arg Ile Gly Ser Asn Gly Ala Glu Arg Ile Ala Thr Asn His Glu	185	190	195	691
aca atc ggg gac ggt cgg gcc gat gaa aat gca atg gac cta ttc aat Thr Ile Gly Asp Gly Pro Ala Asp Glu Asn Ala Met Asp Leu Phe Asn	200	205	210	739
aat gca caa ggc cga cag atc gga gcc gga ttc att aat agt aag gat Asn Ala Gln Gly Arg Gln Ile Gly Ala Gly Phe Ile Asn Ser Lys Asp	215	220	225	787
gaa act agc gcg ctc gcg ata tgc gcg ctg tgg aca aat ctc ggt aga Glu Thr Ser Ala Leu Ala Ile Cys Ala Leu Trp Thr Asn Leu Gly Arg	230	235	240	835
cta aaa act cta aaa taagcaagggt gccctctgat gct Leu Lys Thr Leu Lys	250			873
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taatcgcgtt	tcaggacacc	tacatgatca	ggagctcttt	ttg tta aac aga gtc		115
				Leu Leu Asn Arg Val	5	
agt cgt att gca ggc gct tct gca atc aca cta tgc atc ggc tta acc						163
Ser Arg Ile Ala Gly Ala Ser Ala Ile Thr Leu Cys Ile Gly Leu Thr	10		15		20	
aca ata cta agc cct act tcg act gca caa agc ctg gaa cag atc acc						211
Thr Ile Leu Ser Pro Thr Ser Thr Ala Gln Ser Leu Glu Gln Ile Thr	25		30		35	
cct tta cct gaa tct gca atc gac ctg aac gcc gag att cac gta aac						259
Pro Leu Pro Glu Ser Ala Ile Asp Leu Asn Ala Glu Ile His Val Asn	40		45		50	
aca agc gac att tca gct gaa cag atc ctt ggt gat caa gat gaa atc						307
Thr Ser Asp Ile Ser Ala Glu Gln Ile Leu Gly Ala Gln Asp Glu Ile	55		60		65	
aca act atg tac gat tct cat gac ccc tac gag tac ttc gat acc ctg						355
Thr Thr Met Tyr Asp Ser His Asp Pro Tyr Glu Tyr Phe Asp Thr Leu	70		75		80	85
acc gac atc gaa cag cgt toa ata ata gca gcg ctt aaa cgg gat ccg						403
Thr Asp Ile Glu Gln Arg Ser Ile Ile Ala Ala Leu Lys Arg Asp Pro	90		95		100	

agt tca ctc caa caa cgc caa gaa acc cgt ctc gcg gca cag tcc gac 451
 Ser Ser Leu Gln Gln Arg Gln Glu Thr Arg Leu Ala Ala Gln Ser Asp
 105 110 115

ccc tac aaa att tac ata tca ggc ctc gaa atg ctt tca tgc atc aat 499
 Pro Tyr Lys Ile Tyr Ile Ser Gly Leu Glu Met Leu Ser Cys Ile Asn
 120 125 130

cta gtt gat gtt gta tca tgc ggg att gca aac caa gca gca acc aaa 547
 Leu Val Asp Val Val Ser Cys Gly Ile Ala Asn Gln Ala Ala Thr Lys
 135 140 145

gca aat aat gag gct gtc gca cga tac cca ggc gat tcc ctt cgc aac 595
 Ala Asn Asn Glu Ala Val Ala Arg Tyr Pro Gly Asp Ser Leu Arg Asn
 150 155 160 165

ggc aaa ggc gat gca ttt cgg cat tgc tca tgg aac gct ctg atg acg 643
 Gly Lys Gly Asp Ala Phe Arg His Cys Ser Trp Asn Ala Leu Met Thr
 170 175 180

ata cga atc ggg agc aat gga gct gaa aga att gca aca aac cac gag 691
 Ile Arg Ile Gly Ser Asn Gly Ala Glu Arg Ile Ala Thr Asn His Glu
 185 190 195

aca atc ggg gac ggt cgg gcc gat gaa aat gca atg gac cta ttc aat 739
 Thr Ile Gly Asp Gly Pro Ala Asp Glu Asn Ala Met Asp Leu Phe Asn
 200 205 210

aat gca caa ggc cga cag atc gga gcc gga ttc att aat agt aag gat 787
 Asn Ala Gln Gly Arg Gln Ile Gly Ala Gly Phe Ile Asn Ser Lys Asp
 215 220 225

gaa act agc gcg ctc gcg ata tgc gcg ctg tgg aca aat ctc ggt aga 835
 Glu Thr Ser Ala Leu Ala Ile Cys Ala Leu Trp Thr Asn Leu Gly Arg
 230 235 240 245

cta aaa act cta aaa taagcaaggt gccctctgat gct 873
 Leu Lys Thr Leu Lys
 250

<210> 76

<211> 250

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 76

Leu Leu Asn Arg Val Ser Arg Ile Ala Gly Ala Ser Ala Ile Thr Leu
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Cys Ile Gly Leu Thr Thr Ile Leu Ser Pro Thr Ser Thr Ala Gln Ser
 20 25 30

Leu Glu Gln Ile Thr Pro Leu Pro Glu Ser Ala Ile Asp Leu Asn Ala
 35 40 45

Glu Ile His Val Asn Thr Ser Asp Ile Ser Ala Glu Gln Ile Leu Gly
 50 55 60

Ala Gln Asp Glu Ile Thr Thr Met Tyr Asp Ser His Asp Pro Tyr Glu

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65              70              75              80
Tyr Phe Asp Thr Leu Thr Asp Ile Glu Gln Arg Ser Ile Ile Ala Ala
      85              90              95
Leu Lys Arg Asp Pro Ser Ser Leu Gln Gln Arg Gln Glu Thr Arg Leu
      100             105             110
Ala Ala Gln Ser Asp Pro Tyr Lys Ile Tyr Ile Ser Gly Leu Glu Met
      115             120             125
Leu Ser Cys Ile Asn Leu Val Asp Val Val Ser Cys Gly Ile Ala Asn
      130             135             140
Gln Ala Ala Thr Lys Ala Asn Asn Glu Ala Val Ala Arg Tyr Pro Gly
      145             150             155             160
Asp Ser Leu Arg Asn Gly Lys Gly Asp Ala Phe Arg His Cys Ser Trp
      165             170             175
Asn Ala Leu Met Thr Thr Ile Arg Ile Gly Ser Asn Gly Ala Glu Arg Ile
      180             185             190
Ala Thr Asn His Glu Thr Ile Gly Asp Gly Pro Ala Asp Glu Asn Ala
      195             200             205
Met Asp Leu Phe Asn Asn Ala Gln Gly Arg Gln Ile Gly Ala Gly Phe
      210             215             220
Ile Asn Ser Lys Asp Glu Thr Ser Ala Leu Ala Ile Cys Ala Leu Trp
      225             230             235             240
Thr Asn Leu Gly Arg Leu Lys Thr Leu Lys
      245             250

<210> 77
<211> 609
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(586)
<223> RXN00067

<400> 77
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aatcattatt ttcctcactt tcagctaaaa ggaccatgca atg gta gac gct cag 115
                                     Met Val Asp Ala Gln
                                     1 5

cgc ccc aaa gca ggc atc ttc ggt agc cac aca gaa gaa aca tgg gtg 163
Arg Pro Lys Ala Gly Ile Phe Gly Ser His Thr Glu Glu Thr Trp Val
      10 15 20

tgg ctc ggt aat gaa ctt ttc gac gag tcc ggc gag gtc atc gcc gac 211
Trp Leu Gly Asn Glu Leu Phe Asp Glu Ser Gly Glu Val Ile Ala Asp
      25 30 35

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gtt cgc tcc gac gtc ctc tac gtg gat cgc gaa cga cta ctc atc gaa 259
Val Arg Ser Asp Val Leu Tyr Val Asp Arg Glu Leu Leu Ile Glu
      40                      45                      50

tcc acc ccc ggc acc atg cgt ttt cgt tgc cgc gca aca ctg tcc ggg 307
Ser Thr Pro Gly Thr Met Arg Phe Arg Cys Arg Ala Thr Leu Ser Gly
      55                      60                      65

ggg gag gtc tat acg atg act cag aat tct ttc act gtg ggg gat ctc 355
Gly Glu Val Tyr Thr Met Thr Gln Asn Ser Phe Thr Val Gly Asp Leu
      70                      75                      80                      85

act gcg gtg tgc ggg cgc cgg acg tat tca cta aaa agg gtg tgc ccg 403
Thr Ala Val Cys Gly Arg Arg Thr Tyr Ser Leu Lys Arg Val Ser Pro
      90                      95                      100

tgg cgt aaa gaa cgc ctg atc acc aac aat ggg gtg gaa gtg gcg cgg 451
Trp Arg Lys Glu Arg Leu Ile Thr Asn Asn Gly Val Glu Val Ala Arg
      105                      110                      115

ctt cgc cgc atg acc agc ggt aaa gtc gaa ttc att gtg ggc acc gcg 499
Leu Arg Pro Met Thr Ser Gly Lys Val Glu Phe Ile Val Gly Thr Ala
      120                      125                      130

ggc agc gag gcg ttg ccg ttc gtc gac gca gta ttt ttg agc tgg gcg 547
Gly Ser Glu Ala Leu Pro Phe Val Asp Ala Val Phe Leu Ser Trp Ala
      135                      140                      145

tgc gtc ctg gtg gat tgc gcc gtg cgc cgg ccg aaa att taaaagcttt 596
Cys Val Leu Val Asp Ser Ala Val Arg Arg Pro Lys Ile
      150                      155                      160

ttgcttatcg acg 609

<210> 78
<211> 162
<212> PRT
<213> Corynebacterium glutamicum

<400> 78
Met Val Asp Ala Gln Arg Pro Lys Ala Gly Ile Phe Gly Ser His Thr
  1          5          10          15

Glu Glu Thr Trp Val Trp Leu Gly Asn Glu Leu Phe Asp Glu Ser Gly
      20          25          30

Glu Val Ile Ala Asp Val Arg Ser Asp Val Leu Tyr Val Asp Arg Glu
      35          40          45

Arg Leu Leu Ile Glu Ser Thr Pro Gly Thr Met Arg Phe Arg Cys Arg
      50          55          60

Ala Thr Leu Ser Gly Gly Glu Val Tyr Thr Met Thr Gln Asn Ser Phe
      65          70          75          80

Thr Val Gly Asp Leu Thr Ala Val Cys Gly Arg Arg Thr Tyr Ser Leu
      85          90          95

Lys Arg Val Ser Pro Trp Arg Lys Glu Arg Leu Ile Thr Asn Asn Gly
      100          105          110

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Val Glu Val Ala Arg Leu Arg Pro Met Thr Ser Gly Lys Val Glu Phe
 115 120 125

Ile Val Gly Thr Ala Gly Ser Glu Ala Leu Pro Phe Val Asp Ala Val
 130 135 140

Phe Leu Ser Trp Ala Cys Val Leu Val Asp Ser Ala Val Arg Arg Pro
 145 150 155 160

Lys Ile

<210> 79
 <211> 609
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(586)
 <223> FRXA00067

<400> 79
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aatcattatt ttctcactt tcagctaaaa ggaccatgca atg gta gac gct cag 115
 Met Val Asp Ala Gln
 1 5

cgc ccc aaa gca ggc atc ttc ggt agc cac aca gaa gaa aca tgg gtg 163
 Arg Pro Lys Ala Gly Ile Phe Gly Ser His Thr Glu Glu Thr Trp Val
 10 15 20

tgg ctc ggt aat gaa ctt ttc gac gag tcc ggc gag gtc atc gcc gac 211
 Trp Leu Gly Asn Glu Leu Phe Asp Glu Ser Gly Glu Val Ile Ala Asp
 25 30 35

gtt cgc tcc gac gtc ctc tac gtg gat cgc gaa cga cta ctc atc gaa 259
 Val Arg Ser Asp Val Leu Tyr Val Asp Arg Glu Arg Leu Leu Ile Glu
 40 45 50

tcc acc ccc ggc acc atg cgt ttt cgt tgc cgc gca aca ctg tcc ggg 307
 Ser Thr Pro Gly Thr Met Arg Phe Arg Cys Arg Ala Thr Leu Ser Gly
 55 60 65

ggt gag gtc tat acg atg act cag aat tct ttc act gtg ggg gat ctc 355
 Gly Glu Val Tyr Thr Met Thr Gln Asn Ser Phe Thr Val Gly Asp Leu
 70 75 80 85

act cgc gtg tgc ggg cgc cgg acg tat tca cta aaa agg gtg tgg ccg 403
 Thr Ala Val Cys Gly Arg Arg Thr Tyr Ser Leu Lys Arg Val Ser Pro
 90 95 100

tgg cgt aaa gaa cgc ctg atc acc aac aat ggg gtg gaa gtg gcg cgg 451
 Trp Arg Lys Glu Arg Leu Ile Thr Asn Asn Gly Val Glu Val Ala Arg
 105 110 115

ctt cgc ccg atg acc agc ggt aaa gtc gaa ttc att gtg ggc acc cgc 499
 Leu Arg Pro Met Thr Ser Gly Lys Val Glu Phe Ile Val Gly Thr Ala

120	125	130	
ggc agc gag gcg ttg ccg ttc gtc gac gca gta ttt ttg agc tgg gcg			547
Gly Ser Glu Ala Leu Pro Phe Val Asp Ala Val Phe Leu Ser Trp Ala			
135	140	145	
tgc gtc ctg gtg gat tcg gcc gtg cgc cgg ccg aaa att taaaagcttt			596
Cys Val Leu Val Asp Ser Ala Val Arg Arg Pro Lys Ile			
150	155	160	
ttgcttatcg acg			609

<210> 80

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 80

Met Val Asp Ala Gln Arg Pro Lys Ala Gly Ile Phe Gly Ser His Thr
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Glu Glu Thr Trp Val Trp Leu Gly Asn Glu Leu Phe Asp Glu Ser Gly
20 25 30

Glu Val Ile Ala Asp Val Arg Ser Asp Val Leu Tyr Val Asp Arg Glu
35 40 45

Arg Leu Leu Ile Glu Ser Thr Pro Gly Thr Met Arg Phe Arg Cys Arg
50 55 60

Ala Thr Leu Ser Gly Gly Glu Val Tyr Thr Met Thr Gln Asn Ser Phe
65 70 75 80

Thr Val Gly Asp Leu Thr Ala Val Cys Gly Arg Arg Thr Tyr Ser Leu
85 90 95

Lys Arg Val Ser Pro Trp Arg Lys Glu Arg Leu Ile Thr Asn Asn Gly
100 105 110

Val Glu Val Ala Arg Leu Arg Pro Met Thr Ser Gly Lys Val Glu Phe
115 120 125

Ile Val Gly Thr Ala Gly Ser Glu Ala Leu Pro Phe Val Asp Ala Val
130 135 140

Phe Leu Ser Trp Ala Cys Val Leu Val Asp Ser Ala Val Arg Arg Pro
145 150 155 160

Lys Ile

<210> 81

<211> 1485

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1462)

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ctttccggga taaaaattgc aacgcactac actgagcagt																	115
Met Asn Asp Glu Asn 1 5																	
att caa agc tcc aac tat cag cca ttc ccg agt ttt gac gat tgg aaa																	163
Ile Gln Ser Ser Asn Tyr Gln Pro Phe Pro Ser Phe Asp Asp Trp Lys 10 15 20																	
cag atc gag gtg tgc ctc tta gat gtc atc gaa tcc tca cgc cat ttt																	211
Gln Ile Glu Val Ser Leu Leu Asp Val Ile Glu Ser Ser Arg His Phe 25 30 35																	
tct gat ttg aaa gat agc act gat cgt tct gcg tta gat gct gcg cta																	259
Ser Asp Leu Lys Asp Ser Thr Asp Arg Ser Ala Leu Asp Ala Ala Leu 40 45 50																	
gag aga gca aaa aga gct gcc gca gtt gat acc aat gcc ata gaa gga																	307
Glu Arg Ala Lys Arg Ala Ala Val Asp Thr Asn Ala Ile Glu Gly 55 60 65																	
atc ttc caa act gat cgc ggt ttt acc cat aca gtt gca acg cag gta																	355
Ile Phe Gln Thr Asp Arg Gly Phe Thr Thr Val Ala Thr Gln Val 70 75 80 85																	
ggg gct tgg gag caa caa atg gcg atg aaa ggc aaa cat gtt aag cct																	403
Gly Ala Trp Glu Gln Gln Met Ala Met Lys Gly Lys His Val Lys Pro 90 95 100																	
gcg ttt gac gat act cta gaa ggc ttt gag tat gtt ctc gat gca gta																	451
Ala Phe Asp Asp Thr Leu Glu Gly Phe Glu Tyr Val Leu Asp Ala Val 105 110 115																	
act ggt aga act cca atc tct cag caa tgg att aga aat ttg cac gcc																	499
Thr Gly Arg Thr Pro Ile Ser Gln Gln Trp Ile Arg Asn Leu His Ala 120 125 130																	
gtc att ctg cgg agc caa gaa agc cac gag gtt ttt aca gcc gtt gga																	547
Val Ile Leu Arg Ser Gln Glu Ser His Glu Val Phe Thr Ala Val Gly 135 140 145																	
gtc caa aat cag gcg ctt cag aaa ggc gag tat aaa act cag cca aat																	595
Val Gln Asn Gln Ala Leu Gln Lys Gly Glu Tyr Lys Thr Gln Pro Asn 150 155 160 165																	
agt cca cag cgc tca gat gga tct gta cat gca tac gcc cca gtt gaa																	643
Ser Pro Gln Arg Ser Asp Gly Ser Val His Ala Tyr Ala Pro Val Glu 170 175 180																	
gat act cct gct gaa atg gct aga ttt att tca gaa ctt gaa tct aag																	691
Asp Thr Pro Ala Glu Met Ala Arg Phe Ile Ser Glu Leu Glu Ser Lys 185 190 195																	
gaa ttc tta gca gcc gag aag gtt att caa gct gcc tat gcc cac tat																	739
Glu Phe Leu Ala Ala Glu Lys Val Ile Gln Ala Ala Tyr Trp Ala His Tyr 200 205 210																	

gct ttc gta tgt att cat cct ttt gca gat ggg aat gga cga gtt gca	787
Ala Phe Val Cys Ile His Pro Phe Ala Asp Gly Asn Gly Arg Val Ala	
215 220 225	
cga gcc ttg gct agt gtt ttt cta tac aaa gat cct ggt gtc cct ctc	835
Arg Ala Leu Ala Ser Val Phe Leu Tyr Lys Asp Pro Gly Val Pro Leu	
230 235 240 245	
gta atc tac caa gat caa cgc aga gat tac atc cat gct cta gaa gca	883
Val Ile Tyr Gln Asp Gln Arg Arg Asp Tyr Ile His Ala Leu Glu Ala	
250 255 260	
gcg gac aag aat aac ccg ctc ctg ctg att aga ttc ttt gct gaa cga	931
Ala Asp Lys Asn Asn Pro Leu Leu Leu Ile Arg Phe Phe Ala Glu Arg	
265 270 275	
gtg acc gat act att aac tct att atc gtt gat ctc act acc ccg atc	979
Val Thr Asp Thr Ile Asn Ser Ile Ile Val Asp Leu Thr Thr Pro Ile	
280 285 290	
gcg ggt aaa tct ggt tcg gct aag ctt tcg gat gcg cta cgc ccc act	1027
Ala Gly Lys Ser Gly Ser Ala Lys Leu Ser Asp Ala Leu Arg Pro Thr	
295 300 305	
cgc gta tta cca gaa tta cat gat gct gca cat agg ctc caa gaa agt	1075
Arg Val Leu Pro Glu Leu His Asp Ala Ala His Arg Leu Gln Glu Ser	
310 315 320 325	
tta ttt aca gaa atc cga tct cga ttg gat gaa gaa gga aaa agg aat	1123
Leu Phe Thr Glu Ile Arg Ser Arg Leu Asp Glu Glu Gly Lys Arg Asn	
330 335 340	
ggg ttg gag ttt cta ctt caa cgg att ttt atc ggt tcc cca ttc aat	1171
Gly Leu Glu Phe Leu Leu Gln Arg Ile Phe Ile Gly Ser Pro Phe Asn	
345 350 355	
ctg cca gag ggc tat aac gct ttc cct gat agc tat tgt ctg acc tta	1219
Leu Pro Glu Gly Tyr Asn Ala Phe Pro Asp Ser Tyr Cys Leu Thr Leu	
360 365 370	
gct ttc aat agc aac tct cca aaa caa atc ttc cac ccg cta tcc ata	1267
Ala Phe Asn Ser Asn Ser Pro Lys Gln Ile Phe His Pro Leu Ser Ile	
375 380 385	
gta ata gca gct cga gat ggg aaa aga gcg agc agc gac ctc gtg gca	1315
Val Ile Ala Ala Arg Asp Gly Lys Arg Ala Ser Ser Asp Leu Val Ala	
390 395 400 405	
gct act tct att gga tac aac ttt cac gct tac gga cgt gaa gtc gag	1363
Ala Thr Ser Ile Gly Tyr Asn Phe His Ala Tyr Gly Arg Glu Val Glu	
410 415 420	
cct gtt gtt act gaa agc ttt cga gaa cgt gtg aaa att tac gcc gac	1411
Pro Val Val Thr Glu Ser Phe Arg Glu Arg Val Lys Ile Tyr Ala Asp	
425 430 435	
ggg att gta gat cac ttc tta acc gaa ctg gct aaa aag ttt caa cag	1459
Gly Ile Val Asp His Phe Leu Thr Glu Leu Ala Lys Lys Phe Gln Gln	
440 445 450	
aat taattgcct atctcggtt tcg	1485

Asn

<210> 82

<211> 454

<212> PRT

<213> Corynebacterium glutamicum

<400> 82

Met Asn Asp Glu Asn Ile Gln Ser Ser Asn Tyr Gln Pro Phe Pro Ser
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Phe Asp Asp Trp Lys Gln Ile Glu Val Ser Leu Leu Asp Val Ile Glu
 20 25 30

Ser Ser Arg His Phe Ser Asp Leu Lys Asp Ser Thr Asp Arg Ser Ala
 35 40 45

Leu Asp Ala Ala Leu Glu Arg Ala Lys Arg Ala Ala Val Asp Thr
 50 55 60

Asn Ala Ile Glu Gly Ile Phe Gln Thr Asp Arg Gly Phe Thr His Thr
 65 70 75 80

Val Ala Thr Gln Val Gly Ala Trp Glu Gln Gln Met Ala Met Lys Gly
 85 90 95

Lys His Val Lys Pro Ala Phe Asp Asp Thr Leu Glu Gly Phe Glu Tyr
 100 105 110

Val Leu Asp Ala Val Thr Gly Arg Thr Pro Ile Ser Gln Gln Trp Ile
 115 120 125

Arg Asn Leu His Ala Val Ile Leu Arg Ser Gln Glu Ser His Glu Val
 130 135 140

Phe Thr Ala Val Gly Val Gln Asn Gln Ala Leu Gln Lys Gly Glu Tyr
 145 150 155 160

Lys Thr Gln Pro Asn Ser Pro Gln Arg Ser Asp Gly Ser Val His Ala
 165 170 175

Tyr Ala Pro Val Glu Asp Thr Pro Ala Glu Met Ala Arg Phe Ile Ser
 180 185 190

Glu Leu Glu Ser Lys Glu Phe Leu Ala Ala Glu Lys Val Ile Gln Ala
 195 200 205

Ala Tyr Ala His Tyr Ala Phe Val Cys Ile His Pro Phe Ala Asp Gly
 210 215 220

Asn Gly Arg Val Ala Arg Ala Leu Ala Ser Val Phe Leu Tyr Lys Asp
 225 230 235 240

Pro Gly Val Pro Leu Val Ile Tyr Gln Asp Gln Arg Arg Asp Tyr Ile
 245 250 255

His Ala Leu Glu Ala Ala Asp Lys Asn Asn Pro Leu Leu Leu Ile Arg
 260 265 270

Phe Phe Ala Glu Arg Val Thr Asp Thr Ile Asn Ser Ile Ile Val Asp
 275 280 285
 Leu Thr Thr Pro Ile Ala Gly Lys Ser Gly Ser Ala Lys Leu Ser Asp
 290 295 300
 Ala Leu Arg Pro Thr Arg Val Leu Pro Glu Leu His Asp Ala Ala His
 305 310 315 320
 Arg Leu Gln Glu Ser Leu Phe Thr Glu Ile Arg Ser Arg Leu Asp Glu
 325 330 335
 Glu Gly Lys Arg Asn Gly Leu Glu Phe Leu Leu Gln Arg Ile Phe Ile
 340 345 350
 Gly Ser Pro Phe Asn Leu Pro Glu Gly Tyr Asn Ala Phe Pro Asp Ser
 355 360 365
 Tyr Cys Leu Thr Leu Ala Phe Asn Ser Asn Ser Pro Lys Gln Ile Phe
 370 375 380
 His Pro Leu Ser Ile Val Ile Ala Ala Arg Asp Gly Lys Arg Ala Ser
 385 390 395 400
 Ser Asp Leu Val Ala Ala Thr Ser Ile Gly Tyr Asn Phe His Ala Tyr
 405 410 415
 Gly Arg Glu Val Glu Pro Val Val Thr Glu Ser Phe Arg Glu Arg Val
 420 425 430
 Lys Ile Tyr Ala Asp Gly Ile Val Asp His Phe Leu Thr Glu Leu Ala
 435 440 445
 Lys Lys Phe Gln Gln Asn
 450

<210> 83

<211> 1485

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> {101}..{1462}

<223> FRXA00077

<400> 83

ctaaattggt ttaacgcgtg aagcagtcgcc gccccgattt attcgaggcg gggactttcg 60

ctttccggga taaaaattgc aacgcactac actgagcagt atg aat gat gag aat 115
 Met Asn Asp Glu Asn
 1 5

att caa agc tcc aac tat cag cca ttc cgg agt ttt gac gat tgg aaa 163
 Ile Gln Ser Ser Asn Tyr Gln Pro Phe Pro Ser Phe Asp Asp Trp Lys
 10 15 20

cag atc gag gtg tgg ctc tta gat gtc atc gaa tcc tca cgc cat ttt 211
 Gln Ile Glu Val Ser Leu Leu Asp Val Ile Glu Ser Ser Arg His Phe
 25 30 35

tct gat ttg aaa gat agc act gat cgt tct gcg tta gat gct gcg cta 259
 Ser Asp Leu Lys Asp Ser Thr Asp Arg Ser Ala Leu Asp Ala Ala Leu
 40 45 50

gag aga gca aaa aga gct gcc gca gtt gat acc aat gcc ata gaa gga 307
 Glu Arg Ala Lys Arg Ala Ala Ala Val Asp Thr Asn Ala Ile Glu Gly
 55 60 65

atc ttc caa act gat cgc ggt ttt acc cat aca gtt gca acg cag gta 355
 Ile Phe Gln Thr Asp Arg Gly Phe Thr His Thr Val Ala Thr Gln Val
 70 75 80 85

ggg gct tgg gag caa caa atg gcg atg aaa ggc aaa cat gtt aag cct 403
 Gly Ala Trp Glu Gln Met Ala Met Lys Gly Lys His Val Lys Pro
 90 95 100

gcg ttt gac gat act cta gaa gcc ttt gag tat gtt ctc gat gca gta 451
 Ala Phe Asp Asp Thr Leu Glu Gly Phe Glu Tyr Val Leu Asp Ala Val
 105 110 115

act ggt aga act cca atc tct cag caa tgg att aga aat ttg cac gcc 499
 Thr Gly Arg Thr Pro Ile Ser Gln Gln Trp Ile Arg Asn Leu His Ala
 120 125 130

gtc att ctg cgg agc caa gaa agc cac gag gtt ttt aca gcc gtt gga 547
 Val Ile Leu Arg Ser Gln Glu Ser His Glu Val Phe Thr Ala Val Gly
 135 140 145

gtc caa aat cag gcg ctt cag aaa ggc gag tat aaa act cag cca aat 595
 Val Gln Asn Gln Ala Leu Gln Lys Gly Glu Tyr Lys Thr Gln Pro Asn
 150 155 160 165

agt cca cag cgc tca gat gga tct gta cat gca tac gcc cca gtt gaa 643
 Ser Pro Gln Arg Ser Asp Gly Ser Val His Ala Tyr Ala Pro Val Glu
 170 175 180

gat act cct gct gaa atg gct aga ttt att tca gaa ctt gaa tct aag 691
 Asp Thr Pro Ala Glu Met Ala Arg Phe Ile Ser Glu Leu Glu Ser Lys
 185 190 195

gaa ttc tta gca gcc gag aag gtt att caa gct gcc tat gcc cac tat 739
 Glu Phe Leu Ala Ala Glu Lys Val Ile Gln Ala Ala Tyr Ala His Tyr
 200 205 210

gct ttc gta tgt att cat cct ttt gca gat ggg aat gga cga gtt gca 787
 Ala Phe Val Cys Ile His Pro Phe Ala Asp Gly Asn Gly Arg Val Ala
 215 220 225

cga gcc ttg gct agt gtt ttt cta tac aaa gat cct ggt gtc cct ctc 835
 Arg Ala Leu Ala Ser Val Phe Leu Tyr Lys Asp Pro Gly Val Pro Leu
 230 235 240 245

gta atc tac caa gat caa cgc aga gat tac atc cat gct cta gaa gca 883
 Val Ile Tyr Gln Asp Gln Arg Arg Asp Tyr Ile His Ala Leu Glu Ala
 250 255 260

gcg gac aag aat aac cgg ctc ctg ctg att aga ttc ttt gct gaa cga 931
 Ala Asp Lys Asn Asn Pro Leu Leu Leu Ile Arg Phe Phe Ala Glu Arg
 265 270 275

gtg acc gat act att aac tct att atc gtt gat ctc act acc ccg atc 979
Val Thr Asp Thr Ile Asn Ser Ile Ile Val Asp Leu Thr Thr Pro Ile
280 285 290

gcg ggt aaa tct ggt tcg gct aag ctt tcg gat gcg cta cgc ccc act 1027
Ala Gly Lys Ser Gly Ser Ala Lys Leu Ser Asp Ala Leu Arg Pro Thr
295 300 305

cgc gta tta cca gaa tta cat gat gct gca cat agg ctc caa gaa agt 1075
Arg Val Leu Pro Glu Leu His Asp Ala Ala His Arg Leu Gln Glu Ser
310 315 320 325

tta ttt aca gaa atc cga tct cga ttg gat gaa gaa gga aaa agg aat 1123
Leu Phe Thr Glu Ile Arg Ser Arg Leu Asp Glu Glu Gly Lys Arg Asn
330 335 340

ggg ttg gag ttt cta ctt caa cgg att ttt atc ggt tcc cca ttc aat 1171
Gly Leu Glu Phe Leu Leu Gln Arg Ile Phe Ile Gly Ser Pro Phe Asn
345 350 355

ctg cca gag ggc tat aac gct ttc cct gat agc tat tgt ctg acc tta 1219
Leu Pro Glu Gly Tyr Asn Ala Phe Pro Asp Ser Tyr Cys Leu Thr Leu
360 365 370

gct ttc aat agc aac tct cca aaa caa atc ttc cac ccg cta tcc ata 1267
Ala Phe Asn Ser Asn Ser Pro Lys Gln Ile Phe His Pro Leu Ser Ile
375 380 385

gta ata gca gct cga gat ggg aaa aga gcg agc agc gac ctc gtg gca 1315
Val Ile Ala Ala Arg Asp Gly Lys Arg Ala Ser Ser Asp Leu Val Ala
390 395 400 405

gct act tct att gga tac aac ttt cac gct tac gga cgt gaa gtc gag 1363
Ala Thr Ser Ile Gly Tyr Asn Phe His Ala Tyr Gly Arg Glu Val Glu
410 415 420

cct gtt gtt act gaa agc ttt cga gaa cgt gtg aaa att tac gcc gac 1411
Pro Val Val Thr Glu Ser Phe Arg Glu Arg Val Lys Ile Tyr Ala Asp
425 430 435

ggg att gta gat cac ttc tta acc gaa ctg gct aaa aag ttt caa cag 1459
Gly Ile Val Asp His Phe Leu Thr Glu Leu Ala Lys Lys Phe Gln Gln
440 445 450

aat taattagcct atctcggtt tcg 1485
Asn

<210> 84

<211> 454

<212> PRT

<213> Corynebacterium glutamicum

<400> 84

Met Asn Asp Glu Asn Ile Gln Ser Ser Asn Tyr Gln Pro Phe Pro Ser
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20 25 30

Ser Ser Arg His Phe Ser Asp Leu Lys Asp Ser Thr Asp Arg Ser Ala
 35 40 45
 Leu Asp Ala Ala Leu Glu Arg Ala Lys Arg Ala Ala Ala Val Asp Thr
 50 55 60
 Asn Ala Ile Glu Gly Ile Phe Gln Thr Asp Arg Gly Phe Thr His Thr
 65 70 75 80
 Val Ala Thr Gln Val Gly Ala Trp Glu Gln Met Ala Met Lys Gly
 85 90 95
 Lys His Val Lys Pro Ala Phe Asp Asp Thr Leu Glu Gly Phe Glu Tyr
 100 105 110
 Val Leu Asp Ala Val Thr Gly Arg Thr Pro Ile Ser Gln Gln Trp Ile
 115 120 125
 Arg Asn Leu His Ala Val Ile Leu Arg Ser Gln Glu Ser His Glu Val
 130 135 140
 Phe Thr Ala Val Gly Val Gln Asn Gln Ala Leu Gln Lys Gly Glu Tyr
 145 150 155 160
 Lys Thr Gln Pro Asn Ser Pro Gln Arg Ser Asp Gly Ser Val His Ala
 165 170 175
 Tyr Ala Pro Val Glu Asp Thr Pro Ala Glu Met Ala Arg Phe Ile Ser
 180 185 190
 Glu Leu Glu Ser Lys Glu Phe Leu Ala Ala Glu Lys Val Ile Gln Ala
 195 200 205
 Ala Tyr Ala His Tyr Ala Phe Val Cys Ile His Pro Phe Ala Asp Gly
 210 215 220
 Asn Gly Arg Val Ala Arg Ala Leu Ala Ser Val Phe Leu Tyr Lys Asp
 225 230 235 240
 Pro Gly Val Pro Leu Val Ile Tyr Gln Asp Gln Arg Arg Asp Tyr Ile
 245 250 255
 His Ala Leu Glu Glu Ala Ala Asp Lys Asn Asn Pro Leu Leu Leu Ile Arg
 260 265 270
 Phe Phe Ala Glu Arg Val Thr Asp Thr Ile Asn Ser Ile Ile Val Asp
 275 280 285
 Leu Thr Thr Pro Ile Ala Gly Lys Ser Gly Ser Ala Lys Leu Ser Asp
 290 295 300
 Ala Leu Arg Pro Thr Arg Val Leu Pro Glu Leu His Asp Ala Ala His
 305 310 315 320
 Arg Leu Gln Glu Ser Leu Phe Thr Glu Ile Arg Ser Arg Leu Asp Glu
 325 330 335
 Glu Gly Lys Arg Asn Gly Leu Glu Phe Leu Leu Gln Arg Ile Phe Ile
 340 345 350
 Gly Ser Pro Phe Asn Leu Pro Glu Gly Tyr Asn Ala Phe Pro Asp Ser

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          355                      360                      365
Tyr Cys Leu Thr Leu Ala Phe Asn Ser Asn Ser Pro Lys Gln Ile Phe
   370                      375                      380
His Pro Leu Ser Ile Val Ile Ala Ala Arg Asp Gly Lys Arg Ala Ser
   385                      390                      395                      400
Ser Asp Leu Val Ala Ala Thr Ser Ile Gly Tyr Asn Phe His Ala Tyr
          405                      410                      415
Gly Arg Glu Val Glu Pro Val Val Thr Glu Ser Phe Arg Glu Arg Val
          420                      425                      430
Lys Ile Tyr Ala Asp Gly Ile Val Asp His Phe Leu Thr Glu Leu Ala
          435                      440                      445
Lys Lys Phe Gln Gln Asn
          450

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<210> 85

<211> 1653

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1630)

<223> RXN00080

<400> 85

atgttcttgt ttccctcatg atgagctccg tgggtctacct cgcattcgat gtggccttgg 60

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gacttaatct tccctccgga cttttgggtg gtggcctttta atg gat att ttg tcc 115
                                     Met Asp Ile Leu Ser
                                     1                               5

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ctc ttg atg gaa ggt ttc gcc ggc gcg cta acg ccg atg aac ctc ctc 163
Leu Leu Met Glu Gly Phe Ala Gly Ala Leu Thr Pro Met Asn Leu Leu
          10                      15                      20

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tgg gtg att gtc ggc tgt ttg ctc ggc acc gcg gtt ggc gtc atg cct 211
Trp Val Ile Val Gly Cys Leu Leu Gly Thr Ala Val Gly Val Met Pro
          25                      30                      35

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```

ggg ctt gga tcc tcc atg gct gtg gcg ctg ctg ctg cca atg acc ttc 259
Gly Leu Gly Ser Ser Met Ala Val Ala Leu Leu Leu Pro Met Thr Phe
          40                      45                      50

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gcg ctt gat cca act gcc gcg ttc att atg ttc tct ggc gta tat ttc 307
Ala Leu Asp Pro Thr Ala Ala Phe Ile Met Phe Ser Gly Val Tyr Phe
          55                      60                      65

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ggg ggt ctc ttc ggt gac tcc acg atg gca att ttg atg aac acc cca 355
Gly Gly Leu Phe Gly Asp Ser Thr Met Ala Ile Leu Met Asn Thr Pro
          70                      75                      80                      85

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ggg cag gca tcg gca atc gcc tca aca ttc gag ggc cac cgc atg gct 403
Gly Gln Ala Ser Ala Ile Ala Ser Thr Phe Glu Gly His Arg Met Ala
          90                      95                      100

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ctt aac ggc cgt gcg cca cag gct ctg gct acc gca gcg atc ggt gcc 451
 Leu Asn Gly Arg Ala Pro Gln Ala Leu Ala Thr Ala Ala Ile Gly Ala
 105 110 115

ttc atc ggc ggt atc gtc tcc tcc ttc atc gtg gtc ttc ctc gca cca 499
 Phe Ile Gly Gly Ile Val Ser Ser Phe Ile Val Val Phe Leu Ala Pro
 120 125 130

acc ctg gcg gaa ctg tcc acc gca ttc ggc ccc gcc gag tac ttc gca 547
 Thr Leu Ala Glu Leu Ser Thr Ala Phe Gly Pro Ala Glu Tyr Phe Ala
 135 140 145

ctg gca ctc ttc gcg ttc gtc gcc acc tcc tcc gtg gtg tcc gac tcc 595
 Leu Ala Leu Phe Ala Phe Val Ala Thr Ser Ser Val Val Ser Asp Ser
 150 155 160 165

gtg ttt aag gga ctt gcg tcc ctc att ttc ggc ctc ggc att gcg acc 643
 Val Phe Lys Gly Leu Ala Ser Leu Ile Phe Gly Leu Gly Ile Ala Thr
 170 175 180

atc ggc atc gat tgc gtc acc ggc atc gag cgc ttc acg ctc ggg gca 691
 Ile Gly Ile Asp Ser Val Thr Gly Ile Glu Arg Phe Thr Leu Gly Ala
 185 190 195

ccg cag ctt ttc gac gga att tcc ctc gtt act gtt acc gtc gcg att 739
 Pro Gln Leu Phe Asp Gly Ile Ser Leu Val Thr Val Thr Val Ala Ile
 200 205 210

ttg gca ctg gga gaa gtg ttt tac att gca gcc cgc gca cgc cgt gac 787
 Leu Ala Leu Gly Glu Val Phe Tyr Ile Ala Ala Arg Ala Arg Arg Asp
 215 220 225

aaa gca aat ctg gag acg cgc tct gca ggc cgt ccg tgg ctt acc gga 835
 Lys Ala Asn Leu Glu Thr Arg Ser Ala Gly Arg Pro Trp Leu Thr Gly
 230 235 240 245

acg gaa ttc aaa gaa gcc gct cca gcc tgg gca cgc gga acc atc att 883
 Thr Glu Phe Lys Glu Ala Ala Pro Ala Trp Ala Arg Gly Thr Ile Ile
 250 255 260

ggt ctg cct ttc ggt gtg atc cct gtt ggt gga tct gaa gtt cca acc 931
 Gly Leu Pro Phe Gly Val Ile Pro Val Gly Gly Ser Glu Val Pro Thr
 265 270 275

ttc ttg gct tac tcc acc gag cgc gca ttg gat aaa cga cgc aaa gat 979
 Phe Leu Ala Tyr Ser Thr Glu Arg Ala Leu Asp Lys Arg Arg Lys Asp
 280 285 290

ccg cag ttc ggc gat aaa ggt gca atc cga gga ctc gct gct cct gaa 1027
 Pro Gln Phe Gly Asp Lys Gly Ala Ile Arg Gly Leu Ala Ala Pro Glu
 295 300 305

gct gca ggt aac gcc acc aca ggc atg gcg atg ggc gct ctt ctt gcc 1075
 Ala Ala Gly Asn Ala Thr Thr Gly Met Ala Met Gly Ala Leu Leu Ala
 310 315 320 325

ctg ggt ctc cca gtc tct gca act gcg gcc atc atg ttg gca gcg ttc 1123
 Leu Gly Leu Pro Val Ser Ala Thr Ala Ala Ile Met Leu Ala Ala Phe
 330 335 340

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cgc cag tac gga atc cag ccc gga cca cta ctc ttc gat cgc aac cct 1171
Arg Gln Tyr Gly Ile Gln Pro Gly Pro Leu Leu Phe Asp Arg Asn Pro
      345                      350                      355

gaa ctt gtc tgg gca ctt ctt gcc agc ttc ttc atc gcg atg atc gtc 1219
Glu Leu Val Trp Ala Leu Leu Ala Ser Phe Phe Ile Ala Met Ile Val
      360                      365                      370

ctg ctg ttc atc aac ctg ccg ttc gca cag ctg tgg gca aag ctc ctg 1267
Leu Leu Phe Phe Ile Asn Leu Pro Phe Ala Gln Leu Trp Ala Lys Leu Leu
      375                      380                      385

ctc att cca aac cac tac ctc tac tcc gcc atc gca ttg ttc tgt gcc 1315
Leu Ile Pro Asn His Tyr Leu Tyr Ser Gly Ile Ala Leu Phe Cys Gly
      390                      395                      400                      405

ctg gcc att tac gcc acc tcc gcc gca gtg ttc gac ctg ctc atg ctg 1363
Leu Gly Ile Tyr Ala Thr Ser Gly Ala Val Phe Asp Leu Leu Met Leu
      410                      415                      420

ctc gcc atc ggt gtc gtg gct ttg atc atg cgt cgc tac ggt tac ccg 1411
Leu Gly Ile Gly Val Val Ala Leu Ile Met Arg Arg Tyr Gly Tyr Pro
      425                      430                      435

ctg gca ccg ctg atg atc ggt atg gtt ctt gga cct ttg gct gaa acc 1459
Leu Ala Pro Leu Met Ile Gly Met Val Leu Gly Pro Leu Ala Glu Thr
      440                      445                      450

tcc ctc cgc gac gca cta ctg tcc tgg gtt gcc gat ttc tcc atc ctc 1507
Ser Leu Arg Asp Ala Leu Leu Ser Ser Val Gly Asp Phe Ser Ile Leu
      455                      460                      465

gtc tcc agc ccc atc acc tgg tct ctc tac gca gtg ctc gcc atc ttc 1555
Val Ser Ser Pro Ile Thr Trp Ser Leu Tyr Ala Val Leu Ala Ile Phe
      470                      475                      480                      485

atc gcg gtc agt gtc atc act gca atc cgc ggt cgt cgc aag cac ctg 1603
Ile Ala Val Ser Val Ile Thr Ala Ile Arg Gly Arg Arg Lys His Leu
      490                      495                      500

act tct cag ctc gaa acc atc gac gct taaagtcgcc gtatagaaac 1650
Thr Ser Gln Leu Glu Thr Ile Asp Ala
      505                      510

agg 1653

<210> 86
<211> 510
<212> PRT
<213> Corynebacterium glutamicum

<400> 86
Met Asp Ile Leu Ser Leu Leu Met Glu Gly Phe Ala Gly Ala Leu Thr
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Pro Met Asn Leu Leu Trp Val Ile Val Gly Cys Leu Leu Gly Thr Ala
      20          25          30

Val Gly Val Met Pro Gly Leu Gly Ser Ser Met Ala Val Ala Leu Leu
      35          40          45

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Leu Pro Met Thr Phe Ala Leu Asp Pro Thr Ala Ala Phe Ile Met Phe
 50 55 60
 Ser Gly Val Tyr Phe Gly Gly Leu Phe Gly Asp Ser Thr Met Ala Ile
 65 70 75 80
 Leu Met Asn Thr Pro Gly Gln Ala Ser Ala Ile Ala Ser Thr Phe Glu
 85 90 95
 Gly His Arg Met Ala Leu Asn Gly Arg Ala Pro Gln Ala Leu Ala Thr
 100 105 110
 Ala Ala Ile Gly Ala Phe Ile Gly Gly Ile Val Ser Ser Phe Ile Val
 115 120 125
 Val Phe Leu Ala Pro Thr Leu Ala Glu Leu Ser Thr Ala Phe Gly Pro
 130 135 140
 Ala Glu Tyr Phe Ala Leu Ala Leu Phe Ala Phe Val Ala Thr Ser Ser
 145 150 155 160
 Val Val Ser Asp Ser Val Phe Lys Gly Leu Ala Ser Leu Ile Phe Gly
 165 170 175
 Leu Gly Ile Ala Thr Ile Gly Ile Asp Ser Val Thr Gly Ile Glu Arg
 180 185 190
 Phe Thr Leu Gly Ala Pro Gln Leu Phe Asp Gly Ile Ser Leu Val Thr
 195 200 205
 Val Thr Val Ala Ile Leu Ala Leu Gly Glu Val Phe Tyr Ile Ala Ala
 210 215 220
 Arg Ala Arg Arg Asp Lys Ala Asn Leu Glu Thr Arg Ser Ala Gly Arg
 225 230 235 240
 Pro Trp Leu Thr Gly Thr Glu Phe Lys Glu Ala Ala Pro Ala Trp Ala
 245 250 255
 Arg Gly Thr Ile Ile Gly Leu Pro Phe Gly Val Ile Pro Val Gly Gly
 260 265 270
 Ser Glu Val Pro Thr Phe Leu Ala Tyr Ser Thr Glu Arg Ala Leu Asp
 275 280 285
 Lys Arg Arg Lys Asp Pro Gln Phe Gly Asp Lys Gly Ala Ile Arg Gly
 290 295 300
 Leu Ala Ala Pro Glu Ala Ala Gly Asn Ala Thr Thr Gly Met Ala Met
 305 310 315 320
 Gly Ala Leu Leu Ala Leu Gly Leu Pro Val Ser Ala Thr Ala Ala Ile
 325 330 335
 Met Leu Ala Ala Phe Arg Gln Tyr Gly Ile Gln Pro Gly Pro Leu Leu
 340 345 350
 Phe Asp Arg Asn Pro Glu Leu Val Trp Ala Leu Leu Ala Ser Phe Phe
 355 360 365

Ile	Ala	Met	Ile	Val	Leu	Leu	Phe	Ile	Asn	Leu	Pro	Phe	Ala	Gln	Leu
370							375					380			
Trp	Ala	Lys	Leu	Leu	Leu	Ile	Pro	Asn	His	Tyr	Leu	Tyr	Ser	Gly	Ile
385					390					395					400
Ala	Leu	Phe	Cys	Gly	Leu	Gly	Ile	Tyr	Ala	Thr	Ser	Gly	Ala	Val	Phe
				405					410					415	
Asp	Leu	Leu	Met	Leu	Leu	Gly	Ile	Gly	Val	Val	Ala	Leu	Ile	Met	Arg
			420					425					430		
Arg	Tyr	Gly	Tyr	Pro	Leu	Ala	Pro	Leu	Met	Ile	Gly	Met	Val	Leu	Gly
		435					440					445			
Pro	Leu	Ala	Glu	Thr	Ser	Leu	Arg	Asp	Ala	Leu	Leu	Ser	Ser	Val	Gly
	450					455					460				
Asp	Phe	Ser	Ile	Leu	Val	Ser	Ser	Pro	Ile	Thr	Trp	Ser	Leu	Tyr	Ala
465					470					475					480
Val	Leu	Ala	Ile	Phe	Ile	Ala	Val	Ser	Val	Ile	Thr	Ala	Ile	Arg	Gly
				485					490					495	
Arg	Arg	Lys	His	Leu	Thr	Ser	Gln	Leu	Glu	Thr	Ile	Asp	Ala		
			500						505				510		

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<210> 87
<211> 543
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(520)
<223> FRXA00080
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400> 87	ttggcagcgt tccgccagta cggaaatccag ccoggaccac tactcttcca tegcaaccct	60
gaacttgtct gggcacttct tgccagcttc ttctatcgcg	atg atc gtc ctg ctg Met Ile Val Leu Leu	115
	1 5	
ttc atc aac ctg ccg ttc gca cag ctg tgg gca aag ctc ctg ctc att		163
Phe Ile Asn Leu	Pro Phe Ala Gln Leu Trp Ala Lys Leu Leu Leu Ile	
	10 15 20	
cca aac cac tac ctc tac tcc gcc atc gca ttg ttc tgt gcc ctg gcc		211
Pro Asn His Tyr Leu Tyr Ser Gly Ile Ala Leu Phe Cys Gly Leu Gly		
	25 30 35	
att tac gcc acc tcc gcc gca gtg ttc gac ctg ctc atg ctg ctc gcc		259
Ile Tyr Ala Thr Ser Gly Ala Val Phe Asp Leu Leu Met Leu Leu Gly		
	40 45 50	
atc ggt gtc gtg gct ttg atc atg cgt cgc tac ggt tac ccg ctg gca		307
Ile Gly Val Val Ala Leu Ile Met Arg Arg Tyr Gly Tyr Pro Leu Ala		
	55 60 65	

```

ccg ctg atg atc ggt atg gtt ctt gga cct ttg gct gaa acc tcc ctc 355
Pro Leu Met Ile Gly Met Val Leu Gly Pro Leu Ala Glu Thr Ser Leu
70 75 80 85

cgc gac gca cta ctg tcc tcg gtt ggc gat ttc tcc atc ctc gtc tcc 403
Arg Asp Ala Leu Leu Ser Ser Val Gly Asp Phe Ser Ile Leu Val Ser
90 95 100

agc ccc atc acc tgg tct ctc tac gca gtg ctc gcc atc ttc atc gcg 451
Ser Pro Ile Thr Trp Ser Leu Tyr Ala Val Leu Ala Ile Phe Ile Ala
105 110 115

gtc agt gtc atc act gca atc cgc ggt cgt cgc aag cac ctg act tct 499
Val Ser Val Ile Thr Ala Ile Arg Gly Arg Arg Lys His Leu Thr Ser
120 125 130

cag ctc gaa acc atc gac gct taaagtcccc gtatagaac agg 543
Gln Leu Glu Thr Ile Asp Ala
135 140

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<210> 88

<211> 140

<212> PRT

<213> Corynebacterium glutamicum

<400> 88

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Met Ile Val Leu Leu Phe Ile Asn Leu Pro Phe Ala Gln Leu Trp Ala
1 5 10 15

```

```

Lys Leu Leu Leu Ile Pro Asn His Tyr Leu Tyr Ser Gly Ile Ala Leu
20 25 30

```

```

Phe Cys Gly Leu Gly Ile Tyr Ala Thr Ser Gly Ala Val Phe Asp Leu
35 40 45

```

```

Leu Met Leu Leu Gly Ile Gly Val Val Ala Leu Ile Met Arg Arg Tyr
50 55 60

```

```

Gly Tyr Pro Leu Ala Pro Leu Met Ile Gly Met Val Leu Gly Pro Leu
65 70 75 80

```

```

Ala Glu Thr Ser Leu Arg Asp Ala Leu Leu Ser Ser Val Gly Asp Phe
85 90 95

```

```

Ser Ile Leu Val Ser Ser Pro Ile Thr Trp Ser Leu Tyr Ala Val Leu
100 105 110

```

```

Ala Ile Phe Ile Ala Val Ser Val Ile Thr Ala Ile Arg Gly Arg Arg
115 120 125

```

```

Lys His Leu Thr Ser Gln Leu Glu Thr Ile Asp Ala
130 135 140

```

<210> 89

<211> 651

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> {101}..(628)

<223> RXN00087

<400> 89

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tcgtcagtc acaaacgttt tcccaccocgg aggtctcccc gtgtctaccg aaatccacaa 60
cgcccccccc aaggcccccaa ctgggcttgg ctgggtgctc atg atc ggc gga ata 115
Met Ile Gly Gly Ile
1 5

atc ggc ctc att ttg tgg gtg atc atc atg gcc gaa aaa ctt gcc atc 163
Ile Gly Leu Ile Leu Ser Val Ile Ile Met Ala Glu Lys Leu Ala Ile
10 15 20

ctc gag gat ccc ggt cac atc acc agc tgc gat ttc aat gca gtc cta 211
Leu Glu Asp Pro Gly His Ile Thr Ser Cys Asp Phe Asn Ala Val Leu
25 30 35

gct tgt ggc gat gtc atg cgt tcc ggc caa gct aac gcg ttc ggc atc 259
Ala Cys Gly Asp Val Met Arg Ser Gly Gln Ala Asn Ala Phe Gly Ile
40 45 50

ccg aat ccg ctc atc ggc atc gcc ggt ttc gcc gct gtc gcc atc atc 307
Pro Asn Pro Leu Ile Gly Ile Ala Gly Phe Ala Ala Val Ala Ile Ile
55 60 65

ggc gcc ggc atc ctc gcg gcc gcc ggg ttc cgc ggt tgg ttc tgg ttc 355
Gly Ala Gly Ile Leu Ala Gly Gly Gly Phe Arg Gly Trp Phe Trp Phe
70 75 80 85

ggc gcc cag gcc gga ctc act ttt gcc atg atg ttc tgc cac tgg ctc 403
Gly Ala Gln Ala Gly Leu Thr Phe Ala Met Met Phe Cys His Trp Leu
90 95 100

gcc tac caa tcc atg tcc gtc atc cgc gcg ctc tgc cct tac tgc atg 451
Ala Tyr Gln Ser Met Ser Val Ile Arg Ala Leu Cys Pro Tyr Cys Met
105 110 115

ggc gtg tgg acc gta tgg atc atc atg ttc gtg ctg gtc act gca tgg 499
Gly Val Trp Thr Val Ser Ile Ile Met Phe Val Leu Val Thr Ala Trp
120 125 130

aat gtg aaa act ttc agc gcc tcc gac agc acg ttc gtc aac gca ctg 547
Asn Val Lys Thr Phe Ser Gly Ser Asp Ser Thr Phe Val Asn Ala Leu
135 140 145

tac aaa tac aag tgg gtc atc gcg atc gtc tgg ctg ctg ctc atc gca 595
Tyr Lys Tyr Lys Trp Val Ile Ala Ile Val Trp Leu Leu Leu Ile Ala
150 155 160 165

gcc gca gct gtg tgg tca ttc cgc tac atg ttc taggcattta aggtcttcag 648
Ala Ala Ala Val Trp Ser Phe Arg Tyr Met Phe
170 175

gcc 651

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<210> 90

<211> 176

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 90

Met Ile Gly Gly Ile Ile Gly Leu Ile Leu Ser Val Ile Ile Met Ala
 1 5 10 15

Glu Lys Leu Ala Ile Leu Glu Asp Pro Gly His Ile Thr Ser Cys Asp
 20 25 30

Phe Asn Ala Val Leu Ala Cys Gly Asp Val Met Arg Ser Gly Gln Ala
 35 40 45

Asn Ala Phe Gly Ile Pro Asn Pro Leu Ile Gly Ile Ala Gly Phe Ala
 50 55 60

Ala Val Ala Ile Ile Gly Ala Gly Ile Leu Ala Gly Gly Gly Phe Arg
 65 70 75 80

Gly Trp Phe Trp Phe Gly Ala Gln Ala Gly Leu Thr Phe Ala Met Met
 85 90 95

Phe Cys His Trp Leu Ala Tyr Gln Ser Met Ser Val Ile Arg Ala Leu
 100 105 110

Cys Pro Tyr Cys Met Gly Val Trp Thr Val Ser Ile Ile Met Phe Val
 115 120 125

Leu Val Thr Ala Trp Asn Val Lys Thr Phe Ser Gly Ser Asp Ser Thr
 130 135 140

Phe Val Asn Ala Leu Tyr Lys Tyr Lys Trp Val Ile Ala Ile Val Trp
 145 150 155 160

Leu Leu Leu Ile Ala Ala Ala Ala Val Trp Ser Phe Arg Tyr Met Phe
 165 170 175

<210> 91

<211> 651

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(628)

<223> FRXA00087

<400> 91

tcgtcagtc acaaacgttt tcccaccgg aggtctcccc gtgtctaccg aaatocacaa 60

cgccccacc aaggcccaaa cttggcttgg ctgggtgctc atg atc ggc gga ata 115
 Met Ile Gly Gly Ile
 1 5

atc ggc ctg att ttg tgg gtg atc atc atg gcc gaa aaa ctt gcc atc 163
 Ile Gly Leu Ile Leu Ser Val Ile Ile Met Ala Glu Lys Leu Ala Ile
 10 15 20

ctc gag gat ccc ggt cac atc acc agc tgc gat ttc aat gca gtc cta 211
 Leu Glu Asp Pro Gly His Ile Thr Ser Cys Asp Phe Asn Ala Val Leu
 25 30 35

 gct tgt ggc gat gtc atg cgt tcc ggc caa gct aac gcg ttc ggc atc 259
 Ala Cys Gly Asp Val Met Arg Ser Gly Gln Ala Asn Ala Phe Gly Ile
 40 45 50

 ccg aat ccg ctc atc ggc atc gcc ggt ttc gcc gct gtc gcc atc atc 307
 Pro Asn Pro Leu Ile Gly Ile Ala Gly Phe Ala Ala Val Ala Ile Ile
 55 60 65

 ggc gcc ggc atc ctc gcg ggc ggc ggg ttc cgc ggt tgg ttc tgg ttc 355
 Gly Ala Gly Ile Leu Ala Gly Gly Gly Phe Arg Gly Trp Phe Trp Phe
 70 75 80 85

 ggc gcc gag gcc gga ctc act ttt gcc atg atg ttc tgc cac tgg ctc 403
 Gly Ala Gln Ala Gly Leu Thr Phe Ala Met Met Phe Cys His Trp Leu
 90 95 100

 gcc tac caa tcc atg tcc gtc atc cgc gcg ctc tgc cct tac tgc atg 451
 Ala Tyr Gln Ser Met Ser Val Ile Arg Ala Leu Cys Pro Tyr Cys Met
 105 110 115

 ggc gtg tgg acc gta tcg atc atc atg ttc gtg ctg gtc act gca tgg 499
 Gly Val Trp Thr Val Ser Ile Ile Met Phe Val Leu Val Thr Ala Trp
 120 125 130

 aat gtg aaa act ttc agc ggc tcc gac agc acg ttc gtc aac gca ctg 547
 Asn Val Lys Thr Phe Ser Gly Ser Asp Ser Thr Phe Val Asn Ala Leu
 135 140 145

 tac aaa tac aag tgg gtc atc gcg atc gtc tgg ctg ctg ctc atc gca 595
 Tyr Lys Tyr Lys Trp Val Ile Ala Ile Val Trp Leu Leu Leu Ile Ala
 150 155 160 165

 gcc gca gct gtg tgg tca ttc cgc tac atg ttc taggcattta aggcatttcag 648
 Ala Ala Ala Val Trp Ser Phe Arg Tyr Met Phe
 170 175

 gcc 651

<210> 92

<211> 176

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 92

Met Ile Gly Gly Ile Ile Gly Leu Ile Leu Ser Val Ile Ile Met Ala
 1 5 10 15

Glu Lys Leu Ala Ile Leu Glu Asp Pro Gly His Ile Thr Ser Cys Asp
 20 25 30

Phe Asn Ala Val Leu Ala Cys Gly Asp Val Met Arg Ser Gly Gln Ala
 35 40 45

Asn Ala Phe Gly Ile Pro Asn Pro Leu Ile Gly Ile Ala Gly Phe Ala
 50 55 60

Ala Val Ala Ile Ile Gly Ala Gly Ile Leu Ala Gly Gly Gly Phe Arg
 65 70 75 80

Gly Trp Phe Trp Phe Gly Ala Gln Ala Gly Leu Thr Phe Ala Met Met
 85 90 95

Phe Cys His Trp Leu Ala Tyr Gln Ser Met Ser Val Ile Arg Ala Leu
 100 105 110

Cys Pro Tyr Cys Met Gly Val Trp Thr Val Ser Ile Ile Met Phe Val
 115 120 125

Leu Val Thr Ala Trp Asn Val Lys Thr Phe Ser Gly Ser Asp Ser Thr
 130 135 140

Phe Val Asn Ala Leu Tyr Lys Tyr Lys Trp Val Ile Ala Ile Val Trp
 145 150 155 160

Leu Leu Leu Ile Ala Ala Ala Val Trp Ser Phe Arg Tyr Met Phe
 165 170 175

<210> 93

<211> 426

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(403)

<223> RXN00096

<400> 93

ggggaacctg gggtaaaagg agaagtattc attaccccaa taacctacta ggtgggggtg 60

acacgcatag tcgacagcca gacgtggcag aatagtgtgc atg act aat gca ggt 115
 Met Thr Asn Ala Gly
 1 5

gac aac ttc gag atc agg atg cct tct ggc acg gat gac cca ttg tcc 163
 Asp Asn Phe Glu Ile Arg Met Pro Ser Gly Thr Asp Asp Pro Leu Ser
 10 15 20

gat gcg gag atc caa aag tat cgc gag gag atc aac cgc ttg gac cgc 211
 Asp Ala Glu Ile Gln Lys Tyr Arg Glu Glu Ile Asn Arg Leu Asp Arg
 25 30 35

gaa atc ctc gat gcg gtg aaa cgc cgc acg aag att tcc caa acc atc 259
 Glu Ile Leu Asp Ala Val Lys Arg Arg Thr Lys Ile Ser Gln Thr Ile
 40 45 50

gga aaa aca cgc atg agc tcg ggc gga aca cgt ctc gtg cac acc cga 307
 Gly Lys Thr Arg Met Ser Ser Gly Gly Thr Arg Leu Val His Thr Arg
 55 60 65

gaa gta gca atc atc aac caa ttc cgt gaa gag atc ggc gag gaa ggc 355
 Glu Val Ala Ile Ile Asn Gln Phe Arg Glu Glu Ile Gly Glu Glu Gly
 70 75 80 85

```
cct gcc ctc gct gga att ttg ctg cgc atg gga cgc gga aaa ctc gga 403
Pro Ala Leu Ala Gly Ile Leu Leu Arg Met Gly Arg Gly Lys Leu Gly
          90          95          100
```

```
taagttatcc acaggtagaa aaa 426
```

```
<210> 94
<211> 101
<212> PRT
<213> Corynebacterium glutamicum
```

```
<400> 94
Met Thr Asn Ala Gly Asp Asn Phe Glu Ile Arg Met Pro Ser Gly Thr
 1          5          10          15
Asp Asp Pro Leu Ser Asp Ala Glu Ile Gln Lys Tyr Arg Glu Glu Ile
          20          25          30
Asn Arg Leu Asp Arg Glu Ile Leu Asp Ala Val Lys Arg Arg Thr Lys
          35          40          45
```

```
Ile Ser Gln Thr Ile Gly Lys Thr Arg Met Ser Ser Gly Gly Thr Arg
          50          55          60
```

```
Leu Val His Thr Arg Glu Val Ala Ile Ile Asn Gln Phe Arg Glu Glu
          65          70          75          80
```

```
Ile Gly Glu Glu Gly Pro Ala Leu Ala Gly Ile Leu Leu Arg Met Gly
          85          90          95
```

```
Arg Gly Lys Leu Gly
          100
```

```
<210> 95
<211> 426
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(403)
<223> FRXA00096
```

```
<400> 95
ggggaacctg gggtaaaagg agaagtattc attaccccaa taacctacta ggtgggggtgg 60
```

```
acacgcatag tcgacagcca gacgtggcag aatagtgtgc atg act aat gca ggt 115
          Met Thr Asn Ala Gly
          1          5
```

```
gac aac ttc gag atc agg atg cct tct ggc acg gat gac cca ttg tcc 163
Asp Asn Phe Glu Ile Arg Met Pro Ser Gly Thr Asp Asp Pro Leu Ser
          10          15          20
```

```
gat gcg gag atc caa aag tat cgc gag gag atc aac cgc ttg gac cgc 211
Asp Ala Glu Ile Gln Lys Tyr Arg Glu Glu Ile Asn Arg Leu Asp Arg
          25          30          35
```

```

gaa atc ctc gat gcg gtg aaa cgc cgc acg aag att tcc caa acc atc 259
Glu Ile Leu Asp Ala Val Lys Arg Arg Thr Lys Ile Ser Gln Thr Ile
      40                      45                      50

gga aaa aca cgc atg agc tcg ggc gga aca cgt ctc gtg cac acc cga 307
Gly Lys Thr Arg Met Ser Ser Gly Gly Thr Arg Leu Val His Thr Arg
      55                      60                      65

gaa gta gca atc atc aac cag ttc cgt gaa gag atc ggc gag gaa ggc 355
Glu Val Ala Ile Ile Asn Gln Phe Arg Glu Ile Gly Glu Glu Gly
      70                      75                      80                      85

cct gcc ctc gct gga att ttg ctg cgc atg gga cgc gga aaa ctc gga 403
Pro Ala Leu Ala Gly Ile Leu Leu Arg Met Gly Arg Gly Lys Leu Gly
      90                      95                      100

taagttatcc acaggtagaa aaa 426

```

```

<210> 96
<211> 101
<212> PRT
<213> Corynebacterium glutamicum

```

```

<400> 96
Met Thr Asn Ala Gly Asp Asn Phe Glu Ile Arg Met Pro Ser Gly Thr
  1                      5                      10                      15

Asp Asp Pro Leu Ser Asp Ala Glu Ile Gln Lys Tyr Arg Glu Glu Ile
      20                      25                      30

Asn Arg Leu Asp Arg Glu Ile Leu Asp Ala Val Lys Arg Arg Thr Lys
      35                      40                      45

Ile Ser Gln Thr Ile Gly Lys Thr Arg Met Ser Ser Gly Gly Thr Arg
      50                      55                      60

Leu Val His Thr Arg Glu Val Ala Ile Ile Asn Gln Phe Arg Glu Glu
      65                      70                      75                      80

Ile Gly Glu Glu Gly Pro Ala Leu Ala Gly Ile Leu Leu Arg Met Gly
      85                      90                      95

Arg Gly Lys Leu Gly
      100

```

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<210> 97
<211> 1299
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(1276)
<223> RXN00097

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<400> 97
tcagggtttt agccgttgat ggcgagagtt atccacaggt ttttagcgag ctggtttccg 60
acgaagaaaa tagtgatag gttacagggc agaatccoga atg gag gtg cct tcc 115

```

	Met	Glu	Val	Pro	Ser	
	1				5	
ttg ttt acc aac ttc ttc gca gtc aac aac cca gac agt ccg ccc gca	163					
Leu Phe Thr Asn Phe Phe Ala Val Asn Asn Pro Asp Ser Pro Pro Ala						
	10				15	20
cga caa aaa acc aaa ctc aga gaa ctg gaa cac cgc ttc tgg caa gaa	211					
Arg Gln Lys Thr Lys Leu Arg Glu Leu Glu His Arg Phe Trp Gln Glu						
	25				30	35
cac ctg cca ggc gac gac gat gac cat tcc acc gca atc tcc agc ctc	259					
His Leu Pro Gly Asp Asp Asp His Ser Thr Ala Ile Ser Ser Leu						
	40				45	50
gcc atc gtc aca ggt cta aca aaa cgc cag gtc tcc cgc ata tcc atc	307					
Ala Ile Val Thr Gly Leu Thr Lys Ala Gln Val Ser Arg Ile Ser Ile						
	55				60	65
gcg ttt gcc acg ctc gcc gac ttg ccc gaa ctc aaa gcc ctg caa caa	355					
Ala Phe Ala Thr Leu Ala Asp Leu Pro Glu Leu Lys Ala Leu Gln Gln						
	70				75	80
aag ctg tac cac ctc gac ctc tcc cga ctg atc acc att agc aac gaa	403					
Lys Leu Tyr His Leu Asp Leu Ser Arg Leu Ile Thr Ile Ser Asn Glu						
	90				95	100
ctc gcc ggc atc aac ccc gac aac ctc gcc ggc gcc gac gca atc ctc	451					
Leu Ala Gly Ile Asn Pro Asp Asn Leu Ala Gly Ala Asp Ala Ile Leu						
	105				110	115
acc gaa tac ctc acc gcc acc agc ccc aac cag att ctg cca agc ccg	499					
Thr Glu Tyr Leu Thr Ala Thr Ser Pro Asn Gln Ile Leu Pro Ser Pro						
	120				125	130
gcg tcc ata gga cgc aag ata aaa gaa ata aga gat ttg ctt gac gac	547					
Ala Ser Ile Gly Arg Lys Ile Lys Glu Ile Arg Asp Leu Leu Asp Asp						
	135				140	145
gca aga gcc acc ggt tgc cgc ggt acc caa gac gac agc tct ttc gga	595					
Ala Arg Ala Thr Gly Ser Arg Gly Thr Gln Asp Asp Ser Ser Phe Gly						
	150				155	160
gtg acc ttc tcc cca gac gga acc gcc gaa atc gga gcc tcc gtc gat	643					
Val Thr Phe Ser Pro Asp Gly Thr Ala Glu Ile Gly Ala Ser Val Asp						
	170				175	180
gct gtg gac ggg cac atc atc aac gac gcc gtc acc caa cac ccg aag	691					
Ala Val Asp Gly His Ile Ile Asn Asp Ala Val Thr Gln His Ala Lys						
	185				190	195
aaa aac gac ctc acc tac ggc gaa gct ttc agc gac atc ctt ccg aac	739					
Lys Asn Asp Leu Thr Tyr Gly Glu Ala Phe Ser Asp Ile Leu Arg Asn						
	200				205	210
aat atc caa gtc aag gta gtc ctc aac ttg tac acc gcc aaa gac ctc	787					
Asn Ile Gln Val Lys Val Val Leu Asn Leu Tyr Thr Ala Lys Asp Leu						
	215				220	225
gcc aac gcc cca gtg tgg gcc agc gga atc gcc tgg ttg gat gcc aag	835					
Ala Asn Ala Pro Val Trp Ala Ser Gly Ile Gly Trp Leu Asp Ala Lys						

230	235	240	245	
act gga aca ttc tgg tca gag aaa gcc aac aaa gaa caa gac atg gat				883
Thr Gly Thr Phe Trp Ser Glu Lys Ala Asn Lys Glu Gln Asp Met Asp	250	255	260	
gcg gct gcc aaa atc agc acc gac aaa cac gat cct cca cca gcg ttg				931
Ala Ala Ala Lys Ile Ser Thr Asp Lys His Asp Pro Pro Ala Leu	265	270	275	
cgt gac gca ctc att ggt cgt gat ggc acc tgc cga ttc cct ggc tgt				979
Arg Asp Ala Leu Ile Gly Arg Asp Gly Thr Cys Arg Phe Pro Gly Cys	280	285	290	
tca gtc cca gcg ctc aaa acc caa gcc gac cac cgc atc ccc tac gaa				1027
Ser Val Pro Ala Leu Lys Thr Gln Ala Asp His Arg Ile Pro Tyr Glu	295	300	305	
gaa ggc gga gaa act tgc cta ggc gga atc ggc tgc ctc tgt caa cac				1075
Glu Gly Gly Glu Thr Cys Leu Gly Gly Ile Gly Cys Leu Cys Gln His	310	315	320	325
cac cac aac atg aaa acc gac ggc cga gtc acc tac ctt ctc gat ccc				1123
His His Asn Met Lys Thr Asp Gly Arg Val Thr Tyr Leu Leu Asp Pro	330	335	340	
ttc tcc ggc atc atc gtc tgg ctc atg gga gac gga aca tgg gca gtg				1171
Phe Ser Gly Ile Ile Val Trp Leu Met Gly Asp Gly Thr Trp Ala Val	345	350	355	
tca gaa ccc aac ggg ccg ctc aat ccc aaa aat gcg aga tgg gcg caa				1219
Ser Glu Pro Asn Gly Pro Leu Asn Pro Lys Asn Ala Arg Trp Ala Gln	360	365	370	
aca gtc gcc caa cac cgg gca cgc cac cac aag cgt tgg gtt aag gag				1267
Thr Val Ala Gln His Arg Ala Arg His His Lys Arg Trp Val Lys Glu	375	380	385	
gac gcc aag tagccggatg gccacgtcga aaa				1299
Asp Ala Lys				
390				

<210> 98

<211> 392

<212> PRT

<213> Corynebacterium glutamicum

<400> 98

Met	Glu	Val	Pro	Ser	Leu	Phe	Thr	Asn	Phe	Phe	Ala	Val	Asn	Asn	Pro
1					5				10					15	

Asp	Ser	Pro	Pro	Ala	Arg	Gln	Lys	Thr	Lys	Leu	Arg	Glu	Leu	Glu	His
				20					25					30	

Arg	Phe	Trp	Gln	Glu	His	Leu	Pro	Gly	Asp	Asp	Asp	Asp	His	Ser	Thr
		35						40				45			

Ala	Ile	Ser	Ser	Leu	Ala	Ile	Val	Thr	Gly	Leu	Thr	Lys	Ala	Gln	Val

50

55

60

Ser Arg Ile Ser Ile Ala Phe Ala Thr Leu Ala Asp Leu Pro Glu Leu
 65 70 75 80
 Lys Ala Leu Gln Gln Lys Leu Tyr His Leu Asp Leu Ser Arg Leu Ile
 85 90 95
 Thr Ile Ser Asn Glu Leu Ala Gly Ile Asn Pro Asp Asn Leu Ala Gly
 100 105 110
 Ala Asp Ala Ile Leu Thr Glu Tyr Leu Thr Ala Thr Ser Pro Asn Gln
 115 120 125
 Ile Leu Pro Ser Pro Ala Ser Ile Gly Arg Lys Ile Lys Glu Ile Arg
 130 135 140
 Asp Leu Leu Asp Asp Ala Arg Ala Thr Gly Ser Arg Gly Thr Gln Asp
 145 150 155 160
 Asp Ser Ser Phe Gly Val Thr Phe Ser Pro Asp Gly Thr Ala Glu Ile
 165 170 175
 Gly Ala Ser Val Asp Ala Val Asp Gly His Ile Ile Asn Asp Ala Val
 180 185 190
 Thr Gln His Ala Lys Lys Asn Asp Leu Thr Tyr Gly Glu Ala Phe Ser
 195 200 205
 Asp Ile Leu Arg Asn Asn Ile Gln Val Lys Val Val Leu Asn Leu Tyr
 210 215 220
 Thr Ala Lys Asp Leu Ala Asn Ala Pro Val Trp Ala Ser Gly Ile Gly
 225 230 235 240
 Trp Leu Asp Ala Lys Thr Gly Thr Phe Trp Ser Glu Lys Ala Asn Lys
 245 250 255
 Glu Gln Asp Met Asp Ala Ala Ala Lys Ile Ser Thr Asp Lys His Asp
 260 265 270
 Pro Pro Pro Ala Leu Arg Asp Ala Leu Ile Gly Arg Asp Gly Thr Cys
 275 280 285
 Arg Phe Pro Gly Cys Ser Val Pro Ala Leu Lys Thr Gln Ala Asp His
 290 295 300
 Arg Ile Pro Tyr Glu Glu Gly Gly Glu Thr Cys Leu Gly Gly Ile Gly
 305 310 315 320
 Cys Leu Cys Gln His His His Asn Met Lys Thr Asp Gly Arg Val Thr
 325 330 335
 Tyr Leu Leu Asp Pro Phe Ser Gly Ile Ile Val Trp Leu Met Gly Asp
 340 345 350
 Gly Thr Trp Ala Val Ser Glu Pro Asn Gly Pro Leu Asn Pro Lys Asn
 355 360 365
 Ala Arg Trp Ala Gln Thr Val Ala Gln His Arg Ala Arg His His Lys
 370 375 380
 Arg Trp Val Lys Glu Asp Ala Lys

385

390

<210> 99
 <211> 1284
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1261)
 <223> FRXA00097

<400> 99
 ttgatgggca gagttatcca caggttttta gcgagctggt ttccgacgaa gaaaatagtg 60
 gataggttac agggcagaat ccggaatgga ggtgccttcc ttg ttt acc aac ttc 115
 Leu Phe Thr Asn Phe
 1 5
 ttc gca gtc aac aac cca gac agt ccg ccc gca cga caa aaa acc aaa 163
 Phe Ala Val Asn Asn Pro Asp Ser Pro Pro Ala Arg Gln Lys Thr Lys
 10 15 20
 ctc aga gaa ctg gaa cac cgc ttc tgg caa gaa cac ctg cca ggc gac 211
 Leu Arg Glu Leu Glu His Arg Phe Trp Gln Glu His Leu Pro Gly Asp
 25 30 35
 gac gat gac cat tcc acc gca atc tcc agc ctc gcc atc gtc aca ggt 259
 Asp Asp Asp His Ser Thr Ala Ile Ser Ser Leu Ala Ile Val Thr Gly
 40 45 50
 cta aca aaa gcg cag gtc tcc cgc ata tcc atc gcg ttt gcc acg ctc 307
 Leu Thr Lys Ala Gln Val Ser Arg Ile Ser Ile Ala Phe Ala Thr Leu
 55 60 65
 gcc gac ttg ccc gaa ctc aaa gcc ctg caa caa aag ctg tac cac ctc 355
 Ala Asp Leu Pro Glu Leu Lys Ala Leu Gln Gln Lys Leu Tyr His Leu
 70 75 80 85
 gac ctc tcc cga ctg atc acc att agc aac gaa ctc gcc ggc atc aac 403
 Asp Leu Ser Arg Leu Ile Thr Ile Ser Asn Glu Leu Ala Gly Ile Asn
 90 95 100
 ccc gac aac ctc gcc ggc gcc gac gca atc ctc acc gaa tac ctc acc 451
 Pro Asp Asn Leu Ala Gly Ala Asp Ala Ile Leu Thr Glu Tyr Leu Thr
 105 110 115
 gcc acc agc ccc aac cag att ctg cca agc ccg gcg tcc ata gga cgc 499
 Ala Thr Ser Pro Asn Gln Ile Leu Pro Ser Pro Ala Ser Ile Gly Arg
 120 125 130
 aag ata aaa gaa ata aga gat ttg ctt gac gac gca aga gcc acc ggt 547
 Lys Ile Lys Glu Ile Arg Asp Leu Leu Asp Asp Ala Arg Ala Thr Gly
 135 140 145
 tcg cgc ggt acc caa gac gac agc tct ttc gga gtg acc ttc tcc cca 595
 Ser Arg Gly Thr Gln Asp Asp Ser Ser Phe Gly Val Thr Phe Ser Pro
 150 155 160 165
 gac gga acc gcc gaa atc gga gcc tcc gtc gat gct gtg gac ggg cac 643

Asp Gly Thr Ala Glu Ile Gly Ala Ser Val Asp Ala Val Asp Gly His	
170 175 180	
atc atc aac gac gcc gtc acc caa cac gcg aag aaa aac gac ctc acc	691
Ile Ile Asn Asp Ala Val Thr Gln His Ala Lys Lys Asn Asp Leu Thr	
185 190 195	
tac ggc gaa get ttc agc gac atc ctt cgg aac aat atc caa gtc aag	739
Tyr Gly Glu Ala Phe Ser Asp Ile Leu Arg Asn Asn Ile Gln Val Lys	
200 205 210	
gta gtc ctc aac ttg tac acc gcc aaa gac ctc gcc aac gcc cca gtg	787
Val Val Leu Asn Leu Tyr Thr Ala Lys Asp Leu Ala Asn Ala Pro Val	
215 220 225	
tgg gcc agc gga atc gcc tgg ttg gat gcc aag act gga aca ttc tgg	835
Trp Ala Ser Gly Ile Gly Trp Leu Asp Ala Lys Thr Gly Thr Phe Trp	
230 235 240 245	
tca gag aaa gcc aac aaa gaa caa gac atg gat gcg gct gcc aaa atc	883
Ser Glu Lys Ala Asn Lys Glu Gln Asp Met Asp Ala Ala Ala Lys Ile	
250 255 260	
agc acc gac aaa cac gat cct cca cca gcg ttg cgt gac gca ctc att	931
Ser Thr Asp Lys His Asp Pro Pro Pro Ala Leu Arg Asp Ala Leu Ile	
265 270 275	
ggt cgt gat ggc acc tgc cga ttc cct ggc tgt tca gtc cca gcg ctc	979
Gly Arg Asp Gly Thr Cys Arg Phe Pro Gly Cys Ser Val Pro Ala Leu	
280 285 290	
aaa acc caa gcc gac cac cgc atc ccc tac gaa gaa ggc gga gaa act	1027
Lys Thr Gln Ala Asp His Arg Ile Pro Tyr Glu Glu Gly Gly Glu Thr	
295 300 305	
tgc cta ggc gga atc gcc tgc ctc tgt caa cac cac cac aac atg aaa	1075
Cys Leu Gly Gly Ile Gly Cys Leu Cys Gln His His His Asn Met Lys	
310 315 320 325	
acc gac ggc cga gtc acc tac ctt etc gat ccc ttc tcc ggc atc atc	1123
Thr Asp Gly Arg Val Thr Tyr Leu Leu Asp Pro Phe Ser Gly Ile Ile	
330 335 340	
gtc tgg ctc atg gga gac gga aca tgg gca gtg tca gaa ccc aac ggg	1171
Val Trp Leu Met Gly Asp Gly Thr Trp Ala Val Ser Glu Pro Asn Gly	
345 350 355	
cgg ctc aat ccc aaa aat gcg aga tgg gcg caa aca gtc gcc caa cac	1219
Pro Leu Asn Pro Lys Asn Ala Arg Trp Ala Gln Thr Val Ala Gln His	
360 365 370	
cgg gca cgc cac cac aag cgt tgg gtt aag gag gac gcc aag	1261
Arg Ala Arg His His Lys Arg Trp Val Lys Glu Asp Ala Lys	
375 380 385	
tagccggatg gccacgtcga aaa	1284

<210> 100
 <211> 387
 <212> PRT

<213> *Corynebacterium glutamicum*

<400> 100

Leu Phe Thr Asn Phe Phe Ala Val Asn Asn Pro Asp Ser Pro Pro Ala
 1 5 10 15

Arg Gln Lys Thr Lys Leu Arg Glu Leu Glu His Arg Phe Trp Gln Glu
 20 25 30

His Leu Pro Gly Asp Asp Asp His Ser Thr Ala Ile Ser Ser Leu
 35 40 45

Ala Ile Val Thr Gly Leu Thr Lys Ala Gln Val Ser Arg Ile Ser Ile
 50 55 60

Ala Phe Ala Thr Leu Ala Asp Leu Pro Glu Leu Lys Ala Leu Gln Gln
 65 70 75 80

Lys Leu Tyr His Leu Asp Leu Ser Arg Leu Ile Thr Ile Ser Asn Glu
 85 90 95

Leu Ala Gly Ile Asn Pro Asp Asn Leu Ala Gly Ala Asp Ala Ile Leu
 100 105 110

Thr Glu Tyr Leu Thr Ala Thr Ser Pro Asn Gln Ile Leu Pro Ser Pro
 115 120 125

Ala Ser Ile Gly Arg Lys Ile Lys Glu Ile Arg Asp Leu Leu Asp Asp
 130 135 140

Ala Arg Ala Thr Gly Ser Arg Gly Thr Gln Asp Asp Ser Ser Phe Gly
 145 150 155 160

Val Thr Phe Ser Pro Asp Gly Thr Ala Glu Ile Gly Ala Ser Val Asp
 165 170 175

Ala Val Asp Gly His Ile Ile Asn Asp Ala Val Thr Gln His Ala Lys
 180 185 190

Lys Asn Asp Leu Thr Tyr Gly Glu Ala Phe Ser Asp Ile Leu Arg Asn
 195 200 205

Asn Ile Gln Val Lys Val Val Leu Asn Leu Tyr Thr Ala Lys Asp Leu
 210 215 220

Ala Asn Ala Pro Val Trp Ala Ser Gly Ile Gly Trp Leu Asp Ala Lys
 225 230 235 240

Thr Gly Thr Phe Trp Ser Glu Lys Ala Asn Lys Glu Gln Asp Met Asp
 245 250 255

Ala Ala Ala Lys Ile Ser Thr Asp Lys His Asp Pro Pro Pro Ala Leu
 260 265 270

Arg Asp Ala Leu Ile Gly Arg Asp Gly Thr Cys Arg Phe Pro Gly Cys
 275 280 285

Ser Val Pro Ala Leu Lys Thr Gln Ala Asp His Arg Ile Pro Tyr Glu
 290 295 300

Glu Gly Gly Glu Thr Cys Leu Gly Gly Ile Gly Cys Leu Cys Gln His

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<210> 101
<211> 612
<212> DNA
<213> Corynebacterium glutamicum
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<400>	101					
tgcattccct	aacgggaatg	cagctttt	tggtcctagt	gc aaatcgaa	atctcatgtg	60
atttacttaa	aacctaatta	aatctactat	cggagatctc	atg aaa ctt ctc aag		115
				Met Lys Leu Leu Lys		
				1	5	
ttt gct gca gca gga acc ttc gca cta gcc ctg gct ggc tgc aca cag						163
Phe Ala Ala Ala Gly Thr Phe Ala Leu Ala Leu Ala Gly Cys Thr Gln						
	10			15	20	
act gag tct ctc gta gca aca atc gaa tct gca acc tct gca gca cag						211
Thr Glu Ser Leu Val Ala Thr Ile Glu Ser Ala Thr Ser Ala Ala Gln						
	25			30	35	
gca tcc gga aac gac gta gaa gga gac caa acc tcc gcg ttc gaa ctc						259
Ala Ser Gly Asn Asp Val Glu Gly Asp Gin Thr Ser Ala Phe Glu Leu						
	40			45	50	
tcc gtt ggc gaa tgc ttc aac gac acc tac gaa gaa gaa atc tcc gaa						307
Ser Val Gly Glu Cys Phe Asn Asp Thr Tyr Glu Glu Glu Ile Ser Glu						
	55			60	65	
gta ccc atc gtc gac tgc gca gaa cct cac gac aac gag atc tac tac						355
Val Pro Ile Val Asp Cys Ala Glu Pro His Asp Asn Glu Ile Tyr Tyr						
	70			75	80	85
ctc tac gac atc gaa ggc gac gac ttc cca acc gac atc acc acc aca						403
Leu Tyr Asp Ile Glu Gly Asp Asp Phe Pro Thr Asp Ile Thr Thr Thr						
	90			95	100	
ggc tac gaa ggc tgc ctc cca aca ttt gaa ggc ttc gta gga gct cct						451
Gly Tyr Glu Gly Cys Leu Pro Thr Phe Glu Gly Phe Val Gly Ala Pro						

105	110	115	
tac gaa acc tcc atc tac gag gtc	tac cca atg acc cca acc ttt ggc	499	
Tyr Glu Thr Ser Ile Tyr Glu Val Tyr	Pro Met Thr Pro Thr Phe Gly		
120	125	130	
tcc tgg aca aac ggc gac cgc gag gta gtg tgc tcc gtg tac ttg gcc	547		
Ser Trp Thr Asn Gly Asp Arg Glu Val Val Cys Ser Val Tyr Leu Ala			
135	140	145	
acc ggt gag cag atg acc gga acc gca gca gga acc gcg cag	589		
Thr Gly Glu Gln Met Thr Gly Thr Ala Ala Gly Thr Ala Gln			
150	155	160	
tagattttgg ataggggaatt ttg	612		

<210> 102

<211> 163

<212> PRT

<213> Corynebacterium glutamicum

<400> 102

Met Lys Leu Leu Lys Phe Ala Ala Ala Gly Thr Phe Ala Leu Ala Leu

1

5

10

15

Ala Gly Cys Thr Gln Thr Glu Ser Leu Val Ala Thr Ile Glu Ser Ala

20

25

30

Thr Ser Ala Ala Gln Ala Ser Gly Asn Asp Val Glu Gly Asp Gln Thr

35

40

45

Ser Ala Phe Glu Leu Ser Val Gly Glu Cys Phe Asn Asp Thr Tyr Glu

50

55

60

Glu Glu Ile Ser Glu Val Pro Ile Val Asp Cys Ala Glu Pro His Asp

65

70

75

80

Asn Glu Ile Tyr Tyr Leu Tyr Asp Ile Glu Gly Asp Asp Phe Pro Thr

85

90

95

Asp Ile Thr Thr Thr Gly Tyr Glu Gly Cys Leu Pro Thr Phe Glu Gly

100

105

110

Phe Val Gly Ala Pro Tyr Glu Thr Ser Ile Tyr Glu Val Tyr Pro Met

115

120

125

Thr Pro Thr Phe Gly Ser Trp Thr Asn Gly Asp Arg Glu Val Val Cys

130

135

140

Ser Val Tyr Leu Ala Thr Gly Glu Gln Met Thr Gly Thr Ala Ala Gly

145

150

155

160

Thr Ala Gln

<210> 103

<211> 612

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(589)

<223> FRXA00114

<400> 103

tgcattccct aacgggaatg cagctttttg tgttcctagt gcaaatcgaa atctcatgtg 60

atttacttaa aacctaatta aatctactat cggagatctc atg aaa ctt ctc aag 115
 Met Lys Leu Leu Lys
 1 5

ttt gct gca gca gga acc ttc gca cta gcc ctg gct ggc tgc aca cag 163
 Phe Ala Ala Ala Gly Thr Phe Ala Leu Ala Leu Ala Gly Cys Thr Gln
 10 15 20

act gag tct ctc gta gca aca atc gaa tct gca acc tct gca gca cag 211
 Thr Glu Ser Leu Val Ala Thr Ile Glu Ser Ala Thr Ser Ala Ala Gln
 25 30 35

gca tcc gga aac gac gta gaa gga gac caa acc tcc gcg ttc gaa ctc 259
 Ala Ser Gly Asn Asp Val Glu Gly Asp Gln Thr Ser Ala Phe Glu Leu
 40 45 50

tcc gtt ggc gaa tgc ttc aac gac acc tac gaa gaa gaa atc tcc gaa 307
 Ser Val Gly Glu Cys Phe Asn Asp Thr Tyr Glu Glu Glu Ile Ser Glu
 55 60 65

gta ccc atc gtc gac tgc gca gaa cct cac gac aac gag atc tac tac 355
 Val Pro Ile Val Asp Cys Ala Glu Pro His Asp Asn Glu Ile Tyr Tyr
 70 75 80 85

ctc tac gac atc gaa ggc gac gac ttc cca acc gac atc acc acc aca 403
 Leu Tyr Asp Ile Glu Gly Asp Asp Phe Pro Thr Asp Ile Thr Thr Thr
 90 95 100

ggc tac gaa ggc tgc ctc cca aca ttt gaa ggc ttc gta gga gct cct 451
 Gly Tyr Glu Gly Cys Leu Pro Thr Phe Glu Gly Phe Val Gly Ala Pro
 105 110 115

tac gaa acc tcc atc tac gag gtc tac cca atg acc cca acc ttt ggc 499
 Tyr Glu Thr Ser Ile Tyr Glu Val Tyr Pro Met Thr Pro Thr Phe Gly
 120 125 130

tcc tgg aca aac ggc gac cgc gag gta gtg tgc tcc gtg tac ttg gcc 547
 Ser Trp Thr Asn Gly Asp Arg Glu Val Val Cys Ser Val Tyr Leu Ala
 135 140 145

acc ggt gag cag atg acc gga acc gca gca gga acc gcg cag 589
 Thr Gly Glu Gln Met Thr Gly Thr Ala Ala Gly Thr Ala Gln
 150 155 160

tagatttttg atagggaatt ttg 612

<210> 104

<211> 163

<212> PRT

<213> Corynebacterium glutamicum

<400> 104

Met Lys Leu Leu Lys Phe Ala Ala Ala Gly Thr Phe Ala Leu Ala Leu
 1 5 10 15

Ala Gly Cys Thr Gln Thr Glu Ser Leu Val Ala Thr Ile Glu Ser Ala
 20 25 30

Thr Ser Ala Ala Gln Ala Ser Gly Asn Asp Val Glu Gly Asp Gln Thr
 35 40 45

Ser Ala Phe Glu Leu Ser Val Gly Glu Cys Phe Asn Asp Thr Tyr Glu
 50 55 60

Glu Glu Ile Ser Glu Val Pro Ile Val Asp Cys Ala Glu Pro His Asp
 65 70 75 80

Asn Glu Ile Tyr Tyr Leu Tyr Asp Ile Glu Gly Asp Asp Phe Pro Thr
 85 90 95

Asp Ile Thr Thr Thr Gly Tyr Glu Gly Cys Leu Pro Thr Phe Glu Gly
 100 105 110

Phe Val Gly Ala Pro Tyr Glu Thr Ser Ile Tyr Glu Val Tyr Pro Met
 115 120 125

Thr Pro Thr Phe Gly Ser Trp Thr Asn Gly Asp Arg Glu Val Val Cys
 130 135 140

Ser Val Tyr Leu Ala Thr Gly Glu Gln Met Thr Gly Thr Ala Ala Gly
 145 150 155 160

Thr Ala Gln

<210> 105

<211> 963

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(940)

<223> RXN00120

<400> 105

acaaactctt aatttaataga gacgtaagta gttgatagtt aggggaaata ctcccaaatac 60

ctcacaggaa acgctctgaa tcttttcaaa aaaatgttct atg ctt att ggc atg 115
 Met Leu Ile Gly Met
 1 5

agc aat caa aca gtc aat caa gca gtg tgc tca ggg gtg aaa gca tcc 163
 Ser Asn Gln Thr Val Asn Gln Ala Val Ser Ser Gly Val Lys Ala Ser
 10 15 20

cgg cac agg ttc aat cgt ttt gaa atc aaa tac ttg att aca gag caa 211
 Pro His Arg Phe Asn Arg Phe Glu Ile Lys Tyr Leu Ile Thr Glu Gln
 25 30 35

gat gta cct gca ctc cgc gag cag ttg gca acg agg atg agc acg gat 259

Asp Val Pro Ala Leu Arg Glu Gln Leu Ala Thr Arg Met Ser Thr Asp	
40 45 50	
ccg ctt tcc cca ccc gga ggc tac cga gtg gaa tcc ctt tac ttc gat	307
Pro Leu Ser Pro Pro Gly Gly Tyr Arg Val Glu Ser Leu Tyr Phe Asp	
55 60 65	
tca gcc gat tta cgg tgc tac acc gaa aag atc gag ggt ctg aaa ttc	355
Ser Ala Asp Leu Arg Cys Tyr Thr Glu Lys Ile Glu Gly Leu Lys Phe	
70 75 80 85	
cga agg aaa cta cgg atc cgt acc tac ggt gat gga gtg ctc act cca	403
Arg Arg Lys Leu Arg Ile Arg Thr Tyr Gly Asp Gly Val Leu Thr Pro	
90 95 100	
gaa tcc acc gtg tcg gta gag atc aag cag cgg gtt aac aaa gta act	451
Glu Ser Thr Val Ser Val Glu Ile Lys Gln Arg Val Asn Lys Val Thr	
105 110 115	
caa aag cgt cgg ctg gat ttg ccc ttt ata tat gcg ctc gcc ctg ggc	499
Gln Lys Arg Arg Leu Asp Leu Pro Phe Ile Tyr Ala Leu Ala Leu Gly	
120 125 130	
gat agc acg ggc gcc gcg gta ggc gag cag gtg gac gtc gag aag ctt	547
Asp Ser Thr Gly Ala Ala Val Gly Glu Gln Val Asp Val Glu Lys Leu	
135 140 145	
ctt gaa atc tct ccg gaa aac cag cac gct ttg att cac gaa atg gcg	595
Leu Glu Ile Ser Pro Glu Asn Gln His Ala Leu Ile His Glu Met Ala	
150 155 160 165	
tcg ttt gct aaa aat tat cgg ctg cga ccc atc gcc acc acg aag tat	643
Ser Phe Ala Lys Asn Tyr Arg Leu Arg Pro Ile Ala Thr Thr Lys Tyr	
170 175 180	
cac cgc gag gca ttc gtc ggc gct gat gcg gag gaa agt tcg cga gtc	691
His Arg Glu Ala Phe Val Gly Ala Asp Ala Glu Glu Ser Ser Arg Val	
185 190 195	
acc att gac cac ggt gtt tca ggc cgt gat cgt gat ttt ctg ctt ggc	739
Thr Ile Asp His Gly Val Ser Gly Arg Asp Arg Asp Phe Leu Leu Gly	
200 205 210	
caa gac ctt gaa gac cgc cca acg gtg gcg caa gga ttg gca gtc gtg	787
Gln Asp Leu Glu Asp Arg Pro Thr Val Ala Gln Gly Leu Ala Val Val	
215 220 225	
gaa atc aaa tgc gat gaa cgc gtg ccg ttt tgg ctc act gat atg act	835
Glu Ile Lys Cys Asp Glu Arg Val Pro Phe Trp Leu Thr Asp Met Thr	
230 235 240 245	
gct caa ctg gaa atg tcc gtg att cgg atg tcc aaa tac tgc gaa acc	883
Ala Gln Leu Glu Met Ser Val Ile Arg Met Ser Lys Tyr Cys Glu Thr	
250 255 260	
atc gaa gcg ttt cac aac cgt ccg gca tca gct ttc ggc gct gtc gac	931
Ile Glu Ala Phe His Asn Arg Pro Ala Ser Ala Phe Gly Ala Val Asp	
265 270 275	
ccc atc ttc taaacaagaa aggccctcc aat	963
Pro Ile Phe	

280

<210> 106

<211> 280

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 106

Met Leu Ile Gly Met Ser Asn Gln Thr Val Asn Gln Ala Val Ser Ser
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Gly Val Lys Ala Ser Pro His Arg Phe Asn Arg Phe Glu Ile Lys Tyr
 20 25 30

Leu Ile Thr Glu Gln Asp Val Pro Ala Leu Arg Glu Gln Leu Ala Thr
 35 40 45

Arg Met Ser Thr Asp Pro Leu Ser Pro Pro Gly Gly Tyr Arg Val Glu
 50 55 60

Ser Leu Tyr Phe Asp Ser Ala Asp Leu Arg Cys Tyr Thr Glu Lys Ile
 65 70 75 80

Glu Gly Leu Lys Phe Arg Arg Lys Leu Arg Ile Arg Thr Tyr Gly Asp
 85 90 95

Gly Val Leu Thr Pro Glu Ser Thr Val Ser Val Glu Ile Lys Gln Arg
 100 105 110

Val Asn Lys Val Thr Gln Lys Arg Arg Leu Asp Leu Pro Phe Ile Tyr
 115 120 125

Ala Leu Ala Leu Gly Asp Ser Thr Gly Ala Ala Val Gly Glu Gln Val
 130 135 140

Asp Val Glu Lys Leu Leu Glu Ile Ser Pro Glu Asn Gln His Ala Leu
 145 150 155 160

Ile His Glu Met Ala Ser Phe Ala Lys Asn Tyr Arg Leu Arg Pro Ile
 165 170 175

Ala Thr Thr Lys Tyr His Arg Glu Ala Phe Val Gly Ala Asp Ala Glu
 180 185 190

Glu Ser Ser Arg Val Thr Ile Asp His Gly Val Ser Gly Arg Asp Arg
 195 200 205

Asp Phe Leu Leu Gly Gln Asp Leu Glu Asp Arg Pro Thr Val Ala Gln
 210 215 220

Gly Leu Ala Val Val Glu Ile Lys Cys Asp Glu Arg Val Pro Phe Trp
 225 230 235 240

Leu Thr Asp Met Thr Ala Gln Leu Glu Met Ser Val Ile Arg Met Ser
 245 250 255

Lys Tyr Cys Glu Thr Ile Glu Ala Phe His Asn Arg Pro Ala Ser Ala
 260 265 270

Phe Gly Ala Val Asp Pro Ile Phe

275

280

<210> 107

<211> 777

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(754)

<223> FRXA00120

<400> 107

aatcaaatatc ttgattacag agcaagatgt acctgcactc cgcgagcagt tggcaacgag 60

gatgagcagc	gatccgcttt	ccccaccg	aggctaccga	gtg	gaa	tcc	ctt	tac	115
				Val	Glu	Ser	Leu	Tyr	
				1				5	

ttc	gat	tca	gcc	gat	tta	cgg	tgc	tac	acc	gaa	aag	atc	gag	ggc	ctg	163
Phe	Asp	Ser	Ala	Asp	Leu	Arg	Cys	Tyr	Thr	Glu	Lys	Ile	Glu	Gly	Leu	
				10					15					20		

aaa	ttc	cga	agg	aaa	cta	cgg	atc	cgt	acc	tac	ggc	gat	gga	gtg	ctc	211
Lys	Phe	Arg	Arg	Lys	Leu	Arg	Ile	Arg	Thr	Tyr	Gly	Asp	Gly	Val	Leu	
			25				30						35			

act	cca	gaa	tcc	acc	gtg	tgc	gta	gag	atc	aag	cag	cgg	gtt	aac	aaa	259
Thr	Pro	Glu	Ser	Thr	Val	Ser	Val	Glu	Ile	Lys	Gln	Arg	Val	Asn	Lys	
		40				45					50					

gta	act	caa	aag	cgt	cgg	ctg	gat	ttg	ccc	ttt	ata	tat	gcg	ctc	gcc	307
Val	Thr	Gln	Lys	Arg	Arg	Leu	Asp	Leu	Pro	Phe	Ile	Tyr	Ala	Leu	Ala	
	55				60						65					

ctg	ggc	gat	agc	acg	ggc	gcc	gcg	gta	ggc	gag	cag	gtg	gac	gtc	gag	355
Leu	Gly	Asp	Ser	Thr	Gly	Ala	Ala	Val	Gly	Glu	Gln	Val	Asp	Val	Glu	
	70				75					80				85		

aag	ctt	ctt	gaa	atc	tct	cgc	gaa	aac	cag	cac	gct	ttg	att	cac	gaa	403
Lys	Leu	Leu	Glu	Ile	Ser	Pro	Glu	Asn	Gln	His	Ala	Leu	Ile	His	Glu	
			90					95						100		

atg	gcg	tgc	ttt	gct	aaa	aat	tat	cgc	ctg	cga	ccc	atc	gcc	acc	acg	451
Met	Ala	Ser	Phe	Ala	Lys	Asn	Tyr	Arg	Leu	Arg	Pro	Ile	Ala	Thr	Thr	
			105				110						115			

aag	tat	cac	cgc	gag	gca	ttc	gtc	ggc	gct	gat	gcg	gag	gaa	agt	tcg	499
Lys	Tyr	His	Arg	Glu	Ala	Phe	Val	Gly	Ala	Asp	Ala	Glu	Glu	Ser	Ser	
		120					125					130				

cga	gtc	acc	att	gac	cac	ggc	gtt	tca	ggc	cgt	gat	cgt	gat	ttt	ctg	547
Arg	Val	Thr	Ile	Asp	His	Gly	Val	Ser	Gly	Arg	Asp	Arg	Asp	Phe	Leu	
	135					140					145					

ctt	ggc	caa	gac	ctt	gaa	gac	cgc	cca	acg	gtg	gcg	caa	gga	ttg	gca	595
Leu	Gly	Gln	Asp	Leu	Glu	Asp	Arg	Pro	Thr	Val	Ala	Gln	Gly	Leu	Ala	
	150				155					160				165		

gtc	gtg	gaa	atc	aaa	tgc	gat	gaa	cgc	gtg	cgc	ttt	tgg	ctc	act	gat	643
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Val Val Glu Ile Lys Cys Asp Glu Arg Val Pro Phe Trp Leu Thr Asp
      170                      175
atg act gct caa ctg gaa atg tcc gtg att cgg atg tcc aaa tac tgc 691
Met Thr Ala Gln Leu Glu Met Ser Val Ile Arg Met Ser Lys Tyr Cys
      185                      190
gaa acc atc gaa gcg ttt cac aac cgt ccg gca tca gct ttc ggc gct 739
Glu Thr Ile Glu Ala Phe His Asn Arg Pro Ala Ser Ala Phe Gly Ala
      200                      205                      210
gtc gac ccc atc ttc taaacaagaa aggccctcc aat 777
Val Asp Pro Ile Phe
      215

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<210> 108
<211> 218
<212> PRT
<213> Corynebacterium glutamicum

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<400> 108
Val Glu Ser Leu Tyr Phe Asp Ser Ala Asp Leu Arg Cys Tyr Thr Glu
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Lys Ile Glu Gly Leu Lys Phe Arg Arg Lys Leu Arg Ile Arg Thr Tyr
      20          25          30
Gly Asp Gly Val Leu Thr Pro Glu Ser Thr Val Ser Val Glu Ile Lys
      35          40          45
Gln Arg Val Asn Lys Val Thr Gln Lys Arg Arg Leu Asp Leu Pro Phe
      50          55          60
Ile Tyr Ala Leu Ala Leu Gly Asp Ser Thr Gly Ala Ala Val Gly Glu
      65          70          75          80
Gln Val Asp Val Glu Lys Leu Leu Glu Ile Ser Pro Glu Asn Gln His
      85          90          95
Ala Leu Ile His Glu Met Ala Ser Phe Ala Lys Asn Tyr Arg Leu Arg
      100          105          110
Pro Ile Ala Thr Thr Lys Tyr His Arg Glu Ala Phe Val Gly Ala Asp
      115          120          125
Ala Glu Glu Ser Ser Arg Val Thr Ile Asp His Gly Val Ser Gly Arg
      130          135          140
Asp Arg Asp Phe Leu Leu Gly Gln Asp Leu Glu Asp Arg Pro Thr Val
      145          150          155          160
Ala Gln Gly Leu Ala Val Val Glu Ile Lys Cys Asp Glu Arg Val Pro
      165          170          175
Phe Trp Leu Thr Asp Met Thr Ala Gln Leu Glu Met Ser Val Ile Arg
      180          185          190
Met Ser Lys Tyr Cys Glu Thr Ile Glu Ala Phe His Asn Arg Pro Ala
      195          200          205

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Ser Ala Phe Gly Ala Val Asp Pro Ile Phe
210 215

<210> 109

<211> 1827

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1804)

<223> RXN00128

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cggtgatcgc tccagagaca ccgtgggaag gggagcagca gtg agt aaa att tcg 115
Val Ser Lys Ile Ser
1 5

acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg 163
Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val
10 15 20

gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc 211
Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg
25 30 35

tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg 259
Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro
40 45 50

aat caa gat ccg gat ttg ttg atc cgc gcc ttc ttc agc gca ggt gcg 307
Asn Gln Asp Pro Asp Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala
55 60 65

tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg 355
Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly
70 75 80 85

acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc 403
Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg
90 95 100

att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att 451
Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile
105 110 115

gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat 499
Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr
120 125 130

cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt ccg gaa 547
Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu
135 140 145

gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag 595
Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu
150 155 160 165

aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt	643
Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe	
170 175 180	
gat cct tct ggc cag gtg ttg gtg ggg gat cgg cgt tgg ttg ttc aat	691
Asp Pro Ser Gln Gly Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn	
185 190 195	
gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt	739
Glu Ser Gln Ser Met Ser Thr Leu Met Ala Leu Val Asn Gly	
200 205 210	
cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat	787
Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp	
215 220 225	
gcg tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg	835
Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu	
230 235 240 245	
gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg	883
Gly Asn Leu Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val	
250 255 260	
tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct	931
Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala	
265 270 275	
gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac	979
Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp	
280 285 290	
ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg	1027
Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu	
295 300 305	
ttt gcg ttg cag gat gga tcg ttg tcg agg gtc agt tcc gcc aat gtg	1075
Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val	
310 315 320 325	
agt cca cta cag gcc att ttg agc ggt gga gat atc gat tct gca gcg	1123
Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala	
330 335 340	
att tcc tcc tcc gcc aat gtg gtg gca gcg gta cgc cac gaa aac aac	1171
Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn	
345 350 355	
gag gca gtg ctt act gtt gcc tcc atg gaa gcc gtg act tca gat gcg	1219
Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala	
360 365 370	
ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt	1267
Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser	
375 380 385	
ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga	1315
Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg	
390 395 400 405	
tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg	1363

Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu
410 415 420

cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act 1411
Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr
425 430 435

ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc 1459
Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val
440 445 450

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag 1507
Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu
455 460 465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca 1555
Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro
470 475 480 485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg 1603
Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp
490 495 500

cgc gtc gag cag gac gga tgc gcg att tgc tgc atg ccg agc ggg aat 1651
Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn
505 510 515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac 1699
Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr
520 525 530

gtc act gat tgc cat gcg atg ctt cag ctg ccg act gcc gat aat gat 1747
Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp
535 540 545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg 1795
Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val
550 555 560 565

gtt gcg tac tgatggagct gttcttcccg cgc 1827
Val Ala Tyr

<210> 110

<211> 568

<212> PRT

<213> Corynebacterium glutamicum

<400> 110

Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser
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Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp
20 25 30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile
35 40 45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe
50 55 60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala
 65 70 75 80
 Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr
 85 90 95
 Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn
 100 105 110
 Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu
 115 120 125
 Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile
 130 135 140
 Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp
 145 150 155 160
 Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His
 165 170 175
 Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg
 180 185 190
 Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala
 195 200 205
 Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn
 210 215 220
 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr
 225 230 235 240
 Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe
 245 250 255
 Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro
 260 265 270
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr
 275 280 285
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn
 290 295 300
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val
 305 310 315 320
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp
 325 330 335
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val
 340 345 350
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly
 355 360 365
 Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe
 370 375 380


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Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro
385                      390                      395                      400

Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu
                      405                      410                      415

Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe
420                      425                      430

Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys
435                      440                      445

Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val
450                      455                      460

Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser
465                      470                      475                      480

Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro
485                      490                      495

Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser
500                      505                      510

Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser
515                      520                      525

Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro
530                      535                      540

Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr
545                      550                      555                      560

Arg Ala Ala Pro Val Val Ala Tyr
565

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<210> 111
<211> 1827
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(1804)
<223> FRXA00128

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<400> 111
ccattttccg ttgtgtcttg cctaaagaac cgcattggaaa ttatcgtgaa gcaccgatcc 60

cgttgatcgc tccagagaca ccgtgggaag gggagcagca gtg agt aaa att tcg 115
                      Val Ser Lys Ile Ser
                      1                      5

acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg 163
Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val
                      10                      15                      20

got ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc 211
Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg
                      25                      30                      35

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tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg	259
Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro	
40 45 50	
aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg	307
Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala	
55 60 65	
tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg	355
Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly	
70 75 80 85	
acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc	403
Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg	
90 95 100	
att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att	451
Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile	
105 110 115	
gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat	499
Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr	
120 125 130	
cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt ccg gaa	547
Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu	
135 140 145	
gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag	595
Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu	
150 155 160 165	
aga aac gat ctg ccg aac cat tac act ccg cac gat gtg tat ttc ttt	643
Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe	
170 175 180	
gat cct tct ggc cag gtg ttg gtg ggg gat ccg cgt tgg ttg ttc aat	691
Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn	
185 190 195	
gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt	739
Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly	
200 205 210	
cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat	787
Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp	
215 220 225	
gcg tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg	835
Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu	
230 235 240 245	
gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg	883
Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val	
250 255 260	
tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct	931
Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala	
265 270 275	

gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac	979
Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp	
280 285 290	
ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg	1027
Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu	
295 300 305	
ttt gcg ttg cag gat gga tcg ttg tcg agg gtc agt tcc gcc aat gtg	1075
Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val	
310 315 320 325	
agt cca cta cag gcc att tgg agc ggt gga gat atc gat tct gca gcg	1123
Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala	
330 335 340	
att tcc tcc tcc gcc aat gtg gtg gca gcg gta cgc cac gaa aac aac	1171
Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn	
345 350 355	
gag gca gtg ctt act gtt gcc tcc atg gaa gcc gtg act tca gat gcg	1219
Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala	
360 365 370	
ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt	1267
Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser	
375 380 385	
ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga	1315
Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg	
390 395 400 405	
tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg	1363
Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu	
410 415 420	
cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act	1411
Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr	
425 430 435	
ggg gtc ccg gcc gcc atg atc att gaa gcc aag gtg tac gtg gcc gtc	1459
Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val	
440 445 450	
gta acg cgt cct ggt ccg gcc gag ccg cgc gtg aca aat atc acg gag	1507
Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu	
455 460 465	
gtg gcg ccg agc ttg gcc gag gcg gcg ctg tcg atc aac tgg cgc cca	1555
Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro	
470 475 480 485	
gac gcc att ttg ctt gtg gcc acg tca att cca gag acg ccg ctg tgg	1603
Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp	
490 495 500	
cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat	1651
Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn	
505 510 515	
ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac	1699

400> 112																		
Val	Ser	Lys	Ile	Ser	Thr	Lys	Leu	Lys	Ala	Leu	Thr	Ala	Val	Leu	Ser			
1				5					10					15				
Val	Thr	Thr	Leu	Val	Ala	Gly	Cys	Ser	Thr	Leu	Pro	Gln	Asn	Thr	Asp			
			20					25					30					
Pro	Gln	Val	Leu	Arg	Ser	Phe	Ser	Gly	Ser	Gln	Ser	Thr	Gln	Glu	Ile			
		35					40					45						
Ala	Gly	Pro	Thr	Pro	Asn	Gln	Asp	Pro	Asp	Leu	Leu	Ile	Arg	Gly	Phe			
		50				55					60							
Phe	Ser	Ala	Gly	Ala	Tyr	Pro	Thr	Gln	Gln	Tyr	Glu	Ala	Ala	Lys	Ala			
		65			70					75				80				
Tyr	Leu	Thr	Glu	Gly	Thr	Arg	Ser	Thr	Trp	Asn	Pro	Ala	Ala	Ser	Thr			
			85						90					95				
Arg	Ile	Leu	Asp	Arg	Ile	Asp	Leu	Asn	Thr	Leu	Pro	Gly	Ser	Thr	Asn			
		100					105					110						
Ala	Glu	Arg	Thr	Ile	Ala	Ile	Arg	Gly	Thr	Gln	Val	Gly	Thr	Leu	Leu			
		115					120					125						
Ser	Gly	Gly	Val	Tyr	Gln	Pro	Glu	Asn	Ala	Glu	Phe	Glu	Ala	Glu	Ile			
		130				135					140							
Thr	Met	Arg	Arg	Glu	Asp	Gly	Glu	Trp	Arg	Ile	Asp	Ala	Leu	Pro	Asp			
	145			150						155				160				
Gly	Ile	Leu	Leu	Glu	Arg	Asn	Asp	Leu	Arg	Asn	His	Tyr	Thr	Pro	His			
			165					170					175					
Asp	Val	Tyr	Phe	Phe	Asp	Pro	Ser	Gly	Gln	Val	Leu	Val	Gly	Asp	Arg			
		180						185					190					
Arg	Trp	Leu	Phe	Asn	Glu	Ser	Gln	Ser	Met	Ser	Thr	Val	Leu	Met	Ala			
		195				200						205						

Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn
 210 215 220
 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr
 225 230 235 240
 Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Ala Arg Leu Arg Phe
 245 250 255
 Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro
 260 265 270
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr
 275 280 285
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn
 290 295 300
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val
 305 310 315 320
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp
 325 330 335
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val
 340 345 350
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly
 355 360 365
 Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe
 370 375 380
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro
 385 390 395 400
 Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu
 405 410 415
 Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe
 420 425 430
 Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys
 435 440 445
 Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val
 450 455 460
 Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser
 465 470 475 480
 Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro
 485 490 495
 Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser
 500 505 510
 Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser
 515 520 525
 Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro

530

535

540

Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr
 545 550 555 560

Arg Ala Ala Pro Val Val Ala Tyr
 565

<210> 113

<211> 966

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(943)

<223> RXN00154

<400> 113

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agggaagtgt agtgcagtgct tttgactagg gtggtgagct atg agt ttt tca gac 115
 Met Ser Phe Ser Asp
 1 5

ccc tat gca ggc aat att ttt ggt gga cac tcc cgc aac aag cag ccg 163
 Pro Tyr Ala Gly Asn Ile Phe Gly Gly His Ser Arg Asn Lys Gln Pro
 10 15 20

gag tat ccc gat gtg ccc gca aaa cca ggc ctt gtg gtg gaa gtt cgt 211
 Glu Tyr Pro Asp Val Pro Ala Lys Pro Gly Leu Val Val Glu Val Arg
 25 30 35

gga gat ggc ttc gtc ggc gct gtg acc ggt ttt gaa cgc acc tac gat 259
 Gly Asp Gly Phe Val Gly Ala Val Thr Gly Phe Glu Arg Thr Tyr Asp
 40 45 50

ggt gat ttt gtg cgt ctc gag gac cgc cgc gga cgc gat gcg ctg tac 307
 Gly Asp Phe Val Arg Leu Glu Asp Arg Arg Gly Arg Asp Ala Leu Tyr
 55 60 65

aag ctg cgc aag ggt gcg ttc atg att gat ggg cag atc gtt aac ctc 355
 Lys Leu Arg Lys Gly Ala Phe Met Ile Asp Gly Gln Ile Val Asn Leu
 70 75 80 85

acc cgt ttc gtg gaa aaa caa gca cca cgt aaa tct aat tct ggt tcc 403
 Thr Arg Phe Val Glu Lys Gln Ala Pro Arg Lys Ser Asn Ser Gly Ser
 90 95 100

agg cgt gta gaa aac gcg caa gca aag gtc gcg gcg ccg tca cgc atc 451
 Arg Arg Val Glu Asn Ala Gln Ala Lys Val Ala Ala Pro Ser Arg Ile
 105 110 115

tgg gta gaa ggc atc cat gac gcc gcc atc gtg gag aaa gtg tgg gga 499
 Trp Val Glu Gly Ile His Asp Ala Ala Ile Val Glu Lys Val Trp Gly
 120 125 130

cac gac ctt cgc gtt gag ggc gtc gtg gtg gag tac ctg gaa ggt cta 547
 His Asp Leu Arg Val Glu Gly Val Val Val Glu Tyr Leu Glu Gly Leu
 135 140 145

gac aac ctg gag gaa cgt ctc gcg gaa ttt cag cct ggg cct gga cga 595
 Asp Asn Leu Glu Glu Arg Leu Ala Glu Phe Gln Pro Gly Pro Gly Arg
 150 155 160 165

cgc atc gga gtg ctc gct gat cac ctt gtt gag gga tct aaa gaa act 643
 Arg Ile Gly Val Leu Ala Asp His Leu Val Glu Gly Ser Lys Glu Thr
 170 175 180

cgg atg act aaa tca cta ccc gcg gat gtc gct gtc acc ggc cac ccc 691
 Arg Met Thr Lys Ser Leu Pro Ala Asp Val Ala Val Thr Gly His Pro
 185 190 195

tac atc gat att tgg gct gct gtg aaa cca gag cgt ttg ggg ctt aag 739
 Tyr Ile Asp Ile Trp Ala Ala Val Lys Pro Glu Arg Leu Gly Leu Lys
 200 205 210

gcg tgg cct gag gtg cca tac ggg gag gat tgg aaa acc ggc atc tgc 787
 Ala Trp Pro Glu Val Pro Tyr Gly Glu Asp Trp Lys Thr Gly Ile Cys
 215 220 225

aaa cga gtt ggc tgg tca gac ccc aaa gaa ggc tgg cac cgt gtg tat 835
 Lys Arg Val Gly Trp Ser Asp Pro Lys Glu Gly Trp His Arg Val Tyr
 230 235 240 245

aac gcc gtg aat tcc ttc cgc gat ttg gac tac acc cta att ggg gca 883
 Asn Ala Val Asn Ser Phe Arg Asp Leu Asp Tyr Thr Leu Ile Gly Ala
 250 255 260

gtg gaa cgt ttg gtg gat ttt gtg acc aac ctc gat ttg agt aaa gag 931
 Val Glu Arg Leu Val Asp Phe Val Thr Asn Leu Asp Leu Ser Lys Glu
 265 270 275

gac gtc ctc gcc tgatttttcg ggtgtgtttt tgc 966
 Asp Val Leu Ala
 280

<210> 114

<211> 281

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 114

Met Ser Phe Ser Asp Pro Tyr Ala Gly Asn Ile Phe Gly Gly His Ser
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Arg Asn Lys Gln Pro Glu Tyr Pro Asp Val Pro Ala Lys Pro Gly Leu
 20 25 30

Val Val Glu Val Arg Gly Asp Gly Phe Val Gly Ala Val Thr Gly Phe
 35 40 45

Glu Arg Thr Tyr Asp Gly Asp Phe Val Arg Leu Glu Asp Arg Arg Gly
 50 55 60

Arg Asp Ala Leu Tyr Lys Leu Arg Lys Gly Ala Phe Met Ile Asp Gly
 65 70 75 80

Gln Ile Val Asn Leu Thr Arg Phe Val Glu Lys Gln Ala Pro Arg Lys
 85 90 95

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Ser Asn Ser Gly Ser Arg Arg Val Glu Asn Ala Gln Ala Lys Val Ala
    100                                105                                110

Ala Pro Ser Arg Ile Trp Val Glu Gly Ile His Asp Ala Ala Ile Val
    115                                120                                125

Glu Lys Val Trp Gly His Asp Leu Arg Val Glu Gly Val Val Val Glu
    130                                135                                140

Tyr Leu Glu Gly Leu Asp Asn Leu Glu Glu Arg Leu Ala Glu Phe Gln
    145                                150                                155                                160

Pro Gly Pro Gly Arg Arg Ile Gly Val Leu Ala Asp His Leu Val Glu
    165                                170                                175

Gly Ser Lys Glu Thr Arg Met Thr Lys Ser Leu Pro Ala Asp Val Ala
    180                                185                                190

Val Thr Gly His Pro Tyr Ile Asp Ile Trp Ala Ala Val Lys Pro Glu
    195                                200                                205

Arg Leu Gly Leu Lys Ala Trp Pro Glu Val Pro Tyr Gly Glu Asp Trp
    210                                215                                220

Lys Thr Gly Ile Cys Lys Arg Val Gly Trp Ser Asp Pro Lys Glu Gly
    225                                230                                235                                240

Trp His Arg Val Tyr Asn Ala Val Asn Ser Phe Arg Asp Leu Asp Tyr
    245                                250                                255

Thr Leu Ile Gly Ala Val Glu Arg Leu Val Asp Phe Val Thr Asn Leu
    260                                265                                270

Asp Leu Ser Lys Glu Asp Val Leu Ala
    275                                280

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<210> 115

<211> 966

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(943)

<223> FRXA00154

<400> 115

tagccaagacg gcagtagttt gaagcggtag ataaacggtt gctcgaattt ccatagtgtt 60

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agggaagtgt agtgacgtgc ttgactagg gtggtgagct atg agt ttt tca gac    115
                Met Ser Phe Ser Asp
                1                                5

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ccc tat gca ggc aat att ttt ggt gga cac tcc cgc aac aag cag cgg    163
Pro Tyr Ala Gly Asn Ile Phe Gly Gly His Ser Arg Asn Lys Gln Pro
                10                                15                                20

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gag tat ccc gat gtg ccc gca aaa cca ggc ctt gtg gtg gaa gtt cgt    211
Glu Tyr Pro Asp Val Pro Ala Lys Pro Gly Leu Val Val Glu Val Arg

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	25	30	35	
	gga gat ggc ttc gtc ggc gct gtg acc ggt ttt gaa cgc acc tac gat			259
	Gly Asp Gly Phe Val Gly Ala Val Thr Gly Phe Glu Arg Thr Tyr Asp			
	40	45	50	
	ggt gat ttt gtg cgt ctc gag gac cgc cgc gga cgc gat gcg ctg tac			307
	Gly Asp Phe Val Arg Leu Glu Asp Arg Arg Gly Arg Asp Ala Leu Tyr			
	55	60	65	
	aag ctg cgc aag ggt gcg ttc atg att gat ggg cag atc gtt aac ctc			355
	Lys Leu Arg Lys Gly Ala Phe Met Ile Asp Gly Gln Ile Val Asn Leu			
	70	75	80	85
	acc cgt ttc gtg gaa aaa caa gca cca cgt aaa tct aat tct ggt tcc			403
	Thr Arg Phe Val Glu Lys Gln Ala Pro Arg Lys Ser Asn Ser Gly Ser			
	90	95	100	
	agg cgt gta gaa aac gcg caa gca aag gtc gcg gcg ccg tca cgc atc			451
	Arg Arg Val Glu Asn Ala Gln Ala Lys Val Ala Ala Pro Ser Arg Ile			
	105	110	115	
	tgg gta gaa ggc atc cat gac gcc gcc atc gtg gag aaa gtg tgg gga			499
	Trp Val Glu Gly Ile His Asp Ala Ala Ile Val Glu Lys Val Trp Gly			
	120	125	130	
	cac gac ctt cgc gtt gag ggc gtc gtg gtg gag tac ctg gaa ggt cta			547
	His Asp Leu Arg Val Glu Gly Val Val Val Glu Tyr Leu Glu Gly Leu			
	135	140	145	
	gac aac ctg gag gaa cgt ctc gcg gaa ttt cag cct ggg cct gga cga			595
	Asp Asn Leu Glu Glu Arg Leu Ala Glu Phe Gln Pro Gly Pro Gly Arg			
	150	155	160	165
	cgc atc gga gtg ctc gct gat cac ctt gtt gag gga tct aaa gaa act			643
	Arg Ile Gly Val Leu Ala Asp His Leu Val Glu Gly Ser Lys Glu Thr			
	170	175	180	
	cgg atg act aaa tca cta ccc gcg gat gtc gct gtc acc ggc cac ccc			691
	Arg Met Thr Lys Ser Leu Pro Ala Asp Val Ala Val Thr Gly His Pro			
	185	190	195	
	tac atc gat att tgg gct gct gtg aaa cca gag cgt ttg ggg ctt aag			739
	Tyr Ile Asp Ile Trp Ala Ala Val Lys Pro Glu Arg Leu Gly Leu Lys			
	200	205	210	
	gcg tgg cct gag gtg cca tac ggg gag gat tgg aaa acc ggc atc tgc			787
	Ala Trp Pro Glu Val Pro Tyr Gly Glu Asp Trp Lys Thr Gly Ile Cys			
	215	220	225	
	aaa cga gtt ggc tgg tca gac ccc aaa gaa ggc tgg cac cgt gtg tat			835
	Lys Arg Val Gly Trp Ser Asp Pro Lys Glu Gly Trp His Arg Val Tyr			
	230	235	240	245
	aac gcc gtg aat tcc ttc cgc gat ttg gac tac acc cta att ggg gca			883
	Asn Ala Val Asn Ser Phe Arg Asp Leu Asp Tyr Thr Leu Ile Gly Ala			
	250	255	260	
	gtg gaa cgt ttg gtg gat ttt gtg acc aac ctc gat ttg agt aaa gag			931
	Val Glu Arg Leu Val Asp Phe Val Thr Asn Leu Asp Leu Ser Lys Glu			
	265	270	275	

gac gtc ctc gcc tgatttttcg ggtgtgtttt tgc
 Asp Val Leu Ala
 280

966

<210> 116
 <211> 281
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 116
 Met Ser Phe Ser Asp Pro Tyr Ala Gly Asn Ile Phe Gly Gly His Ser
 1 5 10 15
 Arg Asn Lys Gln Pro Glu Tyr Pro Asp Val Pro Ala Lys Pro Gly Leu
 20 25 30
 Val Val Glu Val Arg Gly Asp Gly Phe Val Gly Ala Val Thr Gly Phe
 35 40 45
 Glu Arg Thr Tyr Asp Gly Asp Phe Val Arg Leu Glu Asp Arg Arg Gly
 50 55 60
 Arg Asp Ala Leu Tyr Lys Leu Arg Lys Gly Ala Phe Met Ile Asp Gly
 65 70 75 80
 Gln Ile Val Asn Leu Thr Arg Phe Val Glu Lys Gln Ala Pro Arg Lys
 85 90 95
 Ser Asn Ser Gly Ser Arg Arg Val Glu Asn Ala Gln Ala Lys Val Ala
 100 105 110
 Ala Pro Ser Arg Ile Trp Val Glu Gly Ile His Asp Ala Ala Ile Val
 115 120 125
 Glu Lys Val Trp Gly His Asp Leu Arg Val Glu Gly Val Val Val Glu
 130 135 140
 Tyr Leu Glu Gly Leu Asp Asn Leu Glu Glu Arg Leu Ala Glu Phe Gln
 145 150 155 160
 Pro Gly Pro Gly Arg Ile Gly Val Leu Ala Asp His Leu Val Glu
 165 170 175
 Gly Ser Lys Glu Thr Arg Met Thr Lys Ser Leu Pro Ala Asp Val Ala
 180 185 190
 Val Thr Gly His Pro Tyr Ile Asp Ile Trp Ala Ala Val Lys Pro Glu
 195 200 205
 Arg Leu Gly Leu Lys Ala Trp Pro Glu Val Pro Tyr Gly Glu Asp Trp
 210 215 220
 Lys Thr Gly Ile Cys Lys Arg Val Gly Trp Ser Asp Pro Lys Glu Gly
 225 230 235 240
 Trp His Arg Val Tyr Asn Ala Val Asn Ser Phe Arg Asp Leu Asp Tyr
 245 250 255
 Thr Leu Ile Gly Ala Val Glu Arg Leu Val Asp Phe Val Thr Asn Leu

260

265

270

Asp Leu Ser Lys Glu Asp Val Leu Ala
 275 280

<210> 117

<211> 477

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(454)

<223> RXN00162

<400> 117

ggagacgtcg aaaagcataa acctggaact ttccggggcc cgcgcccgac tgctttgctg 60

aagccctatc ccgctatattt atttttgaag gaagagttgc gtg tct acc acc acc 115
 Val Ser Thr Thr Thr
 1 5

cca atc cac cct gag cgc aag aaa cgc gtt cgt cag gcc ctc acc atg 163
 Pro Ile His Pro Glu Arg Lys Lys Arg Val Arg Gln Ala Leu Thr Met
 10 15 20

ttc tcc atc gct gcg tgg gtg act ggt gtg ttt ttg ctg gcg ctg gtg 211
 Phe Ser Ile Ala Ala Trp Val Thr Gly Val Phe Leu Leu Ala Leu Val
 25 30 35

gcg gag atg atc atg aag tac ata att ggc atg gat ctt cct gag tgg 259
 Ala Glu Met Ile Met Lys Tyr Ile Ile Gly Met Asp Leu Pro Glu Trp
 40 45 50

gca cga ttc gtt ccg att gca cat gga tgg gtt tac att gtt ttc ttg 307
 Ala Arg Phe Val Pro Ile Ala His Gly Trp Val Tyr Ile Val Phe Leu
 55 60 65

atg acc acc ctg aac ctg ggt ctg aag gcg cgt tgg aat ccg act cgt 355
 Met Thr Thr Leu Asn Leu Gly Leu Lys Ala Arg Trp Asn Pro Thr Arg
 70 75 80 85

tgg gtg acc acc gct atc gca ggt gtg gtt ccg ctg ctg tgc ttt ttt 403
 Trp Val Thr Thr Ala Ile Ala Gly Val Val Pro Leu Leu Ser Phe Phe
 90 95 100

gtt gag cac aac cgc cgc aag gaa gtt act cag aca ttc cag ctg aac 451
 Val Glu His Asn Arg Arg Lys Glu Val Thr Gln Thr Phe Gln Leu Asn
 105 110 115

tca tagttaaata cacaaaaacc tcc 477
 Ser

<210> 118

<211> 118

<212> PRT

<213> *Corynebacterium glutamicum*

```

<400> 118
Val Ser Thr Thr Thr Pro Ile His Pro Glu Arg Lys Lys Arg Val Arg
  1              5              10              15

Gln Ala Leu Thr Met Phe Ser Ile Ala Ala Trp Val Thr Gly Val Phe
      20              25              30

Leu Leu Ala Leu Val Ala Glu Met Ile Met Lys Tyr Ile Ile Gly Met
      35              40              45

Asp Leu Pro Glu Trp Ala Arg Phe Val Pro Ile Ala His Gly Trp Val
      50              55              60

Tyr Ile Val Phe Leu Met Thr Thr Leu Asn Leu Gly Leu Lys Ala Arg
      65              70              75              80

Trp Asn Pro Thr Arg Trp Val Thr Thr Ala Ile Ala Gly Val Val Pro
      85              90              95

Leu Leu Ser Phe Phe Val Glu His Asn Arg Arg Lys Glu Val Thr Gln
      100             105             110

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Thr Phe Gln Leu Asn Ser
      115

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```

<210> 119
<211> 477
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(454)
<223> FRXA00162

```

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<400> 119
ggagacgtcg aaaagcataa acctggaact ttccggggcc cgcgcccgac tgctttgctg 60

aagccctatc ccgctatattt atttttgaag gaagagttgc gtg tct acc acc acc 115
Val Ser Thr Thr Thr
      1              5

cca atc cac cct gag cgc aag aaa cgc gtt cgt cag gcc ctc acc atg 163
Pro Ile His Pro Glu Arg Lys Lys Arg Val Arg Gln Ala Leu Thr Met
      10              15              20

ttc tcc atc gct gcg tgg gtg act ggt gtg ttt ttg ctg gcg ctg gtg 211
Phe Ser Ile Ala Trp Val Thr Gly Val Phe Leu Leu Ala Leu Val
      25              30              35

gcg gag atg atc atg aag tac ata att ggc atg gat ctt cct gag tgg 259
Ala Glu Met Ile Met Lys Tyr Ile Ile Gly Met Asp Leu Pro Glu Trp
      40              45              50

gca cga ttc gtt ccg att gca cat gga tgg gtt tac att gtt ttc ttg 307
Ala Arg Phe Val Pro Ile Ala His Gly Trp Val Tyr Ile Val Phe Leu
      55              60              65

atg acc acc ctg aac ctg ggt ctg aag gcg cgt tgg aat ccg act cgt 355
Met Thr Thr Leu Asn Leu Gly Leu Lys Ala Arg Trp Asn Pro Thr Arg

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70              75              80              85
tgg gtg acc acc gct atc gca ggt gtg gtt ccg ctg ctg tct ttt ttt 403
Trp Val Thr Thr Ala Ile Ala Gly Val Val Pro Leu Leu Ser Phe Phe
          90              95              100

gtt gag cac aac cgc cgc aag gaa gtt act cag aca ttc cag ctg aac 451
Val Glu His Asn Arg Arg Lys Glu Val Thr Gln Thr Phe Gln Leu Asn
          105              110              115

tca tagttaata cacaaaaacc tcc 477
Ser

```

```

<210> 120
<211> 118
<212> PRT
<213> Corynebacterium glutamicum

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```

<400> 120
Val Ser Thr Thr Thr Pro Ile His Pro Glu Arg Lys Lys Arg Val Arg
  1              5              10              15

Gln Ala Leu Thr Met Phe Ser Ile Ala Ala Trp Val Thr Gly Val Phe
          20              25              30

Leu Leu Ala Leu Val Ala Glu Met Ile Met Lys Tyr Ile Ile Gly Met
          35              40              45

Asp Leu Pro Glu Trp Ala Arg Phe Val Pro Ile Ala His Gly Trp Val
          50              55              60

Tyr Ile Val Phe Leu Met Thr Thr Leu Asn Leu Gly Leu Lys Ala Arg
          65              70              75              80

Trp Asn Pro Thr Arg Trp Val Thr Thr Ala Ile Ala Gly Val Val Pro
          85              90              95

Leu Leu Ser Phe Phe Val Glu His Asn Arg Arg Lys Glu Val Thr Gln
          100              105              110

Thr Phe Gln Leu Asn Ser
          115

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<210> 121
<211> 621
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(598)
<223> RXN00167

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<400> 121
cgcacaatcc agtggaaactt ccctatcgct gtgatgcatt ttactttca cgttcggta 60

ccctggcagg cagatcttcc aatctttagg agccctcgcc atg tac ctg ttg aat 115
Met Tyr Leu Leu Asn

```

1

5

cca cca gtc act gaa ccc gag atc ctc act gtc aac gag att ccg acc 163
 Pro Pro Val Thr Glu Pro Glu Ile Leu Thr Val Asn Glu Ile Pro Thr 20
 10 15

gtc gtc gct gtc ttt gac aac cac ccc atg aac gac atg ccc gca gca 211
 Val Val Ala Val Phe Asp Asn His Pro Met Asn Asp Met Pro Ala Ala 35
 25 30

ttc gat caa acc tac caa gtg ctc ttc ccc acc ttg ggt gcc aag ggc 259
 Phe Asp Gln Thr Tyr Gln Val Leu Phe Pro Thr Leu Gly Ala Lys Gly 50
 40 45

atc gcg cca att ggc ccc gga ttt gct ctg tac acc tcc gaa cca act 307
 Ile Ala Pro Ile Gly Pro Gly Phe Ala Leu Tyr Thr Ser Glu Pro Thr 65
 55 60

gac acc gtc agc ttt gaa gtg ggc atc cca gtc agc caa cca ctt gag 355
 Asp Thr Val Ser Phe Glu Val Gly Ile Pro Val Ser Gln Pro Leu Glu 85
 70 75 80

gga gat gtt tca gcc gcc agc ggc atc gtg ctg aaa aac tca gtg gtc 403
 Gly Asp Val Ser Ala Ala Ser Gly Ile Val Leu Lys Asn Ser Val Val 100
 90 95

cct gcc gga aaa att gcg cga atc agc cac atc ggc tca ttc gac gga 451
 Pro Ala Gly Lys Ile Ala Arg Ile Ser His Ile Gly Ser Phe Asp Gly 115
 105 110

ctg agc caa gca tgg ggt tca ttc gtg gaa gct ctt gaa tct gca ggc 499
 Leu Ser Gln Ala Trp Gly Ser Phe Val Glu Ala Leu Glu Ser Ala Gly 130
 120 125

cat gag atc gat atg ccg tgt tgg gag gta tat gtc acc gag cct tcc 547
 His Glu Ile Asp Met Pro Cys Trp Glu Val Tyr Val Thr Glu Pro Ser 145
 135 140

ccc gac atg gat ccc gca aca ctc caa act gat cta tac gtc ctg ttg 595
 Pro Asp Met Asp Pro Ala Thr Leu Gln Thr Asp Leu Thr Val Leu Leu 165
 150 155 160

aag tagagaagct ttctggtcaa gtt 621
 Lys

<210> 122

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 122

Met Tyr Leu Leu Asn Pro Pro Val Thr Glu Pro Glu Ile Leu Thr Val
 1 5 10 15

Asn Glu Ile Pro Thr Val Val Ala Val Phe Asp Asn His Pro Met Asn
 20 25 30

Asp Met Pro Ala Ala Phe Asp Gln Thr Tyr Gln Val Leu Phe Pro Thr
 35 40 45

Leu Gly Ala Lys Gly Ile Ala Pro Ile Gly Pro Gly Phe Ala Leu Tyr
 50 55 60
 Thr Ser Glu Pro Thr Asp Thr Val Ser Phe Glu Val Gly Ile Pro Val
 65 70 75 80
 Ser Gln Pro Leu Glu Gly Asp Val Ser Ala Ala Ser Gly Ile Val Leu
 85 90 95
 Lys Asn Ser Val Val Pro Ala Gly Lys Ile Ala Arg Ile Ser His Ile
 100 105 110
 Gly Ser Phe Asp Gly Leu Ser Gln Ala Trp Gly Ser Phe Val Glu Ala
 115 120 125
 Leu Glu Ser Ala Gly His Glu Ile Asp Met Pro Cys Trp Glu Val Tyr
 130 135 140
 Val Thr Glu Pro Ser Pro Asp Met Asp Pro Ala Thr Leu Gln Thr Asp
 145 150 155 160
 Leu Tyr Val Leu Leu Lys
 165

<210> 123
 <211> 361
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(361)
 <223> FRXA00167

<400> 123
 ccgacaatcc agtggaaactt ccctatcgct gtgatgcatt ttactttcca cggtccggta 60
 ccctggcagg cagatcttcc aatctttagg agccctcgcc atg tac ctg ttg aat 115
 Met Tyr Leu Leu Asn
 1 5
 cca cca gtc act gaa ccc gag atc ctc act gtc aac gag att ccg acc 163
 Pro Pro Val Thr Glu Pro Glu Ile Leu Thr Val Asn Glu Ile Pro Thr
 10 15 20
 gtc gtc get gtc ttt gac aac cac ccc atg aac gac atg ccc gca gca 211
 Val Val Ala Val Phe Asp Asn His Pro Met Asn Asp Met Pro Ala Ala
 25 30 35
 ttc gat caa acc tac caa gtg ctc ttc ccc acc ttg ggt gcc aag ggc 259
 Phe Asp Gln Thr Tyr Gln Val Leu Phe Pro Thr Leu Gly Ala Lys Gly
 40 45 50
 atc gcg cca att ggc ccc gga ttt gct ctg tac acc tcc gaa cca act 307
 Ile Ala Pro Ile Gly Pro Gly Phe Ala Leu Tyr Thr Ser Glu Pro Thr
 55 60 65
 gac acc gtc agc ttt gaa gtg ggc atg cca gtc agc caa cca ctt gag 355
 Asp Thr Val Ser Phe Glu Val Gly Met Pro Val Ser Gln Pro Leu Glu

70 75 80 85 361

gga gag
Gly Glu

<210> 124
<211> 87
<212> PRT
<213> Corynebacterium glutamicum

<400> 124
Met Tyr Leu Leu Asn Pro Pro Val Thr Glu Pro Glu Ile Leu Thr Val
1 5 10 15
Asn Glu Ile Pro Thr Val Val Ala Val Phe Asp Asn His Pro Met Asn
20 25 30
Asp Met Pro Ala Ala Phe Asp Gln Thr Tyr Gln Val Leu Phe Pro Thr
35 40 45
Leu Gly Ala Lys Gly Ile Ala Pro Ile Gly Pro Gly Phe Ala Leu Tyr
50 55 60
Thr Ser Glu Pro Thr Asp Thr Val Ser Phe Glu Val Gly Met Pro Val
65 70 75 80
Ser Gln Pro Leu Glu Gly Glu
85

<210> 125
<211> 281
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(258)
<223> RXN00171

<400> 125
aaa gat cag cag aag cag att cat aac ttg gca gct gag gta aag cgt 48
Lys Asp Gln Gln Lys Gln Ile His Asn Leu Ala Ala Glu Val Lys Arg
1 5 10 15
ctt cgt gag cgt gac gat gca cga gat cag cag cta gga gtg ctt aat 96
Leu Arg Glu Arg Asp Asp Ala Arg Asp Gln Gln Leu Gly Val Leu Asn
20 25 30
gaa gcc atg ttt tca cta cta gga gat gga ctt gac cgt ttt cgt gaa 144
Glu Ala Met Phe Ser Leu Leu Gly Asp Gly Leu Asp Arg Phe Arg Glu
35 40 45
tct ggc gat gag gca tcc ttc aat gct gca ttg aac tat cag gca gtg 192
Ser Gly Asp Glu Ala Ser Phe Asn Ala Ala Leu Asn Tyr Gln Ala Val
50 55 60
gtg gca cca gaa atg ttt aag acc gtg tat ggt gtc gat ccg tct acc 240
Val Ala Pro Glu Met Phe Lys Thr Val Tyr Gly Val Asp Pro Ser Thr

65 70 75 80
 gga gag cct att ccc act taaagtacaa cacagtcttt tca 281
 Gly Glu Pro Ile Pro Thr
 85

<210> 126
 <211> 86
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 126
 Lys Asp Gln Gln Lys Gln Ile His Asn Leu Ala Ala Glu Val Lys Arg
 1 5 10 15
 Leu Arg Glu Arg Asp Asp Ala Arg Asp Gln Gln Leu Gly Val Leu Asn
 20 25 30
 Glu Ala Met Phe Ser Leu Leu Gly Asp Gly Leu Asp Arg Phe Arg Glu
 35 40 45
 Ser Gly Asp Glu Ala Ser Phe Asn Ala Ala Leu Asn Tyr Gln Ala Val
 50 55 60
 Val Ala Pro Glu Met Phe Lys Thr Val Tyr Gly Val Asp Pro Ser Thr
 65 70 75 80
 Gly Glu Pro Ile Pro Thr
 85

<210> 127
 <211> 354
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(331)
 <223> FRXA00171

<400> 127
 cgattaaggt aggggcctta aaaaggggaa taaagaatat tgggccccaga cgaaaactgc 60
 tggcgagatc atcaaagatc agcagaagca gattcataac ttg gca gct gag gta 115
 Leu Ala Ala Glu Val
 1 5
 aag cgt ctt cgt gag cgt gac gat gca cga gat cag cag cta gga gtg 163
 Lys Arg Leu Arg Glu Arg Asp Asp Ala Arg Asp Gln Gln Leu Gly Val
 10 15 20
 ctt aat gaa gcc atg ttt tca cta cta gga gat gga ctt gac cgt ttt 211
 Leu Asn Glu Ala Met Phe Ser Leu Leu Gly Asp Gly Leu Asp Arg Phe
 25 30 35
 cgt gaa tct ggc gat gag gca tcc ttc aat gct gca ttg aac tat cag 259
 Arg Glu Ser Gly Asp Glu Ala Ser Phe Asn Ala Ala Leu Asn Tyr Gln
 40 45 50

gca gtg gtg gca cca gaa atg ttt aag acc gtg tat ggt gtc gat ccg 307
Ala Val Val Ala Pro Glu Met Phe Lys Thr Val Tyr Gly Val Asp Pro
55 60 65

tct acc gga gag cct att ccc act taaagtacaa cacagtcttt tca 354
Ser Thr Gly Glu Pro Ile Pro Thr
70 75

<210> 128

<211> 77

<212> PRT

<213> Corynebacterium glutamicum

<400> 128

Leu Ala Ala Glu Val Lys Arg Leu Arg Glu Arg Asp Asp Ala Arg Asp
1 5 10 15

Gln Gln Leu Gly Val Leu Asn Glu Ala Met Phe Ser Leu Leu Gly Asp
20 25 30

Gly Leu Asp Arg Phe Arg Glu Ser Gly Asp Glu Ala Ser Phe Asn Ala
35 40 45

Ala Leu Asn Tyr Gln Ala Val Val Ala Pro Glu Met Phe Lys Thr Val
50 55 60

Tyr Gly Val Asp Pro Ser Thr Gly Glu Pro Ile Pro Thr
65 70 75

<210> 129

<211> 564

<212> DNA

<213> *Corynebacterium glutamicum*

 $\langle 220 \rangle$

<221> CDS

<222> (101) . . (541)

<223> RXN00194

<400> 129

aaatatgaga acatagtgaq agttaaacca agttctgtag gtgcttggtg cagcgggcgc 60

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gaaggcgtag cactgcaact tgcgaataaa ggagtaaaac  gtg gct ggt tcc tcc    115
                Val Ala Gly Ser Ser
                1             5
```

cac acg att gag cct gag atc tac cgc ggt gta tcc acc ctt gat gag 163
His Thr Ile Glu Pro Glu Ile Tyr Arg Gly Val Ser Thr Leu Asp Glu
 10 15 20

cct tgc gct gca tgg gga tgg cac ggt ctc aag cgc aac acc atc caa 211
Pro Ser Ala Ala Trp Gly Trp His Gly Leu Lys Arg Asn Thr Ile Gln
25 30 35

ctc gct ggc tgg att tcc gtt ctg ttc atg ctt gga tac aac ttc ggt 259
Leu Ala Gly Trp Ile Ser Val Leu Phe Met Leu Gly Tyr Asn Phe Gly
40 45 50

aac cac aag qgc cac gtt qaa acc atc tqg ctt ctc gtc atc acc gcc 307

```

Asn His Lys Gly His Val Glu Thr Ile Trp Leu Leu Val Ile Thr Ala
 55                                60
ctt ctg gtc atc ggc ctg ctg atc cac ctg ttc gag cca aag ctc ttc 355
Leu Leu Val Ile Gly Leu Leu Ile His Leu Phe Glu Pro Lys Leu Phe
 70                                80                                85
cag gtt cgc acc atc act tcc cgc aac aag cct gtc ggc cac gtc gag 403
Gln Val Arg Thr Ile Thr Ser Arg Asn Lys Pro Val Gly His Val Glu
 90                                95                                100
cca gac tgg acc tac gac cag gca acc ctc acc ggc acc tgg ggt aac 451
Pro Asp Trp Thr Tyr Asp Gln Ala Thr Leu Thr Gly Thr Trp Gly Asn
105                                110                                115
ctc act gac tcc cag ctt cgc tcc gtc aac atc gag cca agc cgt gtc 499
Leu Thr Asp Ser Gln Leu Arg Ser Val Asn Ile Glu Pro Ser Arg Val
120                                125                                130
gct cac ctg cgt gct gca gat tct gcg aaa gaa cta gac aac 541
Ala His Leu Arg Ala Ala Asp Ser Ala Lys Glu Leu Asp Asn
135                                140                                145

tagtttttta aaaagaaaat gcg 564

<210> 130
<211> 147
<212> PRT
<213> Corynebacterium glutamicum

<400> 130
Val Ala Gly Ser Ser His Thr Ile Glu Pro Glu Ile Tyr Arg Gly Val
 1 5 10 15
Ser Thr Leu Asp Glu Pro Ser Ala Ala Trp Gly Trp His Gly Leu Lys
 20 25 30
Arg Asn Thr Ile Gln Leu Ala Gly Trp Ile Ser Val Leu Phe Met Leu
 35 40 45

Gly Tyr Asn Phe Gly Asn His Lys Gly His Val Glu Thr Ile Trp Leu
 50 55 60
Leu Val Ile Thr Ala Leu Leu Val Ile Gly Leu Leu Ile His Leu Phe
 65 70 75 80
Glu Pro Lys Leu Phe Gln Val Arg Thr Ile Ser Arg Asn Lys Pro
 85 90 95
Val Gly His Val Glu Pro Asp Trp Thr Tyr Asp Gln Ala Thr Leu Thr
100 105 110
Gly Thr Trp Gly Asn Leu Thr Asp Ser Gln Leu Arg Ser Val Asn Ile
115 120 125
Glu Pro Ser Arg Val Ala His Leu Arg Ala Ala Asp Ser Ala Lys Glu
130 135 140
Leu Asp Asn
145

```

<210> 131
 <211> 385
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(385)
 <223> FRXA00194

<400> 131
 aaatatgaga acatagtgag agttaaacca agttctgtag gtgcttggtg cagcgggcgc 60
 gaaggcgtag cactgcaact tgcgaataaa ggagtaaaac gtg gct ggt tcc tcc 115
 Val Ala Gly Ser Ser
 1 5
 cac acg att gag cct gag atc tac cgc ggt gta tcc acc ctt gat gag 163
 His Thr Ile Glu Pro Glu Ile Tyr Arg Gly Val Ser Thr Leu Asp Glu
 10 15 20
 cct tcg gct gca tgg gga tgg cac ggt ctc aag cgc aac acc atc caa 211
 Pro Ser Ala Ala Trp Gly Trp His Gly Leu Lys Arg Asn Thr Ile Gln
 25 30 35
 ctc gct ggc tgg att tcc gtt ctg ttc atg ctt gga tac aac ttc ggt 259
 Leu Ala Gly Trp Ile Ser Val Leu Phe Met Leu Gly Tyr Asn Phe Gly
 40 45 50
 aac cac aag ggc cac gtt gaa acc atc tgg ctt ctc gtc atc acc gcc 307
 Asn His Lys Gly His Val Glu Thr Ile Trp Leu Val Ile Thr Ala
 55 60 65
 ctt ctg gtc atc ggc ctg ctg atc cac ctg ttc gag cca aaa gct ctt 355
 Leu Leu Val Ile Gly Leu Leu Ile His Leu Phe Glu Pro Lys Ala Leu
 70 75 80 85
 cca ggt tcg cac cat cac ttc tcg caa caa 385
 Pro Gly Ser His His His Phe Ser Gln Gln
 90 95

<210> 132
 <211> 95
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 132
 Val Ala Gly Ser Ser His Thr Ile Glu Pro Glu Ile Tyr Arg Gly Val
 1 5 10 15
 Ser Thr Leu Asp Glu Pro Ser Ala Ala Trp Gly Trp His Gly Leu Lys
 20 25 30
 Arg Asn Thr Ile Gln Leu Ala Gly Trp Ile Ser Val Leu Phe Met Leu
 35 40 45
 Gly Tyr Asn Phe Gly Asn His Lys Gly His Val Glu Thr Ile Trp Leu
 50 55 60

Leu Val Ile Thr Ala Leu Leu Val Ile Gly Leu Leu Ile His Leu Phe
65 70 75 80

Glu Pro Lys Ala Leu Pro Gly Ser His His His Phe Ser Gln Gln
85 90 95

<210> 133

<211> 1335

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1312)

<223> RXN00197

<400> 133

gtc gat gata ttttggcaac cgaatctgag gcacgcgcgc gtgcgaatgc ttgatacaac 60

cggttggcaa ccaacttgta agctaaggag ctccgcctc gtg gca gcc tat ctt 115
Val Ala Ala Tyr Leu
1 5

ctt ggt gtc gta tta ttt ttc ctc ggc atc gca gta acc atc gcg ctt 163
Leu Gly Val Val Leu Phe Phe Leu Gly Ile Ala Val Thr Ile Ala Leu
10 15 20

cac gag tgg ggg cac ttc atc aca gcg cgc att ttc gga atg aaa gtg 211
His Glu Trp Gly His Phe Ile Thr Ala Arg Ile Phe Gly Met Lys Val
25 30 35

cgg cgt ttc ttc atc ggt ttc ggc cgg acg gtg ttt gcc aaa aga cgc 259
Arg Arg Phe Phe Ile Gly Phe Gly Pro Thr Val Phe Ala Lys Arg Arg
40 45 50

ggc gaa acc gtg tac ggc ctt aaa gcg att cgg gtc ggc ggt ttt tgt 307
Gly Glu Thr Val Tyr Gly Leu Lys Ala Ile Pro Val Gly Gly Phe Cys
55 60 65

gac atc gcg ggg atg act gcc caa gat gaa ctt gat cgg gaa gac ctg 355
Asp Ile Ala Gly Met Thr Ala Gln Asp Glu Leu Asp Pro Glu Asp Leu
70 75 80 85

cgg cgc gcc atg tat cta aag ccc tgg tgg cag cgc ata att gtg ctt 403
Pro Arg Ala Met Tyr Leu Lys Pro Trp Trp Gln Arg Ile Ile Val Leu
90 95 100

tcc ggc ggc gtg atc atg aat ctg atc gtc ggc ttt ttg gtg ctt tac 451
Ser Gly Gly Val Ile Met Asn Leu Ile Val Gly Phe Leu Val Leu Tyr
105 110 115

ggc gtg gcg gtg agc tcc gga atc cgg aat cgg gat gtg gat acc acc 499
Gly Val Ala Val Ser Ser Gly Ile Pro Asn Pro Asp Val Asp Thr Thr
120 125 130

gcg aca gtc gac acc gtt cag tgc gtg cgg gaa acc caa att tcc gca 547
Ala Thr Val Asp Thr Val Gln Cys Val Pro Glu Thr Gln Ile Ser Ala
135 140 145

act gaa ctg tcc tcc tgc gta ggt tca ggc cca gcg ggc gac gcc ggc	595
Thr Glu Leu Ser Ser Cys Val Gly Ser Gly Pro Ala Gly Asp Ala Gly	
150 155 160 165	
att gag cac ggc gat aag att ttg gcc gtc aac ggc caa gag atg gca	643
Ile Glu His Gly Asp Lys Ile Leu Ala Val Asn Gly Gln Glu Met Ala	
170 175 180	
agc ttc acc gcc atc cgc gat gcg atc ctc gag ctc cca ggc gaa acg	691
Ser Phe Thr Ala Ile Arg Asp Ala Ile Leu Glu Leu Pro Gly Glu Thr	
185 190 195	
gca acg ctg acg att gaa cgg gag gga acg ctt ttc gac gtc gac ctc	739
Ala Thr Leu Thr Ile Glu Arg Glu Gly Thr Leu Phe Asp Val Asp Leu	
200 205 210	
cag gtt gcc tct gtc acc cgt ctc gcc tct gac ggt tca gaa att acc	787
Gln Val Ala Ser Val Thr Arg Leu Ala Ser Asp Gly Ser Glu Ile Thr	
215 220 225	
gtc ggc gcg gtg ggc atg tcg agc ctt cca cgg acc gat gtg tac aaa	835
Val Gly Ala Val Gly Met Ser Ser Leu Pro Thr Asp Val Tyr Lys	
230 235 240 245	
aaa tac ggc cca atc gag ggt gtg gga gca act gca cgt ttc acc ggc	883
Lys Tyr Gly Pro Ile Glu Gly Val Gly Ala Thr Ala Arg Phe Thr Gly	
250 255 260	
gac atg atc agc gcc acg tgg gat ggc ctc aaa gcc ttc cgg gcg aaa	931
Asp Met Ile Ser Ala Thr Trp Asp Gly Leu Lys Ala Phe Pro Ala Lys	
265 270 275	
atc cca ggg gtc gtc gca tcc atc ttc ggt gca gaa cga gat gta gaa	979
Ile Pro Gly Val Val Ala Ser Ile Phe Gly Ala Glu Arg Asp Val Glu	
280 285 290	
agc ccc atg agt gtg gtg ggc gcc gta cgc atc ggc ggc gaa ttt gtc	1027
Ser Pro Met Ser Val Val Gly Ala Val Arg Ile Gly Gly Glu Phe Val	
295 300 305	
gaa cgt tcc atg tgg gac atg ttc atg atg atg ctg gcc agc ctg aac	1075
Glu Arg Ser Met Trp Asp Met Phe Met Met Met Leu Ala Ser Leu Asn	
310 315 320 325	
ttc ttc ctc gcg ctg ttt aac ctc gtg ccg ctg cca coa ctt gat ggc	1123
Phe Phe Leu Ala Leu Phe Asn Leu Val Pro Leu Pro Pro Leu Asp Gly	
330 335 340	
gga cac att gcc gtg gtg atc tat gaa aaa atc cgc gac ttc ttc cgc	1171
Gly His Ile Ala Val Val Ile Tyr Glu Lys Ile Arg Asp Phe Phe Arg	
345 350 355	
aaa ctg cgc gga aaa cca gcg ggc ggc cca gcg gat tac acc aaa cta	1219
Lys Leu Arg Gly Lys Pro Ala Gly Gly Pro Ala Asp Tyr Thr Lys Leu	
360 365 370	
atg ccc gtc acc gta gct gtc gca gcc ttg ctg atg aca gtg gga ggc	1267
Met Pro Val Thr Val Ala Val Ala Ala Leu Leu Met Thr Val Gly Gly	
375 380 385	
ctg gtc att gtc gcc gat gtg gtc aat ccc atc cga ctc ttt ggc	1312

Leu Val Ile Val Ala Asp Val Val Asn Pro Ile Arg Leu Phe Gly
 390 395 400

taacgatacg gaattgaact gcc

1335

<210> 134

<211> 404

<212> PRT

<213> Corynebacterium glutamicum

<400> 134

Val Ala Ala Tyr Leu Leu Gly Val Val Leu Phe Phe Leu Gly Ile Ala
 1 5 10 15

Val Thr Ile Ala Leu His Glu Trp Gly His Phe Ile Thr Ala Arg Ile
 20 25 30

Phe Gly Met Lys Val Arg Arg Phe Phe Ile Gly Phe Gly Pro Thr Val
 35 40 45

Phe Ala Lys Arg Arg Gly Glu Thr Val Tyr Gly Leu Lys Ala Ile Pro
 50 55 60

Val Gly Gly Phe Cys Asp Ile Ala Gly Met Thr Ala Gln Asp Glu Leu
 65 70 75 80

Asp Pro Glu Asp Leu Pro Arg Ala Met Tyr Leu Lys Pro Trp Trp Gln
 85 90 95

Arg Ile Ile Val Leu Ser Gly Gly Val Ile Met Asn Leu Ile Val Gly
 100 105 110

Phe Leu Val Leu Tyr Gly Val Ala Val Ser Ser Gly Ile Pro Asn Pro
 115 120 125

Asp Val Asp Thr Thr Ala Thr Val Asp Thr Val Gln Cys Val Pro Glu
 130 135 140

Thr Gln Ile Ser Ala Thr Glu Leu Ser Ser Cys Val Gly Ser Gly Pro
 145 150 155 160

Ala Gly Asp Ala Gly Ile Glu His Gly Asp Lys Ile Leu Ala Val Asn
 165 170 175

Gly Gln Glu Met Ala Ser Phe Thr Ala Ile Arg Asp Ala Ile Leu Glu
 180 185 190

Leu Pro Gly Glu Thr Ala Thr Leu Thr Ile Glu Arg Glu Gly Thr Leu
 195 200 205

Phe Asp Val Asp Leu Gln Val Ala Ser Val Thr Arg Leu Ala Ser Asp
 210 215 220

Gly Ser Glu Ile Thr Val Gly Ala Val Gly Met Ser Ser Leu Pro Pro
 225 230 235 240

Thr Asp Val Tyr Lys Lys Tyr Gly Pro Ile Glu Gly Val Gly Ala Thr
 245 250 255

Ala Arg Phe Thr Gly Asp Met Ile Ser Ala Thr Trp Asp Gly Leu Lys

260

265

270

Ala Phe Pro Ala Lys Ile Pro Gly Val Val Ala Ser Ile Phe Gly Ala
275 280 285

Glu Arg Asp Val Glu Ser Pro Met Ser Val Val Gly Ala Val Arg Ile
290 295 300

Gly Gly Glu Phe Val Glu Arg Ser Met Trp Asp Met Phe Met Met Met
305 310 315 320

Leu Ala Ser Leu Asn Phe Phe Leu Ala Leu Phe Asn Leu Val Pro Leu
325 330 335

Pro Pro Leu Asp Gly Gly His Ile Ala Val Val Ile Tyr Glu Lys Ile
340 345 350

Arg Asp Phe Phe Arg Lys Leu Arg Gly Lys Pro Ala Gly Gly Pro Ala
355 360 365

Asp Tyr Thr Lys Leu Met Pro Val Thr Val Ala Val Ala Ala Leu Leu
370 375 380

Met Thr Val Gly Gly Leu Val Ile Val Ala Asp Val Val Asn Pro Ile
385 390 395 400

Arg Leu Phe Gly

<210> 135

<211> 1111

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1111)

<223> FRXA00197

<400> 135

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cggttgga ccaacttgta agctaaggag cttccgcctc gtg gca gcc tat ctt 115
Val Ala Ala Tyr Leu
1 5

ctt ggt gtc gta tta ttt ttc ctc ggc atc gca gta acc atc gcg ctt 163
Leu Gly Val Val Leu Phe Phe Leu Gly Ile Ala Val Thr Ile Ala Leu
10 15 20

cac gag tgg ggg cac ttc atc aca gcg cgc att ttc gga atg aaa gtg 211
His Glu Trp Gly His Phe Ile Thr Ala Arg Ile Phe Gly Met Lys Val
25 30 35

cgg cgt ttc ttc atc ggt ttc ggc ccg acg gtg ttt gcc aaa aga cgc 259
Arg Arg Phe Phe Ile Gly Phe Gly Pro Thr Val Phe Ala Lys Arg Arg
40 45 50

ggc gaa acc gtg tac ggc ctt aaa gcg att ccg gtc ggc ggt ttt tgt 307
Gly Glu Thr Val Tyr Gly Leu Lys Ala Ile Pro Val Gly Gly Phe Cys

55	60	65	
gac atc gcg ggg atg act gcc caa gat gaa ctt gat ccg gaa gac ctg Asp Ile Ala Gly Met Thr Ala Gln Asp Glu Leu Asp Leu	75	80	355
70		85	
ccg cgc gcc atg tat cta aag ccc tgg tgg cag cgc ata att gtg ctt Pro Arg Ala Met Tyr Leu Lys Pro Trp Trp Gln Arg Ile Ile Val Leu	90	95	403
		100	
tcc gcc gcg gtg atc atg aat ctg atc gtc gcc ttt ttg gtg ctt tac Ser Gly Gly Val Ile Met Asn Leu Ile Val Gly Phe Leu Val Leu Tyr	105	110	451
		115	
ggc gtg gcg gtg agc tcc gga atc ccg aat ccg gat gtg gat acc acc Gly Val Ala Val Ser Ser Gly Ile Pro Asn Pro Asp Val Asp Thr Thr	120	125	499
		130	
gcg aca gtc gac acc gtt cag tgc gtg ccg gaa acc caa att tcc gca Ala Thr Val Asp Thr Val Gln Cys Val Pro Glu Thr Gln Ile Ser Ala	135	140	547
		145	
act gaa ctg tcc tcc tgc gta ggt tca gcc cca gcg gcc gac gcc gcc Thr Glu Leu Ser Ser Cys Val Gly Ser Gly Pro Ala Gly Asp Ala Gly	150	155	595
		160	
att gag cac gcc gat aag att ttg gcc gtc aac gcc caa gag atg gca Ile Glu His Gly Asp Lys Ile Leu Ala Val Asn Gly Gln Glu Met Ala	170	175	643
		180	
agc ttc acc gcc atc cgc gat gcg atc ctc gag ctc cca gcc gaa acg Ser Phe Thr Ala Ile Arg Asp Ala Ile Leu Glu Leu Pro Gly Glu Thr	185	190	691
		195	
gca acg ctg acg att gaa cgg gag gga acg ctt ttc gac gtc gac ctc Ala Thr Leu Thr Ile Glu Arg Glu Gly Thr Leu Phe Asp Val Asp Leu	200	205	739
		210	
cag gtt gcc tct gtc acc cgt ctc gcc tct gac ggt tca gaa att acc Gln Val Ala Ser Val Thr Arg Leu Ala Ser Asp Gly Ser Glu Ile Thr	215	220	787
		225	
gtc gcc gcg gtg gcc atg tgc agc ctt cca ccg acc gat gtg tac aaa Val Gly Ala Val Gly Met Ser Ser Leu Pro Pro Thr Asp Val Tyr Lys	230	235	835
		240	
aaa tac gcc cca atc gag ggt gtg gga gca act gca cgt ttc acc gcc Lys Tyr Gly Pro Ile Glu Gly Val Gly Ala Thr Ala Arg Phe Thr Gly	250	255	883
		260	
gac atg atc agc gcc acg tgg gat gcc ctc aaa gcc ttc ccg gcg aaa Asp Met Ile Ser Ala Thr Trp Asp Gly Leu Lys Ala Phe Pro Ala Lys	265	270	931
		275	
atc cca ggg gtc gtc gca tcc atc ttc ggt gca gaa cga gat gta gaa Ile Pro Gly Val Val Ala Ser Ile Phe Gly Ala Glu Arg Asp Val Glu	280	285	979
		290	
agc ccc atg agt gtg gtg ggc gcg tca cgc atc ggc gcc gaa ttt gtc Ser Pro Met Ser Val Val Gly Ala Ser Arg Ile Gly Glu Phe Val	295	300	1027
		305	

gaa cgt tcc atg tgg gac atg ttc atg atg atg ctg gcc agc ctg aac 1075
 Glu Arg Ser Met Trp Asp Met Phe Met Met Met Leu Ala Ser Leu Asn
 310 315 320 325

ttc ttc ctc gcg ctg ttt aac ctc gtg ccg ctg cca 1111
 Phe Phe Leu Ala Leu Phe Asn Leu Val Pro Leu Pro
 330 335

<210> 136

<211> 337

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 136

Val Ala Ala Tyr Leu Leu Gly Val Val Leu Phe Phe Leu Gly Ile Ala
 1 5 10 15

Val Thr Ile Ala Leu His Glu Trp Gly His Phe Ile Thr Ala Arg Ile
 20 25 30

Phe Gly Met Lys Val Arg Arg Phe Phe Ile Gly Phe Gly Pro Thr Val
 35 40 45

Phe Ala Lys Arg Arg Gly Glu Thr Val Tyr Gly Leu Lys Ala Ile Pro
 50 55 60

Val Gly Gly Phe Cys Asp Ile Ala Gly Met Thr Ala Gln Asp Glu Leu
 65 70 75 80

Asp Pro Glu Asp Leu Pro Arg Ala Met Tyr Leu Lys Pro Trp Trp Gln
 85 90 95

Arg Ile Ile Val Leu Ser Gly Gly Val Ile Met Asn Leu Ile Val Gly
 100 105 110

Phe Leu Val Leu Tyr Gly Val Ala Val Ser Ser Gly Ile Pro Asn Pro
 115 120 125

Asp Val Asp Thr Thr Ala Thr Val Asp Thr Val Gln Cys Val Pro Glu
 130 135 140

Thr Gln Ile Ser Ala Thr Glu Leu Ser Ser Cys Val Gly Ser Gly Pro
 145 150 155 160

Ala Gly Asp Ala Gly Ile Glu His Gly Asp Lys Ile Leu Ala Val Asn
 165 170 175

Gly Gln Glu Met Ala Ser Phe Thr Ala Ile Arg Asp Ala Ile Leu Glu
 180 185 190

Leu Pro Gly Glu Thr Ala Thr Leu Thr Ile Glu Arg Glu Gly Thr Leu
 195 200 205

Phe Asp Val Asp Leu Gln Val Ala Ser Val Thr Arg Leu Ala Ser Asp
 210 215 220

Gly Ser Glu Ile Thr Val Gly Ala Val Gly Met Ser Ser Leu Pro Pro
 225 230 235 240

Thr Asp Val Tyr Lys Lys Tyr Gly Pro Ile Glu Gly Val Gly Ala Thr
245 255

Ala Arg Phe Thr Gly Asp Met Ile Ser Ala Thr Trp Asp Gly Leu Lys
260 265 270

Ala Phe Pro Ala Lys Ile Pro Gly Val Val Ala Ser Ile Phe Gly Ala
275 280 285

Glu Arg Asp Val Glu Ser Pro Met Ser Val Val Gly Ala Ser Arg Ile
290 295 300

Gly Gly Glu Phe Val Glu Arg Ser Met Trp Asp Met Phe Met Met Met
305 310 315 320

Leu Ala Ser Leu Asn Phe Phe Leu Ala Leu Phe Asn Leu Val Pro Leu
325 330 335

Pro

<210> 137
<211> 1113
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(1090)
<223> RXN00216

<400> 137
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ttggatcagg caccatctgc cacacggagt ctttaagaaaa ttg ggc gct tat ggt 115
Leu Gly Ala Tyr Gly
1 5

tta ggt gag ctt cct gga aaa tcc gcc gcg gaa gcc gcc gac att att 163
Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu Ala Ala Asp Ile Ile
10 15 20

cag ggt gaa acg ggc gat ctt ctc cat att cct cag ctt ccg gcg cga 211
Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro Gln Leu Pro Ala Arg
25 30 35

ggt ttg ggt gct gat ctg atc ggt cga acc gtc ggt ctg ctg gac atg 259
Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val Gly Leu Leu Asp Met
40 45 50

atc aac gtt gat cgc ggg gcc cga tct tgg gtg atg agc aca cgc ccc 307
Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val Met Ser Thr Arg Pro
55 60 65

agc aga ttg acg cac ctg acc ggc gat ttc ctt gac atg gat ttg gat 355
Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu Asp Met Asp Leu Asp
70 75 80 85

gcg tgc gag gaa acc tgg gga acg ggc gtc gac aag cta aaa atc caa 403
Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp Lys Leu Lys Ile Gln

	90	95	100	
gtt gct ggt ccc tgg act tta ggt gcg cgc att gag ttg gcc aat ggc				451
Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile Glu Leu Ala Asn Gly	105	110	115	
cat cgc gtt ttg tct gat cgc ggt gcg atg cgt gat ctc acg cag gcg				499
His Arg Val Leu Ser Asp Arg Gly Ala Met Arg Asp Leu Thr Gln Ala	120	125	130	
ctg atc gcc ggc atc gat gcg cat gca cgc aag gtt gct ggg cga ttt				547
Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys Val Ala Gly Arg Phe	135	140	145	
gcg gcc gaa gtg cag gtg caa att gat gag ccg gag ctg aaa tcg ctt				595
Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro Glu Leu Lys Ser Leu	150	155	160	165
atc gac ggc tcc ctc cct ggc act tcc acc ttt gac att att cct gcg				643
Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe Asp Ile Ile Pro Ala	170	175	180	
gtg aat gtc gct gat gcc agt gaa cgt ttg cag cag gtc ttt agc tcg				691
Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln Gln Val Phe Ser Ser	185	190	195	
att gag ggg ccg aca tat ctc aac ctc acc ggc cag att cct act tgg				739
Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly Gln Ile Pro Thr Trp	200	205	210	
gat gtg gct cgg ggt gcg ggc gcc gat act gtg cag att tcc atg gat				787
Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val Gln Ile Ser Met Asp	215	220	225	
caa gtc cgt gga aat gaa cat ttg gat ggt ttt ggt gaa acc atc acc				835
Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe Gly Glu Thr Ile Thr	230	235	240	245
agt gga att cgt ctt ggt ttg ggc att acg aca gga aaa gat gtc gta				883
Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr Gly Lys Asp Val Val	250	255	260	
gat gaa ctg ctc gag cga ccg cgg caa aag gcc gtt gag gta gca cgc				931
Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala Val Glu Val Ala Arg	265	270	275	
ttt ttt gat cgt tta ggt gtg ggc cga aac tat ctc gtg gat gct gtt				979
Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr Leu Val Asp Ala Val	280	285	290	
gat att cat ccg ggt gag gat ttg gtg cag ggg acc atc acc gag gcc				1027
Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly Thr Ile Thr Glu Ala	295	300	305	
gcg cag gct tat cgc atg gcc cgg gtg atg tcg gag atg ttg tcg aag				1075
Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser Glu Met Leu Ser Lys	310	315	320	325
gat tca tgc gac ctt taaggcttta ccggcgctgg gtg				1113
Asp Ser Cys Asp Leu	330			

<210> 138
 <211> 330
 <212> PRT
 <213> *Corynebacterium glutamicum*

 <400> 138
 Leu Gly Ala Tyr Gly Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu
 1 5 10 15
 Ala Ala Asp Ile Ile Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro
 20 25 30
 Gln Leu Pro Ala Arg Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val
 35 40 45
 Gly Leu Leu Asp Met Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val
 50 55 60
 Met Ser Thr Arg Pro Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu
 65 70 75 80
 Asp Met Asp Leu Asp Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp
 85 90 95
 Lys Leu Lys Ile Gln Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile
 100 105 110
 Glu Leu Ala Asn Gly His Arg Val Leu Ser Asp Arg Gly Ala Met Arg
 115 120 125
 Asp Leu Thr Gln Ala Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys
 130 135 140
 Val Ala Gly Arg Phe Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro
 145 150 155 160
 Glu Leu Lys Ser Leu Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe
 165 170 175
 Asp Ile Ile Pro Ala Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln
 180 185 190
 Gln Val Phe Ser Ser Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly
 195 200 205
 Gln Ile Pro Thr Trp Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val
 210 215 220
 Gln Ile Ser Met Asp Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe
 225 230 235 240
 Gly Glu Thr Ile Thr Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr
 245 250 255
 Gly Lys Asp Val Val Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala
 260 265 270
 Val Glu Val Ala Arg Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr
 275 280 285

Leu Val Asp Ala Val Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly
 290 295 300

Thr Ile Thr Glu Ala Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser
 305 310 315 320

Glu Met Leu Ser Lys Asp Ser Cys Asp Leu
 325 330

<210> 139

<211> 1269

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}..(1246)

<223> RXN00222

<400> 139

agggaaaaac taccgccgc ctggacaaaag tcacgatgt actccgcgtc ottggactcg 60

agctttctgt tggaattcac gatccctca aggttaatca atg acc ccc act gcc 115
 Met Thr Pro Thr Ala
 1 5

gat atc tgg ttt aaa gat act ttg gct gct cat ttc aca cgc gac gcc 163
 Asp Ile Trp Phe Lys Asp Thr Leu Ala Ala His Phe Thr Arg Asp Gly
 10 15 20

gac cag acc aca ttc tcc tac aca gct gat tac gca ggt cca cgg att 211
 Asp Gln Thr Thr Phe Ser Tyr Thr Ala Asp Tyr Ala Gly Pro Pro Ile
 25 30 35

gcc acg tcc ctg ccc atc aat tct gaa ccc gtg att acg cgc tct gga 259
 Ala Thr Ser Leu Pro Ile Asn Ser Glu Pro Val Ile Thr Arg Ser Gly
 40 45 50

gcg atc cca cca ttt ttc gcg gga tta ctc ccc gaa ggt cgt cgc tta 307
 Ala Ile Pro Pro Phe Phe Ala Gly Leu Leu Pro Glu Gly Arg Arg Leu
 55 60 65

agt tca ctc cgg aga aac att aaa gcc tct gcc gat gat gaa ctt tca 355
 Ser Ser Leu Arg Arg Asn Ile Lys Ala Ser Ala Asp Asp Glu Leu Ser
 70 75 80 85

ctc ctt cta gca gtg gga gct gat cct gtt ggt gca gtc gct atc ttc 403
 Leu Leu Leu Ala Val Gly Ala Asp Pro Val Gly Ala Val Ala Ile Phe
 90 95 100

ccc cat ggt gaa aat aca caa cct gca cca ccc aca gtt gat ttt gac 451
 Pro His Gly Glu Asn Thr Gln Pro Ala Pro Thr Val Asp Phe Asp
 105 110 115

gat gaa ctt gat ttc tcg gct gca cta acc gag tcc ggg att gcg gat 499
 Asp Glu Leu Asp Phe Ser Ala Ala Leu Thr Glu Ser Gly Ile Ala Asp
 120 125 130

ccc gtt gca ctg gcc ggt gtc caa gac aaa gcc tct gca cgc acc atc 547

Pro Val Ala Leu Ala Gly Val Gln Asp Lys Ala Ser Ala Arg Thr Ile
135 140 145

gcg gtc ccc gtt gca agc gat gcc atc ttg aaa ctc tcc ccg cct gaa 595
Ala Val Pro Val Ala Ser Asp Ala Ile Leu Lys Leu Ser Pro Pro Glu
150 155 160 165

tac cct tac ttg gtg gaa aac gaa gca gct tgt tac cag ttg ctg acc 643
Tyr Pro Tyr Leu Val Glu Asn Glu Ala Ala Cys Tyr Gln Leu Leu Thr
170 175 180

aaa aat aag ctt cgc att gaa ctg tcc aaa gta gaa gtt ctc cat gac 691
Lys Asn Lys Leu Arg Ile Glu Leu Ser Lys Val Glu Val Leu His Asp
185 190 195

aaa cac gcc agg tcc gga ctc tta gtt cac cgc ttt gac cgc aca ccc 739
Lys His Gly Arg Ser Gly Leu Leu Val His Arg Phe Asp Arg Thr Pro
200 205 210

aaa gcc aaa atc ccc gtc gag gat gca gga cag gtc ttg gga atc tgg 787
Lys Gly Lys Ile Pro Val Glu Asp Ala Gly Gln Val Leu Gly Ile Trp
215 220 225

cct gca gat aaa tac tta gtg agc tac gag gac atc gca caa gcc ctc 835
Pro Ala Asp Lys Tyr Leu Val Ser Tyr Glu Asp Ile Ala Gln Ala Leu
230 235 240 245

act aaa gtg tgc gcc tcc ccc atc ttg gcg atg cgc aat ctc gcc ttc 883
Thr Lys Val Cys Ala Ser Pro Ile Leu Ala Met Arg Asn Leu Ala Phe
250 255 260

caa atc gca gtc gcg tgg ctc agc gcc aat ggt gat ctt cat gcc aag 931
Gln Ile Ala Val Ala Trp Leu Ser Gly Asn Gly Asp Leu His Ala Lys
265 270 275

aac atc tcc att atc aac aaa gcc cgc gga ttt gag atc agc ccc atc 979
Asn Ile Ser Ile Ile Asn Lys Gly Arg Gly Phe Glu Ile Ser Pro Ile
280 285 290

tat gac atc cct gcc acc gca gta tat gcc gac acc acg atg gca tta 1027
Tyr Asp Ile Pro Ala Thr Ala Val Tyr Gly Asp Thr Thr Met Ala Leu
295 300 305

gaa atc cag gga tcc aaa aag gat ctc agc caa aag aaa ttc cta aaa 1075
Glu Ile Gln Gly Ser Lys Lys Asp Leu Ser Gln Lys Lys Phe Leu Lys
310 315 320 325

ttc tgt aca tcc atc gga cta cca gaa aaa aca gcc atg tgc gtt gcg 1123
Phe Cys Thr Ser Ile Gly Leu Pro Glu Lys Thr Ala Met Ser Val Ala
330 335 340

aac gct gca ctg ttg gca aca gaa aat gcc gca gag aca att ctt gct 1171
Asn Ala Ala Leu Leu Ala Thr Glu Asn Ala Ala Glu Thr Ile Leu Ala
345 350 355

tcg gga aat ttt gat aca cgg atg aat cga gat ctg gcc agg gtt ctc 1219
Ser Gly Asn Phe Asp Thr Arg Met Asn Arg Asp Leu Ala Arg Val Leu
360 365 370

aaa cat cga cga agc gca tgg gga gct taattgcgctt gtttaagagg 1266
Lys His Arg Arg Ser Ala Trp Gly Ala

375

380

tcg

1269

<210> 140

<211> 382

<212> PRT

<213> Corynebacterium glutamicum

<400> 140

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Phe	Thr	Arg	Asp	Gly	Asp	Gln	Thr	Thr	Phe	Ser	Tyr	Thr	Ala	Asp	Tyr
			20					25					30		

Ala	Gly	Pro	Pro	Ile	Ala	Thr	Ser	Leu	Pro	Ile	Asn	Ser	Glu	Pro	Val
		35					40					45			

Ile	Thr	Arg	Ser	Gly	Ala	Ile	Pro	Pro	Phe	Phe	Ala	Gly	Leu	Leu	Pro
	50					55						60			

Glu	Gly	Arg	Arg	Leu	Ser	Ser	Leu	Arg	Arg	Asn	Ile	Lys	Ala	Ser	Ala
	65					70				75					80

Asp	Asp	Glu	Leu	Ser	Leu	Leu	Leu	Ala	Val	Gly	Ala	Asp	Pro	Val	Gly
				85					90					95	

Ala	Val	Ala	Ile	Phe	Pro	His	Gly	Glu	Asn	Thr	Gln	Pro	Ala	Pro	Pro
			100					105					110		

Thr	Val	Asp	Phe	Asp	Asp	Glu	Leu	Asp	Phe	Ser	Ala	Ala	Leu	Thr	Glu
		115					120						125		

Ser	Gly	Ile	Ala	Asp	Pro	Val	Ala	Leu	Ala	Gly	Val	Gln	Asp	Lys	Ala
	130					135						140			

Ser	Ala	Arg	Thr	Ile	Ala	Val	Pro	Val	Ala	Ser	Asp	Ala	Ile	Leu	Lys
	145				150					155				160	

Leu	Ser	Pro	Pro	Glu	Tyr	Pro	Tyr	Leu	Val	Glu	Asn	Glu	Ala	Ala	Cys
				165				170					175		

Tyr	Gln	Leu	Leu	Thr	Lys	Asn	Lys	Leu	Arg	Ile	Glu	Leu	Ser	Lys	Val
		180					185						190		

Glu	Val	Leu	His	Asp	Lys	His	Gly	Arg	Ser	Gly	Leu	Leu	Val	His	Arg
		195					200						205		

Phe	Asp	Arg	Thr	Pro	Lys	Gly	Lys	Ile	Pro	Val	Glu	Asp	Ala	Gly	Gln
	210					215					220				

Val	Leu	Gly	Ile	Trp	Pro	Ala	Asp	Lys	Tyr	Leu	Val	Ser	Tyr	Glu	Asp
	225				230				235					240	

Ile	Ala	Gln	Ala	Leu	Thr	Lys	Val	Cys	Ala	Ser	Pro	Ile	Leu	Ala	Met
			245					250					255		

Arg	Asn	Leu	Ala	Phe	Gln	Ile	Ala	Val	Ala	Trp	Leu	Ser	Gly	Asn	Gly
		260					265						270		

Asp Leu His Ala Lys Asn Ile Ser Ile Ile Asn Lys Gly Arg Gly Phe
 275 280 285
 Glu Ile Ser Pro Ile Tyr Asp Ile Pro Ala Thr Ala Val Tyr Gly Asp
 290 295 300
 Thr Thr Met Ala Leu Glu Ile Gln Gly Ser Lys Lys Asp Leu Ser Gln
 305 310 315 320
 Lys Lys Phe Leu Lys Phe Cys Thr Ser Ile Gly Leu Pro Glu Lys Thr
 325 330 335
 Ala Met Ser Val Ala Asn Ala Ala Leu Leu Ala Thr Glu Asn Ala Ala
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 355 360 365
 Leu Ala Arg Val Leu Lys His Arg Arg Ser Ala Trp Gly Ala
 370 375 380

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 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <222> (101)..(1246)
 <223> FRXA00222

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 Met Thr Pro Thr Ala
 1 5
 gat atc tgg ttt aaa gat act ttg gct gct cat ttc aca cgc gac ggc 163
 Asp Ile Trp Phe Lys Asp Thr Leu Ala Ala His Phe Thr Arg Asp Gly
 10 15 20
 gac cag acc aca ttc tcc tac aca gct gat tac gca ggt cca ccg att 211
 Asp Gln Thr Thr Phe Ser Tyr Thr Ala Asp Tyr Ala Gly Pro Pro Ile
 25 30 35
 gcc acg tcc ctg ccc atc aat tct gaa ccc gtg att acg cgc tct gga 259
 Ala Thr Ser Leu Pro Ile Asn Ser Glu Pro Val Ile Thr Arg Ser Gly
 40 45 50
 gcg atc cca cca ttt ttc gcg gga tta ctc ccc gaa ggt cgt cgc tta 307
 Ala Ile Pro Pro Phe Phe Ala Gly Leu Leu Pro Glu Gly Arg Arg Leu
 55 60 65
 agt tca ctc cgg aga aac att aaa gcc tct gcc gat gat gaa ctt tca 355
 Ser Ser Leu Arg Arg Asn Ile Lys Ala Ser Ala Asp Asp Glu Leu Ser
 70 75 80 85
 ctc ctt cta gca gtg gga gct gat cct gtt ggt gca gtc gct atc ttc 403

Leu	Leu	Leu	Ala	Val	Gly	Ala	Asp	Pro	Val	Gly	Ala	Val	Ala	Ile	Phe	
				90					95					100		
ccc	cat	ggt	gaa	aat	aca	caa	cct	gca	cca	ccc	aca	ggt	gat	ttt	gac	451
Pro	His	Gly	Glu	Asn	Thr	Gln	Pro	Ala	Pro	Pro	Thr	Val	Asp	Phe	Asp	
			105				110					115				
gat	gaa	ctt	gat	ttc	tcg	gct	gca	cta	acc	gag	tcc	ggg	att	gcg	gat	499
Asp	Glu	Leu	Asp	Phe	Ser	Ala	Ala	Leu	Thr	Glu	Ser	Gly	Ile	Ala	Asp	
		120				125					130					
ccc	ggt	gca	ctg	gcc	ggt	gtc	caa	gac	aaa	gcc	tct	gca	cgc	acc	atc	547
Pro	Val	Ala	Leu	Ala	Gly	Val	Gln	Asp	Lys	Ala	Ser	Ala	Arg	Thr	Ile	
	135				140					145						
gcg	gtc	ccc	ggt	gca	agc	gat	gcc	atc	ttg	aaa	ctc	tcc	ccg	cct	gaa	595
Ala	Val	Pro	Val	Ala	Ser	Asp	Ala	Ile	Leu	Lys	Leu	Ser	Pro	Pro	Glu	
150				155					160					165		
tac	cct	tac	ttg	gtg	gaa	aac	gaa	gca	gct	tgt	tac	cag	ttg	ctg	acc	643
Tyr	Pro	Tyr	Leu	Val	Glu	Asn	Glu	Ala	Ala	Cys	Tyr	Gln	Leu	Leu	Thr	
			170					175						180		
aaa	aat	aag	ctt	cgc	att	gaa	ctg	tcc	aaa	gta	gaa	ggt	ctc	cat	gac	691
Lys	Asn	Lys	Leu	Arg	Ile	Glu	Leu	Ser	Lys	Val	Glu	Val	Leu	His	Asp	
			185				190						195			
aaa	cac	ggc	agg	tcc	gga	ctc	tta	gtt	cac	cgc	ttt	gac	cgc	aca	ccc	739
Lys	His	Gly	Arg	Ser	Gly	Leu	Leu	Val	His	Arg	Phe	Asp	Arg	Thr	Pro	
		200				205					210					
aaa	ggc	aaa	atc	ccc	gtc	gag	gat	gca	gga	cag	gtc	ttg	gga	atc	tgg	787
Lys	Gly	Lys	Ile	Pro	Val	Glu	Asp	Ala	Gly	Gln	Val	Leu	Gly	Ile	Trp	
	215				220					225						
cct	gca	gat	aaa	tac	tta	gtg	agc	tac	gag	gac	atc	gca	caa	gcc	ctc	835
Pro	Ala	Asp	Lys	Tyr	Leu	Val	Ser	Tyr	Glu	Asp	Ile	Ala	Gln	Ala	Leu	
230				235					240					245		
act	aaa	gtg	tgc	gcc	tcc	ccc	atc	ttg	gcg	atg	cgc	aat	ctc	gcc	ttc	883
Thr	Lys	Val	Cys	Ala	Ser	Pro	Ile	Leu	Ala	Met	Arg	Asn	Leu	Ala	Phe	
			250					255					260			
caa	atc	gca	gtc	gcg	tgg	ctc	agc	ggc	aat	ggt	gat	ctt	cat	gcc	aag	931
Gln	Ile	Ala	Val	Ala	Trp	Leu	Ser	Gly	Asn	Gly	Asp	Leu	His	Ala	Lys	
		265				270							275			
aac	atc	tcc	att	atc	aac	aaa	ggc	cgc	gga	ttt	gag	atc	agc	ccc	atc	979
Asn	Ile	Ser	Ile	Ile	Asn	Lys	Gly	Arg	Gly	Phe	Glu	Ile	Ser	Pro	Ile	
		280				285					290					
tat	gac	atc	cct	gcc	acc	gca	gta	tat	ggc	gac	acc	acg	atg	gca	tta	1027
Tyr	Asp	Ile	Pro	Ala	Thr	Ala	Val	Tyr	Gly	Asp	Thr	Thr	Met	Ala	Leu	
	295				300					305						
gaa	atc	cag	gga	tcc	aaa	aag	gat	ctc	agc	caa	aag	aaa	ttc	cta	aaa	1075
Glu	Ile	Gln	Gly	Ser	Lys	Lys	Asp	Leu	Ser	Gln	Lys	Lys	Phe	Leu	Lys	
310				315					320				325			
ttc	tgt	aca	tcc	atc	gga	cta	cca	gaa	aaa	aca	gcc	atg	tcg	gtt	gcg	1123
Phe	Cys	Thr	Ser	Ile	Gly	Leu	Pro	Glu	Lys	Thr	Ala	Met	Ser	Val	Ala	

	330	335	340	
aac gct gca ctg ttg gca aca gaa aat gcc gca gag aca att ctt gct				1171
Asn Ala Ala Leu Leu Ala Thr Glu Asn Ala Ala Glu Thr Ile Leu Ala	345	350	355	
tcg gga aat ttt gat aca cgg atg aat cga gat ctg gcc agg gtt ctc				1219
Ser Gly Asn Phe Asp Thr Arg Met Asn Arg Asp Leu Ala Arg Val Leu	360	365	370	
aaa cat cga cga agc gca tgg gga gct taattcgccct gtttaagagg				1266
Lys His Arg Arg Ser Ala Trp Gly Ala	375	380		
tcg				1269
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<212>	PRT			
<213>	Corynebacterium glutamicum			
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Ala Gly Pro Pro Ile Ala Thr Ser Leu Pro Ile Asn Ser Glu Pro Val				
35 40 45				
Ile Thr Arg Ser Gly Ala Ile Pro Pro Phe Phe Ala Gly Leu Leu Pro				
50 55 60				
Glu Gly Arg Arg Leu Ser Ser Leu Arg Arg Asn Ile Lys Ala Ser Ala				
65 70 75 80				
Asp Asp Glu Leu Ser Leu Leu Leu Ala Val Gly Ala Asp Pro Val Gly				
85 90 95				
Ala Val Ala Ile Phe Pro His Gly Glu Asn Thr Gln Pro Ala Pro Pro				
100 105 110				
Thr Val Asp Phe Asp Asp Glu Leu Asp Phe Ser Ala Ala Leu Thr Glu				
115 120				
Ser Gly Ile Ala Asp Pro Val Ala Leu Ala Gly Val Gln Asp Lys Ala				
130 135 140				
Ser Ala Arg Thr Ile Ala Val Pro Val Ala Ser Asp Ala Ile Leu Lys				
145 150 155 160				
Leu Ser Pro Pro Glu Tyr Pro Tyr Leu Val Glu Asn Glu Ala Ala Cys				
165 170 175				
Tyr Gln Leu Leu Thr Lys Asn Lys Leu Arg Ile Glu Leu Ser Lys Val				
180 185 190				
Glu Val Leu His Asp Lys His Gly Arg Ser Gly Leu Leu Val His Arg				
195 200 205				

Phe Asp Arg Thr Pro Lys Gly Lys Ile Pro Val Glu Asp Ala Gly Gln
210 215 220

Val Leu Gly Ile Trp Pro Ala Asp Lys Tyr Leu Val Ser Tyr Glu Asp
225 230 235 240

Ile Ala Gln Ala Leu Thr Lys Val Cys Ala Ser Pro Ile Leu Ala Met
245 250 255

Arg Asn Leu Ala Phe Gln Ile Ala Val Ala Trp Leu Ser Gly Asn Gly
260 265 270

Asp Leu His Ala Lys Asn Ile Ser Ile Ile Asn Lys Gly Arg Gly Phe
275 280 285

Glu Ile Ser Pro Ile Tyr Asp Ile Pro Ala Thr Ala Val Tyr Gly Asp
290 295 300

Thr Thr Met Ala Leu Glu Ile Gln Gly Ser Lys Lys Asp Leu Ser Gln
305 310 315 320

Lys Lys Phe Leu Lys Phe Cys Thr Ser Ile Gly Leu Pro Glu Lys Thr
325 330 335

Ala Met Ser Val Ala Asn Ala Ala Leu Leu Ala Thr Glu Asn Ala Ala
340 345 350

Glu Thr Ile Leu Ala Ser Gly Asn Phe Asp Thr Arg Met Asn Arg Asp
355 360 365

Leu Ala Arg Val Leu Lys His Arg Arg Ser Ala Trp Gly Ala
370 375 380

<210> 143

<211> 633

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(610)

<223> RXN00232

<400> 143

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caccaccggc agcactcga aacgtgttta tacttgaact atg aac gac agg gct 115
Met Asn Asp Arg Ala
1 5

cac caa cga ata ggc gac atc gag cga tcc caa gcc ctc gac cga ctt 163
His Gln Arg Ile Gly Asp Ile Glu Arg Ser Gln Ala Leu Asp Arg Leu
10 15 20

ggg tca tat ttt gca gac gga tac ctc gac atc gac gaa ttc gat acc 211
Gly Ser Tyr Phe Ala Asp Gly Tyr Leu Asp Ile Asp Glu Phe Asp Thr
25 30 35

cga acc ggc gcc gca gca atc gca cgc aca gcc ggt gaa ata gat gtc 259

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Arg Thr Gly Ala Ala Ala Ile Ala Arg Thr Ala Gly Glu Ile Asp Val
    40                      45                      50

ttg ttc aca gat ctt ccc gaa caa cag gca agc acc gcc gtg aca ccc 307
Leu Phe Thr Asp Leu Pro Glu Gln Gln Ala Ser Thr Ala Val Thr Pro
    55                      60                      65

gtg caa gac gat acc gag aaa gaa tta gac ctg gtc cta cag cga gga 355
Val Gln Asp Asp Thr Glu Lys Glu Leu Asp Leu Val Leu Gln Arg Gly
    70                      75                      80                      85

aag aag ctc aag cag atc gac tcc gcc att tgg gct gtc gtg atg gtc 403
Lys Lys Leu Lys Glu Ile Asp Ser Ala Ile Trp Ala Val Val Met Val
    90                      95                      100

tcg ttc ttc cta ggc ttg ttt gtt ttc aac gtg cca tat ttc tgg gtt 451
Ser Phe Phe Ile Leu Gly Leu Phe Val Phe Asn Val Pro Tyr Phe Trp Val
    105                      110                      115

gtg ttc atc ctt ggc gga gcg gcc tcc gcg ggt gcg cga ttc ttg ctc 499
Val Phe Ile Leu Gly Gly Ala Ala Ser Ala Gly Ala Arg Phe Leu Leu
    120                      125                      130

aaa gta gat gac gcc gat gaa aaa ctc ttt gag gaa ctc cac agc aag 547
Lys Val Asp Asp Ala Asp Glu Lys Leu Phe Glu Glu Leu His Ser Lys
    135                      140                      145

gaa caa agc gaa cgc gaa gca cgc cta cgc att gcg gca caa cgt cga 595
Glu Gln Ser Glu Arg Glu Ala Arg Leu Arg Ile Ala Ala Gln Arg Arg
    150                      155                      160                      165

cgc gag ttg gaa caa tagccacaaa agctatcaag ccc 633
Arg Glu Leu Glu Gln
    170

<210> 144
<211> 170
<212> PRT
<213> Corynebacterium glutamicum

<400> 144
Met Asn Asp Arg Ala His Gln Arg Ile Gly Asp Ile Glu Arg Ser Gln
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Ala Leu Asp Arg Leu Gly Ser Tyr Phe Ala Asp Gly Tyr Leu Asp Ile
    20                      25                      30

Asp Glu Phe Asp Thr Arg Thr Gly Ala Ala Ala Ile Ala Arg Thr Ala
    35                      40                      45

Gly Glu Ile Asp Val Leu Phe Thr Asp Leu Pro Glu Gln Gln Ala Ser
    50                      55                      60

Thr Ala Val Thr Pro Val Gln Asp Asp Thr Glu Lys Glu Leu Asp Leu
    65                      70                      75                      80

Val Leu Gln Arg Gly Lys Lys Leu Lys Gln Ile Asp Ser Ala Ile Trp
    85                      90                      95

Ala Val Val Met Val Ser Phe Phe Leu Gly Leu Phe Val Phe Asn Val

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100 105 110
 Pro Tyr Phe Trp Val Val Phe Ile Leu Gly Gly Ala Ala Ser Ala Gly
 115 120 125
 Ala Arg Phe Leu Leu Lys Val Asp Asp Ala Asp Glu Lys Leu Phe Glu
 130 135 140
 Glu Leu His Ser Lys Glu Gln Ser Glu Arg Glu Ala Arg Leu Arg Ile
 145 150 155 160
 Ala Ala Gln Arg Arg Arg Glu Leu Glu Gln
 165 170

 <210> 145
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 <212> DNA
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 <223> FRXA00232

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 caccaccggc agcactcgaa aacgtgttta tacttgaact atg aac gac agg gct 115
 Met Asn Asp Arg Ala
 1 5
 cac caa cga ata ggc gac atc gag cga tcc caa gcc ctc gac cga ctt 163
 His Gln Arg Ile Gly Asp Ile Glu Arg Ser Gln Ala Leu Asp Arg Leu
 10 15 20
 ggg tca tat ttt gca gac gga tac ctc gac atc gac gaa ttc gat acc 211
 Gly Ser Tyr Phe Ala Asp Gly Tyr Leu Asp Ile Asp Glu Phe Asp Thr
 25 30 35
 cga acc ggc gcc gca gca atc gca cgc aca gcc ggt gaa ata gat gtc 259
 Arg Thr Gly Ala Ala Ala Ile Ala Arg Thr Ala Gly Glu Ile Asp Val
 40 45 50
 ttg ttc aca gat ctt ccc gaa caa cag gca agc acc gcc gtg aca ccc 307
 Leu Phe Thr Asp Leu Pro Glu Gln Gln Ala Ser Thr Ala Val Thr Pro
 55 60 65
 gtg caa gac gat acc gag aaa gaa tta gac ctg gtc cta cag cga gga 355
 Val Gln Asp Asp Thr Glu Lys Glu Leu Asp Leu Val Leu Gln Arg Gly
 70 75 80 85
 aag aag ctc aag cag atc gac tcc gcc att tgg gct gtc gtg atg gtc 403
 Lys Lys Leu Lys Gln Ile Asp Ser Ala Ile Trp Ala Val Val Met Val
 90 95 100
 tcg ttc ttc cta ggc ttg ttt gtt ttc aac gtg cca tat ttc tgg gtt 451
 Ser Phe Phe Leu Gly Leu Phe Val Phe Asn Val Pro Tyr Phe Trp Val
 105 110 115
 gtg ttc atc ctt ggc gga gcg gcc tcc gcg ggt gcg cga ttc ttg ctc 499

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Val Phe Ile Leu Gly Gly Ala Ala Ser Ala Gly Ala Arg Phe Leu Leu
    120                      125                      130

aaa gta gat gac gcc gat gaa aaa ctc ttt gag gaa ctc cac agc aag   547
Lys Val Asp Asp Ala Asp Glu Lys Leu Phe Glu Glu Leu His Ser Lys
    135                      140                      145

gaa caa agc gaa cgc gaa gca cgc cta cgc att gcg gca caa cgt cga   595
Glu Gln Ser Glu Arg Glu Ala Arg Leu Arg Ile Ala Ala Gln Arg Arg
    150                      155                      160                      165

cgc gag ttg gaa caa tagccacaaa agctatc   627
Arg Glu Leu Glu Gln
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<210> 146
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Ala Leu Asp Arg Leu Gly Ser Tyr Phe Ala Asp Gly Tyr Leu Asp Ile
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Asp Glu Phe Asp Thr Arg Thr Gly Ala Ala Ala Ile Ala Arg Thr Ala
    35           40           45

Gly Glu Ile Asp Val Leu Phe Thr Asp Leu Pro Glu Gln Gln Ala Ser
    50           55           60

Thr Ala Val Thr Pro Val Gln Asp Asp Thr Glu Lys Glu Leu Asp Leu
    65           70           75           80

Val Leu Gln Arg Gly Lys Lys Leu Lys Gln Ile Asp Ser Ala Ile Trp
    85           90           95

Ala Val Val Met Val Ser Phe Phe Leu Gly Leu Phe Val Phe Asn Val
    100          105          110

Pro Tyr Phe Trp Val Val Phe Ile Leu Gly Gly Ala Ala Ser Ala Gly
    115          120          125

Ala Arg Phe Leu Leu Lys Val Asp Asp Ala Asp Glu Lys Leu Phe Glu
    130          135          140

Glu Leu His Ser Lys Glu Gln Ser Glu Arg Glu Ala Arg Leu Arg Ile
    145          150          155          160

Ala Ala Gln Arg Arg Arg Glu Leu Glu Gln
    165          170

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<210> 147
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<212> DNA
<213> Corynebacterium glutamicum

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<220>

<221> CDS

<222> (101)..(826)

<223> RXN00236

<400> 147

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agcaatggga ttgggatgcg gttcgggtttt ggccgtcatc atg gtg atc tca ttt 115
                               Met Val Ile Ser Phe
                               1 5

gtt gga tgg gcg ctc agc ttc atg gat gga acg gca cct att cgc caa 163
Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr Ala Pro Ile Arg Gln
                               10 15 20

ctc cag caa atc cct gaa gat gtt ccg ccg gcg cgt ggt gta gaa gtt 211
Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala Arg Gly Val Glu Val
                               25 30 35

ccg caa att gat aca gag gca gat gga cgc aca tcc aac cat ttg cgt 259
Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr Ser Asn His Leu Arg
                               40 45 50

ttt tgg gcg gaa cca att gct caa gat act ggt gtg tcc gct caa gcg 307
Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly Val Ser Ala Gln Ala
                               55 60 65

att gcg gct tat gga aac gca gag ctc atc gcg agt act gcg tgg cct 355
Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala Ser Thr Ala Trp Pro
                               70 75 80 85

ggc tgc aat ctg ggg tgg aat acc ttg gca ggt atc ggc cag gtg gaa 403
Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly Ile Gly Gln Val Glu
                               90 95 100

acc cgt cac ggt acc tac aac ggc aaa atg ttc ggg ggc agt tcc ctg 451
Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe Gly Gly Ser Ser Leu
                               105 110 115

gat gaa aat gga gtt gca acc cct cca atc atc ggc gtt cca ctt gat 499
Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile Gly Val Pro Leu Asp
                               120 125 130

ggt tca ccg ggg ttt gcg gaa att ccc gac act gat ggt ggg gaa tta 547
Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr Asp Gly Gly Glu Leu
                               135 140 145

gat ggc gat act gaa tat gat cgc gcg gta ggt ccc atg cag ttc att 595
Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly Pro Met Gln Phe Ile
                               150 155 160 165

ccg gaa acg tgg cga ctt atg gga ttg gat gca aac ggt gat ggg gta 643
Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala Asn Gly Asp Gly Val
                               170 175 180

gcg gac ccc aac caa att gat gac gca gca ttg agt gcc gca aac ctg 691
Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu Ser Ala Ala Asn Leu
                               185 190 195

ttg tgt tcc aac gat cgt gac ttg tcc act cct gaa gga tgg acc gca 739

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Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro Glu Gly Trp Thr Ala
 200 205
 gct gtt cat tct tac aac atg tct aat cag tat ttg atg gac gtt cga 787
 Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr Leu Met Asp Val Arg
 215 220
 gat gct gcc gcg tcc tac gct tta cga cag ccg gcg atc taaaacttaa 836
 Asp Ala Ala Ala Ser Tyr Ala Leu Arg Gln Pro Ala Ile
 230 235 240
 caagcgcaac ccc 849

<210> 148
 <211> 242
 <212> PRT
 <213> *Corynebacterium glutamicum*

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 Arg Gly Val Glu Val Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr
 35 40 45
 Ser Asn His Leu Arg Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly
 50 55 60
 Val Ser Ala Gln Ala Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala
 65 70 75 80
 Ser Thr Ala Trp Pro Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly
 85 90 95
 Ile Gly Gln Val Glu Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe
 100 105 110
 Gly Gly Ser Ser Leu Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile
 115 120 125
 Gly Val Pro Leu Asp Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr
 130 135 140
 Asp Gly Gly Glu Leu Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly
 145 150 155 160
 Pro Met Gln Phe Ile Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala
 165 170 175
 Asn Gly Asp Gly Val Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu
 180 185 190
 Ser Ala Ala Asn Leu Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro
 195 200 205
 Glu Gly Trp Thr Ala Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr
 210 215 220

Leu Met Asp Val Arg Asp Ala Ala Ala Ser Tyr Ala Leu Arg Gln Pro
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Ala Ile

<210> 149

<211> 849

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(826)

<223> FRXA00236

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 Met Val Ile Ser Phe
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gtt gga tgg gcg ctc agc ttc atg gat gga acg gca cct att cgc caa 163
 Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr Ala Pro Ile Arg Gln
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ctc cag caa atc cct gaa gat gtt ccg ccg gcg cgt ggt gta gaa gtt 211
 Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala Arg Gly Val Glu Val
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ccg caa att gat aca gag gca gat gga cgc aca tcc aac cat ttg cgt 259
 Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr Ser Asn His Leu Arg
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ttt tgg gcg gaa cca att gct caa gat act ggt gtg tcc gct caa gcg 307
 Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly Val Ser Ala Gln Ala
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att gcg gct tat gga aac gca gag ctc atc gcg agt act gcg tgg cct 355
 Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala Ser Thr Ala Trp Pro
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ggc tgc aat ctg ggg tgg aat acc ttg gca ggt atc ggc cag gtg gaa 403
 Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly Ile Gly Gln Val Glu
 90 95 100

acc cgt cac ggt acc tac aac ggc aaa atg ttc ggg ggc agt tcc ctg 451
 Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe Gly Ser Ser Leu
 105 110 115

gat gaa aat gga gtt gca acc cct cca atc atc ggc gtt cca ctt gat 499
 Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile Gly Val Pro Leu Asp
 120 125 130

ggc tca ccg ggg ttt gcg gaa att ccc gac act gat ggt ggg gaa tta 547
 Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr Asp Gly Gly Glu Leu
 135 140 145

gat ggc gat act gaa tat gat cgc gcg gta ggt ccc atg cag ttc att 595
Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly Pro Met Gln Phe Ile
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ccg gaa acg tgg cga ctt atg gga ttg gat gca aac ggt gat ggg gta 643
Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala Asn Gly Asp Gly Val
170 175 180

gcg gac ccc aac caa att gat gac gca gca ttg agt gcc gca aac ctg 691
Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu Ser Ala Ala Asn Leu
185 190 195

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Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro Glu Gly Trp Thr Ala
200 205 210

gct gtt cat tct tac aac atg tct aat cag tat ttg atg gac gtt cga 787
Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr Leu Met Asp Val Arg
215 220 225

gat gct gcc gcg tcc tac gct tta cga cag ccg gcg atc taaaacttaa 836
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caagcgcaac ccc 849

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<212> PRT
<213> Corynebacterium glutamicum

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35 40 45
Ser Asn His Leu Arg Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly
50 55 60
Val Ser Ala Gln Ala Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala
65 70 75 80
Ser Thr Ala Trp Pro Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly
85 90 95
Ile Gly Gln Val Glu Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe
100 105 110
Gly Gly Ser Ser Leu Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile
115 120 125
Gly Val Pro Leu Asp Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr
130 135 140
Asp Gly Gly Glu Leu Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly

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 Thr Leu Thr Val Ile Ala Leu Val Asn Thr Ala Ala Val Ile Asn Val
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atc tac cag cca tac ccg acg ttg ggt tct ttc aat ccc gtg cca acg 499
 Ile Tyr Gln Pro Tyr Pro Thr Leu Gly Ser Phe Asn Pro Val Pro Thr
 120 125 130

gct gtg tcc atg tcg tat gca gat ttt gaa tct cag acc act gcc cgg 547
 Ala Val Ser Met Ser Tyr Ala Asp Phe Glu Ser Gln Thr Thr Ala Pro
 135 140 145

acg atg gat gac cgt gaa gtc ggt gcc ctt gtg cag gtg ccg cta gct 595
 Thr Met Asp Asp Arg Glu Val Gly Ala Leu Val Gln Val Pro Leu Ala
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gga aca aca gat gat tcc acc tcc gcc ttt gat gcg cgc gat gcc tac 643
 Gly Thr Thr Asp Asp Ser Thr Ser Gly Phe Asp Ala Arg Asp Ala Tyr
 170 175 180

gcc tat att ccg cct gcg tat tgg gat aat cct tcc cta caa ctg cca 691
 Ala Tyr Ile Pro Pro Ala Tyr Trp Asp Asn Pro Ser Leu Gln Leu Pro
 185 190 195

gtt ttg gtt ctc atg ccc gga aac ccc gcc cag cca gat cag tgg ttt 739
 Val Leu Val Leu Met Pro Gly Asn Pro Gly Gln Pro Asp Gln Trp Phe
 200 205 210

agc agt gga aat gcc gat caa aca gca gat aat ttc caa gca acc cac 787
 Ser Ser Gly Asn Ala Asp Gln Thr Ala Asp Asn Phe Gln Ala Thr His
 215 220 225

gat gcc atc agc ccc att gtc atc agc gtg gat gcc aca gga tca ttc 835
 Asp Gly Ile Ser Pro Ile Val Ile Ser Val Asp Gly Thr Gly Ser Phe
 230 235 240 245

agc gga aac cct gct tgc gtg gat tct gat gcc caa agc gtg atg aca 883
 Ser Gly Asn Pro Ala Cys Val Asp Ser Asp Ala Gln Ser Val Met Thr
 250 255 260

tat cta tcc cac gat gtc ccc atg ttg atc aaa cag aaa ttc cga gtc 931
 Tyr Leu Ser His Asp Val Pro Met Leu Ile Lys Gln Lys Phe Arg Val
 265 270 275

aat cag gat cag cgc acc tgg aca att ggt ggt tta agt tac gcc gcc 979
 Asn Gln Asp Gln Arg Thr Trp Thr Ile Gly Gly Leu Ser Tyr Gly Gly
 280 285 290

acc tgt gct ttg cag atc atg acc aat cac ccc gaa gcg tat ggt tct 1027
 Thr Cys Ala Leu Gln Ile Met Thr Asn His Pro Glu Ala Tyr Gly Ser
 295 300 305

tto ctt gac ttc tcg gcc cag gaa gaa cca aca ctt gcc aca cgc cag 1075
 Phe Leu Asp Phe Ser Gly Gln Glu Glu Pro Thr Leu Gly Thr Arg Gln
 310 315 320 325

caa act gtt gat cag ctt ttc gcc gcc gat gaa gac gca ttc aaa gcc 1123
 Gln Thr Val Asp Gln Leu Phe Gly Gly Asp Glu Asp Ala Phe Lys Ala
 330 335 340

gtt aat cgg gaa gat ctg ctc aat caa gca atc agc tca gga gcg cat 1171
 Val Asn Pro Glu Asp Leu Leu Asn Gln Ala Ile Ser Ser Gly Ala His
 345 350 355

acc tac agc ggg att tcg ggc agg ttt att gct ggt agc aac gat aaa 1219
 Thr Tyr Ser Gly Ile Ser Gly Arg Phe Ile Ala Gly Ser Asn Asp Lys
 360 365 370

agt gca gtg agc gcg ctg tct cat ctt gat aat ttg agc aat cag gcg 1267
 Ser Ala Val Ser Ala Leu Ser His Leu Asp Asn Leu Ser Asn Gln Ala
 375 380 385

ggc atg tcc acc acc ttt gat acc gtg gcc ggt gga cat tcc ttc cag 1315
 Gly Met Ser Thr Thr Phe Asp Thr Val Ala Gly Gly His Ser Phe Gln
 390 395 400 405

gtg tgg cgc gtg gct tta gcg aat act ttt gat tgg gtt gcc aag cgc 1363
 Val Trp Arg Val Ala Leu Ala Asn Thr Phe Asp Trp Val Ala Lys Arg
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 <213> Corynebacterium glutamicum

<400> 152
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Val Val Lys Lys Arg Ser Arg Trp Arg Val Leu Gly Ala Leu Ile Ser
 35 40 45

Ser Ala Val Leu Thr Ser Gly Ala Trp Val Val Ile Glu Lys Leu Trp
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Lys Pro Phe Pro Asp Pro Asn Pro Trp Thr Ile Tyr Leu Ser Ala Gly
 65 70 75 80

Leu Ala Val Phe Pro Leu Leu Ser Ile Leu Phe Arg Thr Gly Arg Thr
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Arg Ile Leu Met Ala Thr Leu Thr Val Ile Ala Leu Val Asn Thr Ala
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Ala Val Ile Asn Val Ile Tyr Gln Pro Tyr Pro Thr Leu Gly Ser Phe
 115 120 125

Asn Pro Val Pro Thr Ala Val Ser Met Ser Tyr Ala Asp Phe Glu Ser
 130 135 140

Gln Thr Thr Ala Pro Thr Met Asp Asp Arg Glu Val Gly Ala Leu Val
 145 150 155 160

Gln Val Pro Leu Ala Gly Thr Thr Asp Asp Ser Thr Ser Gly Phe Asp
 165 170 175
 Ala Arg Asp Ala Tyr Ala Tyr Ile Pro Pro Ala Tyr Trp Asp Asn Pro
 180 185 190
 Ser Leu Gln Leu Pro Val Leu Val Leu Met Pro Gly Asn Pro Gly Gln
 195 200 205
 Pro Asp Gln Trp Phe Ser Ser Gly Asn Ala Asp Gln Thr Ala Asp Asn
 210 215 220
 Phe Gln Ala Thr His Asp Gly Ile Ser Pro Ile Val Ile Ser Val Asp
 225 230 235 240
 Gly Thr Gly Ser Phe Ser Gly Asn Pro Ala Cys Val Asp Ser Asp Ala
 245 250 255
 Gln Ser Val Met Thr Tyr Leu Ser His Asp Val Pro Met Leu Ile Lys
 260 265 270
 Gln Lys Phe Arg Val Asn Gln Asp Gln Arg Thr Trp Thr Ile Gly Gly
 275 280 285
 Leu Ser Tyr Gly Gly Thr Cys Ala Leu Gln Ile Met Thr Asn His Pro
 290 295 300
 Glu Ala Tyr Gly Ser Phe Leu Asp Phe Ser Gly Gln Glu Glu Pro Thr
 305 310 315 320
 Leu Gly Thr Arg Gln Gln Thr Val Asp Gln Leu Phe Gly Gly Asp Glu
 325 330 335
 Asp Ala Phe Lys Ala Val Asn Pro Glu Asp Leu Leu Asn Gln Ala Ile
 340 345 350
 Ser Ser Gly Ala His Thr Tyr Ser Gly Ile Ser Gly Arg Phe Ile Ala
 355 360 365
 Gly Ser Asn Asp Lys Ser Ala Val Ser Ala Leu Ser His Leu Asp Asn
 370 375 380
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<211> 1303

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1303)

<223> FRXA00242

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 Val Asn Glu Trp Arg
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 aca gtc tcg ctt gta gat tcc acg gcg ctg acc gtg atc atc agt gtg 163
 Thr Val Ser Leu Val Asp Ser Thr Ala Leu Thr Val Ile Ile Ser Val
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 gcc gtg ttt act tct gct gtg gct ctg ctc gga gtt gtg aaa aag cgc 211
 Ala Val Phe Thr Ser Ala Val Ala Leu Leu Gly Val Val Lys Lys Arg
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 tct cgg tgg cgg gtt ctc gga gct ctc atc tcc tca gca gtt ctc acc 259
 Ser Arg Trp Arg Val Leu Gly Ala Leu Ile Ser Ser Ala Val Leu Thr
 40 45 50
 agt ggc gca tgg gtg gtt att gaa aag ctg tgg aag cct ttc ccc gac 307
 Ser Gly Ala Trp Val Val Ile Glu Lys Leu Trp Lys Pro Phe Pro Asp
 55 60 65
 ccc aat ccg tgg acc atc tat ctt tcc gct ggt ttg gcg gtt ttt cct 355
 Pro Asn Pro Trp Thr Ile Tyr Leu Ser Ala Gly Leu Ala Val Phe Pro
 70 75 80 85
 ctg ttg agc atc ttg ttc cgc act ggt cgt aca aga ata ctg atg gct 403
 Leu Leu Ser Ile Leu Phe Arg Thr Gly Arg Thr Arg Ile Leu Met Ala
 90 95 100
 aca ctc acc gtg att gca ctg gtt aat acg gcc gca gtc atc aat gtc 451
 Thr Leu Thr Val Ile Ala Leu Val Asn Thr Ala Ala Val Ile Asn Val
 105 110 115
 atc tac cag cca tac ccg acg ttg ggt tct ttc aat ccc gtg cca acg 499
 Ile Tyr Gln Pro Tyr Pro Thr Leu Gly Ser Phe Asn Pro Val Pro Thr
 120 125 130
 gct gtg tcc atg tcg tat gca gat ttt gaa tct cag acc act gcc ccg 547
 Ala Val Ser Met Ser Tyr Ala Asp Phe Glu Ser Gln Thr Thr Ala Pro
 135 140 145
 acg atg gat gac cgt gaa gtc ggt gcc ctt gtg cag gtg ccg cta gct 595
 Thr Met Asp Asp Arg Glu Val Gly Ala Leu Val Gln Val Pro Leu Ala
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 Gly Thr Thr Asp Asp Ser Thr Ser Gly Phe Asp Ala Arg Asp Ala Tyr
 170 175 180
 gcc tat att ccg cct gcg tat tgg gat aat cct tcc cta caa ctg cca 691
 Ala Tyr Ile Pro Pro Ala Tyr Trp Asp Asn Pro Ser Leu Gln Leu Pro
 185 190 195
 gtt ttg gtt ctc atg ccc gga aac ccc gcc cag cca gat cag tgg ttt 739
 Val Leu Val Leu Met Pro Gly Asn Pro Gly Gln Pro Asp Gln Trp Phe
 200 205 210
 agc agt gga aat gcc gat caa aca gca gat aat ttc caa gca acc cac 787


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Ser Ser Gly Asn Ala Asp Gln Thr Ala Asp Asn Phe Gln Ala Thr His
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gat ggc atc agc ccc att gtc atc agc gtg gat ggc aca gga tca ttc 835
Asp Gly Ile Ser Pro Ile Val Ile Ser Val Asp Gly Thr Gly Ser Phe
230                               235                               240                               245

agc gga aac cct gct tgc gtg gat tct gat gcc caa agc gtg atg aca 883
Ser Gly Asn Pro Ala Cys Val Asp Ser Asp Ala Gln Ser Val Met Thr
250                               255                               260

tat cta tcc cac gat gtc ccc atg ttg atc aaa cag aaa ttc cga gtc 931
Tyr Leu Ser His Asp Val Pro Met Leu Ile Lys Gln Lys Phe Arg Val
265                               270                               275

aat cag gat cag cgc acc tgg aca att ggt ggt tta agt tac ggc ggc 979
Asn Gln Asp Gln Arg Thr Trp Thr Ile Gly Gly Leu Ser Tyr Gly Gly
280                               285                               290

acc tgt gct ttg cag atc atg acc aat cac ccc gaa gcg tat ggt tct 1027
Thr Cys Ala Leu Gln Ile Met Thr Asn His Pro Gln Ala Tyr Gly Ser
295                               300                               305

ttc ctt gac ttc tcg ggc cag gaa gaa cca aca ctt ggc aca cgc cag 1075
Phe Leu Asp Phe Ser Gly Gln Glu Glu Pro Thr Leu Gly Thr Arg Gln
310                               315                               320                               325

caa act gtt gat cag ctt ttc ggc ggc gat gaa gac gca ttc aaa gcc 1123
Gln Thr Val Asp Gln Leu Phe Gly Gly Asp Glu Asp Ala Phe Lys Ala
330                               335                               340

gtt aat ccg gaa gat ctg ctc aat caa gca atc agc tca gga gcg cat 1171
Val Asn Pro Glu Asp Leu Leu Asn Gln Ala Ile Ser Ser Gly Ala His
345                               350                               355

acc tac agc ggg att tcg ggc agg ttt att gct ggt agc aac gat aaa 1219
Thr Tyr Ser Gly Ile Ser Gly Arg Phe Ile Ala Gly Ser Asn Asp Lys
360                               365                               370

agt gca gtg agc gcg ctg tct cat ctt gat aat ttg agc aat cag gcg 1267
Ser Ala Val Ser Ala Leu Ser His Leu Asp Asn Leu Ser Asn Gln Ala
375                               380                               385

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<400> 154
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Val Val Lys Lys Arg Ser Arg Trp Arg Val Leu Gly Ala Leu Ile Ser

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Arg	Ile	Leu	Met	Ala	Thr	Leu	Thr	Val	Ile	Ala	Leu	Val	Asn	Thr	Ala
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Gln	Val	Pro	Leu	Ala	Gly	Thr	Thr	Asp	Asp	Ser	Thr	Ser	Gly	Phe	Asp
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Ala	Arg	Asp	Ala	Tyr	Ala	Tyr	Ile	Pro	Pro	Ala	Tyr	Trp	Asp	Asn	Pro
			180					185					190		
Ser	Leu	Gln	Leu	Pro	Val	Leu	Val	Leu	Met	Pro	Gly	Asn	Pro	Gly	Gln
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Pro	Asp	Gln	Trp	Phe	Ser	Ser	Gly	Asn	Ala	Asp	Gln	Thr	Ala	Asp	Asn
			210				215					220			
Phe	Gln	Ala	Thr	His	Asp	Gly	Ile	Ser	Pro	Ile	Val	Ile	Ser	Val	Asp
			225				230					235			240
Gly	Thr	Gly	Ser	Phe	Ser	Gly	Asn	Pro	Ala	Cys	Val	Asp	Ser	Asp	Ala
				245					250					255	
Gln	Ser	Val	Met	Thr	Tyr	Leu	Ser	His	Asp	Val	Pro	Met	Leu	Ile	Lys
			260					265					270		
Gln	Lys	Phe	Arg	Val	Asn	Gln	Asp	Gln	Arg	Thr	Trp	Thr	Ile	Gly	Gly
			275				280						285		
Leu	Ser	Tyr	Gly	Gly	Thr	Cys	Ala	Leu	Gln	Ile	Met	Thr	Asn	His	Pro
			290				295					300			
Glu	Ala	Tyr	Gly	Ser	Phe	Leu	Asp	Phe	Ser	Gly	Gln	Glu	Glu	Pro	Thr
			305				310					315			320
Leu	Gly	Thr	Arg	Gln	Gln	Thr	Val	Asp	Gln	Leu	Phe	Gly	Gly	Asp	Glu
				325					330					335	
Asp	Ala	Phe	Lys	Ala	Val	Asn	Pro	Glu	Asp	Leu	Leu	Asn	Gln	Ala	Ile
			340					345					350		
Ser	Ser	Gly	Ala	His	Thr	Tyr	Ser	Gly	Ile	Ser	Gly	Arg	Phe	Ile	Ala
			355				360					365			

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Leu Ser Asn Gln Ala Gly Met Ser Thr Thr Phe Asp Thr Val Ala Gly
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Gly

<210> 155

<211> 1050

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1027)

<223> RXN00247

<400> 155

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 Met Gln Thr Leu Ile
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ttt atc gcc att gca ggc gtc gca gca cag ett gtt gat ggc ggc ctc 163
 Phe Ile Ala Ile Ala Gly Val Ala Ala Gln Leu Val Asp Gly Gly Leu
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ggc atg ggc ttc ggc gtc acc tca acc acc atc ctc atc atg ctc gca 211
 Gly Met Gly Phe Gly Val Thr Ser Thr Thr Ile Leu Ile Met Leu Ala
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ggt tta ggc cct gcg cag gca tcc gcc gtc gtg cac acc gca gag gtt 259
 Gly Leu Gly Pro Ala Gln Ala Ser Ala Val Val His Thr Ala Glu Val
 40 45 50

gga acc acc tta gtt tct ggt tta agc cac tgg aaa ttt ggc aac gtg 307
 Gly Thr Thr Leu Val Ser Gly Leu Ser His Trp Lys Phe Gly Asn Val
 55 60 65

gat tgg aaa gta gtt gtc cgg ctc ggt atc ccc ggc gct atc ggc gca 355
 Asp Trp Lys Val Val Arg Leu Gly Ile Pro Gly Ala Ile Gly Ala
 70 75 80 85

ttt gct ggc gct acc ttc ttg tcc aat att tcc acc gaa gca gca gca 403
 Phe Ala Gly Ala Thr Phe Leu Ser Asn Ile Ser Thr Glu Ala Ala Ala
 90 95 100

ccg atc acc tcc ctg att ctt gcc ctg atc ggc atg aac cta gtc tgg 451
 Pro Ile Thr Ser Leu Ile Leu Ala Leu Ile Gly Met Asn Leu Val Trp
 105 110 115

cga ttc agc aag gga cgc atc cgc cgc gac tat tcc gat cgc ccg cac 499
 Arg Phe Ser Lys Gly Arg Ile Arg Arg Asp Tyr Ser Asp Arg Pro His
 120 125 130

agc agg gga ttc ctc ggc gga ctc ggt att gtc ggt ggt ttc gtt gac 547

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Ser Arg Gly Phe Leu Gly Gly Leu Gly Ile Val Gly Gly Phe Val Asp
135                               140                               145

gca tcc ggt ggc ggc gga tgg ggt cca gtg acc acc tct acg ctg ctg 595
Ala Ser Gly Gly Gly Gly Trp Gly Pro Val Thr Thr Ser Thr Leu Leu
150                               155                               160

tct ttg gga cgc acc gaa ccc cgc aaa gta gtc ggc acc gtc aac acc 643
Ser Leu Gly Arg Thr Glu Pro Arg Lys Val Val Gly Thr Val Asn Thr
170                               175                               180

gca gaa ttc tta gtc tcc cta gcc gca aca ttg ggc ttc gtc gtg gga 691
Ala Glu Phe Leu Val Ser Leu Ala Ala Thr Leu Gly Phe Val Val Gly
185                               190                               195

ctg tgg gat gac cta gta gct aac ctc tct gca gtt ctc cgg ttg ctc 739
Leu Trp Asp Asp Leu Val Ala Asn Leu Ser Ala Val Leu Ala Leu Leu
200                               205                               210

atc ggc ggc gca atc gca gca cca atc ggc gcc tgg atg atc tct cgc 787
Ile Gly Gly Ala Ile Ala Ala Pro Ile Gly Ala Trp Met Ile Ser Arg
215                               220                               225

gtt aat gca acc gtc ctc ggt ggc ttc gtg ggc acc ctg att gtc aca 835
Val Asn Ala Thr Val Leu Gly Gly Phe Val Gly Thr Leu Ile Val Thr
230                               235                               240

ctg aac ctg cca aag gtg ctc aac gtg gtt ggc ctt gat ttc atc ccc 883
Leu Asn Leu Pro Lys Val Leu Asn Val Val Gly Leu Asp Phe Ile Pro
250                               255                               260

acc ggc ctc atc cag gtc acc gtc ctc ctc atc ggc ctg ccg ctg acg 931
Thr Gly Leu Ile Gln Val Thr Val Leu Leu Ile Gly Leu Pro Leu Thr
265                               270                               275

tac ctc ggc ttc cgc cgc tac cgc aaa aat ctc ctc aac gag acc atc 979
Tyr Leu Gly Phe Arg Arg Tyr Arg Lys Asn Leu Leu Asn Glu Thr Ile
280                               285                               290

tcc agc gaa gtt gtc tcc gaa cca aag ggc caa aag att aaa agc act 1027
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<210> 156
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<212> PRT
<213> Corynebacterium glutamicum

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Val Asp Gly Gly Leu Gly Met Gly Phe Gly Val Thr Ser Thr Thr Ile
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35 40 45

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His Thr Ala Glu Val Gly Thr Thr Leu Val Ser Gly Leu Ser His Trp
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                      100                      105                      110
Met Asn Leu Val Trp Arg Phe Ser Lys Gly Arg Ile Arg Arg Asp Tyr
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Ser Asp Arg Pro His Ser Arg Gly Phe Leu Gly Gly Leu Gly Ile Val
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Gly Gly Phe Val Asp Ala Ser Gly Gly Gly Gly Trp Gly Pro Val Thr
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Thr Ser Thr Leu Leu Ser Leu Gly Arg Thr Glu Pro Arg Lys Val Val
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Gly Thr Val Asn Thr Ala Glu Phe Leu Val Ser Leu Ala Ala Thr Leu
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Gly Phe Val Val Gly Leu Trp Asp Asp Leu Val Ala Asn Leu Ser Ala
                      195                      200                      205
Val Leu Ala Leu Leu Ile Gly Gly Ala Ile Ala Ala Pro Ile Gly Ala
                      210                      215                      220
Trp Met Ile Ser Arg Val Asn Ala Thr Val Leu Gly Gly Phe Val Gly
                      225                      230                      235                      240
Thr Leu Ile Val Thr Leu Asn Leu Pro Lys Val Leu Asn Val Val Gly
                      245                      250                      255
Leu Asp Phe Ile Pro Thr Gly Leu Ile Gln Val Thr Val Leu Leu Ile
                      260                      265                      270
Gly Leu Pro Leu Thr Tyr Leu Gly Phe Arg Arg Tyr Arg Lys Asn Leu
                      275                      280                      285
Leu Asn Glu Thr Ile Ser Ser Glu Val Val Ser Glu Pro Lys Gly Gln
                      290                      295                      300
Lys Ile Lys Ser Thr
305

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<210> 157
<211> 1050
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> {101}..{1027}
<223> FRXA00247

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<400> 157

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aaccccctaac tactgacctc gcaccacttg ttgcagcccg ttaccacgct gcattgagcg 60
cactgctggc acatatctaa gaccgctaag gaaatcagct atg cag aca tta atc 115
Met Gln Thr Leu Ile
1 5
ttt atc gcc att gca ggc gtc gca gca cag ctt gtt gat ggc ggc ctc 163
Phe Ile Ala Ile Ala Gly Val Ala Ala Gln Leu Val Asp Gly Gly Leu
10 15 20
ggc atg ggg ttc ggc gtc acc tca acc acc atc ctc atc atg ctc gca 211
Gly Met Gly Phe Gly Val Thr Ser Thr Thr Ile Leu Ile Met Leu Ala
25 30 35
ggg tta ggc cct gcg cag gca tcc gcc gtc gtg cac acc gca gag gtt 259
Gly Leu Gly Pro Ala Gln Ala Ser Ala Val Val His Thr Ala Glu Val
40 45 50
gga acc acc tta gtt tct ggt tta agc cac tgg aaa ttt ggc aac gtg 307
Gly Thr Thr Leu Val Ser Gly Leu Ser His Trp Lys Phe Gly Asn Val
55 60 65
gat tgg aaa gta gtt gtc cgg ctc ggt atc ccc ggc gct atc ggc gca 355
Asp Trp Lys Val Val Val Arg Leu Gly Ile Pro Gly Ala Ile Gly Ala
70 75 80 85
ttt gct ggc gct acc ttc ttg tcc aat att tcc acc gaa gca gca gca 403
Phe Ala Gly Ala Thr Phe Leu Ser Asn Ile Ser Thr Glu Ala Ala Ala
90 95 100
ccg atc acc tcc ctg att ctt gcc ctg atc ggc atg aac cta gtc tgg 451
Pro Ile Thr Ser Leu Ile Leu Ala Leu Ile Gly Met Asn Leu Val Trp
105 110 115
cga ttc agc aag gga cgc atc cgc cgc gac tat tcc gat cgc ccg cac 499
Arg Phe Ser Lys Gly Arg Ile Arg Arg Asp Tyr Ser Asp Arg Pro His
120 125 130
agc agg gga ttc ctc ggc gga ctc ggt att gtc ggt ggt ttc gtt gac 547
Ser Arg Gly Phe Leu Gly Gly Leu Gly Ile Val Gly Gly Phe Val Asp
135 140 145
gca tcc ggt ggc ggc gga tgg ggt cca gtg acc acc tct acg ctg ctg 595
Ala Ser Gly Gly Gly Trp Gly Pro Val Thr Thr Ser Thr Leu Leu
150 155 160 165
tct ttg gga cgc acc gaa ccc cgc aaa gta gtc ggc acc gtc aac acc 643
Ser Leu Gly Arg Thr Glu Pro Arg Lys Val Val Gly Thr Val Asn Thr
170 175 180
gca gaa ttc tta gtc tcc cta gcc gca aca ttg ggc ttc gtc gtg gga 691
Ala Glu Phe Leu Val Ser Leu Ala Ala Thr Leu Gly Phe Val Val Gly
185 190 195
ctg tgg gat gac cta gta gct aac ctc tct gca gtt ctc gcg ttg ctc 739
Leu Trp Asp Asp Leu Val Ala Asn Leu Ser Ala Val Leu Ala Leu Leu
200 205 210
atc ggc ggc gca atc gca gca cca atc ggc gcc tgg atg atc tct cgc 787

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Ile Gly Gly Ala Ile Ala Ala Pro Ile Gly Ala Trp Met Ile Ser Arg
 215                      220                      225

gtt aat gca acc gtc ctc ggt ggc ttc gtg ggc acc ctg att gtc aca    835
Val Asn Ala Thr Val Leu Gly Gly Phe Val Gly Thr Leu Ile Val Thr
 230                      235                      240                      245

ctg aac ctg cca aag gtg ctc aac gtg gtt ggc ctt gat ttc atc ccc    883
Leu Asn Leu Pro Lys Val Leu Asn Val Val Gly Leu Asp Phe Ile Pro
                      250                      255                      260

acc ggc ctc atc cag gtc acc gtc ctc ctc atc ggc ctg ccg ctg acg    931
Thr Gly Leu Ile Gln Val Thr Val Leu Leu Ile Gly Leu Pro Leu Thr
                      265                      270                      275

tac ctc ggc ttc cgc cgc tac cgc aaa aat ctc ctc aac gag acc atc    979
Tyr Leu Gly Phe Arg Arg Tyr Arg Lys Asn Leu Leu Asn Glu Thr Ile
                      280                      285                      290

tcc agc gaa gtt gtc tcc gaa cca aag ggc caa aag att aaa agc act    1027
Ser Ser Glu Val Val Ser Glu Pro Lys Gly Gln Lys Ile Lys Ser Thr
                      295                      300                      305

taaaacacgc ttttcgacgc cca    1050

<210> 158
<211> 309
<212> PRT
<213> Corynebacterium glutamicum

<400> 158
Met Gln Thr Leu Ile Phe Ile Ala Ile Ala Gly Val Ala Ala Gln Leu
 1                      5                      10                      15

Val Asp Gly Gly Leu Gly Met Gly Phe Gly Val Thr Ser Thr Thr Ile
                      20                      25                      30

Leu Ile Met Leu Ala Gly Leu Gly Pro Ala Gln Ala Ser Ala Val Val
                      35                      40                      45

His Thr Ala Glu Val Gly Thr Thr Leu Val Ser Gly Leu Ser His Trp
                      50                      55                      60

Lys Phe Gly Asn Val Asp Trp Lys Val Val Val Arg Leu Gly Ile Pro
                      65                      70                      75                      80

Gly Ala Ile Gly Ala Phe Ala Gly Ala Thr Phe Leu Ser Asn Ile Ser
                      85                      90                      95

Thr Glu Ala Ala Ala Pro Ile Thr Ser Leu Ile Leu Ala Leu Ile Gly
                      100                      105                      110

Met Asn Leu Val Trp Arg Phe Ser Lys Gly Arg Ile Arg Arg Asp Tyr
                      115                      120                      125

Ser Asp Arg Pro His Ser Arg Gly Phe Leu Gly Gly Leu Gly Ile Val
                      130                      135                      140

Gly Gly Phe Val Asp Ala Ser Gly Gly Gly Gly Trp Gly Pro Val Thr
                      145                      150                      155                      160

```

Thr Ser Thr Leu Leu Ser Leu Gly Arg Thr Glu Pro Arg Lys Val Val
165 170 175

Gly Thr Val Asn Thr Ala Glu Phe Leu Val Ser Leu Ala Ala Thr Leu
180 185 190

Gly Phe Val Val Gly Leu Trp Asp Asp Leu Val Ala Asn Leu Ser Ala
195 200 205

Val Leu Ala Leu Leu Ile Gly Gly Ala Ile Ala Ala Pro Ile Gly Ala
210 215 220

Trp Met Ile Ser Arg Val Asn Ala Thr Val Leu Gly Gly Phe Val Gly
225 230 235 240

Thr Leu Ile Val Thr Leu Asn Leu Pro Lys Val Leu Asn Val Val Gly
245 250 255

Leu Asp Phe Ile Pro Thr Gly Leu Ile Gln Val Thr Val Leu Leu Ile
260 265 270

Gly Leu Pro Leu Thr Tyr Leu Gly Phe Arg Arg Tyr Arg Lys Asn Leu
275 280 285

Leu Asn Glu Thr Ile Ser Ser Glu Val Val Ser Glu Pro Lys Gly Gln
290 295 300

Lys Ile Lys Ser Thr
305

<210> 159

<211> 894

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(871)

<223> RXN00256

<400> 159

aettaataca tcagaaaaac atattgaata cttataaatt tctgacatac tcattaatga 60

gatattcgaa gtctttatca aaatgattaa caaaaggagt atg ttt atg tcg cta 115
Met Phe Met Ser Leu
1 5

aaa act cgc cga ata ttc ggc gca ctt gct gtt tcg cta tca atc tct 163
Lys Thr Arg Arg Ile Phe Gly Ala Leu Ala Val Ser Leu Ser Ile Ser
10 15 20

ttc tca gcc att gct aca cct gca gca tcc gca caa gaa cta gtg gtg 211
Phe Ser Ala Ile Ala Thr Pro Ala Ala Ser Ala Gln Glu Leu Val Val
25 30 35

agc aca tca gca gta aac gaa ttt ggt gta gtt acc agt gac atc acg 259
Ser Thr Ser Ala Val Asn Glu Phe Gly Val Val Thr Ser Asp Ile Thr
40 45 50

gct gag caa att ctt cag gcg caa gat cta atc gct gag atg aaa cag 307
 Ala Glu Gln Ile Leu Gln Ala Gln Asp Leu Ile Ala Glu Met Lys Gln
 55 60 65

tca gag gac ata tat gag tat ttc ggt gcc ttg tct gac gtt gaa cag 355
 Ser Glu Asp Ile Tyr Glu Tyr Phe Gly Ala Leu Ser Asp Val Glu Gln
 70 75 80 85

aga tcc atc att gca gct gta aag gaa aat cca tat ctc att gag aac 403
 Arg Ser Ile Ile Ala Ala Val Lys Glu Asn Pro Tyr Leu Ile Glu Asn
 90 95 100

gaa tca ccc cgt atg aga gtc caa agt gaa aca ccc gac gag gaa aca 451
 Glu Ser Pro Arg Met Arg Val Gln Ser Glu Thr Pro Asp Glu Glu Thr
 105 110 115

cct gat aag aaa aag cgg agc aaa acc tac aag ctc tat atg agc att 499
 Pro Asp Lys Lys Lys Pro Ser Lys Thr Tyr Lys Leu Tyr Met Ser Ile
 120 125 130

ctc gaa atg atg tca tgt atc aat ctt gtt gat gtt cgg tca tgt gcc 547
 Leu Glu Met Met Ser Cys Ile Asn Leu Val Asp Val Pro Ser Cys Ala
 135 140 145

caa gcc ctt aaa gcg gca aat ata gct gaa cgc gag gcc aag gcc cgt 595
 Gln Ala Leu Lys Ala Ala Asn Ile Ala Glu Arg Glu Ala Lys Ala Arg
 150 155 160 165

tac ccc gat tgg gtc act aat ggt aaa ggc gat gcc ctt cgt cat tgt 643
 Tyr Pro Asp Ser Val Thr Asn Gly Lys Gly Asp Ala Leu Arg His Cys
 170 175 180

gca tgg agc gct ctc atg act att cga atc gga aaa gat gca gcc gaa 691
 Ala Trp Ser Ala Leu Met Thr Ile Arg Ile Gly Lys Asp Ala Ala Glu
 185 190 195

aga att ggt aac gct cat gaa acc gtt gtg aga ggt gaa ccc gaa gaa 739
 Arg Ile Gly Asn Ala His Glu Thr Val Val Arg Gly Glu Pro Glu Glu
 200 205 210

aga gaa atg gat ctc atc aat aac gcg ctg ggt aga gac atc ggc gaa 787
 Arg Glu Met Asp Leu Ile Asn Asn Ala Leu Gly Arg Asp Ile Gly Glu
 215 220 225

aga ttc atc atc aat ggc gat gaa acg ggt gcg ctc agt act tgt gta 835
 Arg Phe Ile Ile Asn Gly Asp Glu Thr Gly Ala Leu Ser Thr Cys Val
 230 235 240 245

tcc atg gct aat atc ggg cta ctt cat act ctg ttg taaacaaagg 881
 Ser Met Ala Asn Ile Gly Leu Leu His Thr Leu Leu
 250 255

aagtttctat cat 894

<210> 160

<211> 257

<212> PRT

<213> Corynebacterium glutamicum

<400> 160

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Met Phe Met Ser Leu Lys Thr Arg Arg Ile Phe Gly Ala Leu Ala Val
 1          5          10          15

Ser Leu Ser Ile Ser Phe Ser Ala Ile Ala Thr Pro Ala Ala Ser Ala
      20          25          30

Gln Glu Leu Val Val Ser Thr Ser Ala Val Asn Glu Phe Gly Val Val
 35          40          45

Thr Ser Asp Ile Thr Ala Glu Gln Ile Leu Gln Ala Gln Asp Leu Ile
 50          55          60

Ala Glu Met Lys Gln Ser Glu Asp Ile Tyr Glu Tyr Phe Gly Ala Leu
 65          70          75          80

Ser Asp Val Glu Gln Arg Ser Ile Ile Ala Ala Val Lys Glu Asn Pro
      85          90          95

Tyr Leu Ile Glu Asn Glu Ser Pro Arg Met Arg Val Gln Ser Glu Thr
 100          105          110

Pro Asp Glu Glu Thr Pro Asp Lys Lys Lys Pro Ser Lys Thr Tyr Lys
 115          120          125

Leu Tyr Met Ser Ile Leu Glu Met Met Ser Cys Ile Asn Leu Val Asp
 130          135          140

Val Pro Ser Cys Ala Gln Ala Leu Lys Ala Ala Asn Ile Ala Glu Arg
 145          150          155          160

Glu Ala Lys Ala Arg Tyr Pro Asp Ser Val Thr Asn Gly Lys Gly Asp
      165          170          175

Ala Leu Arg His Cys Ala Trp Ser Ala Leu Met Thr Ile Arg Ile Gly
 180          185          190

Lys Asp Ala Ala Glu Arg Ile Gly Asn Ala His Glu Thr Val Val Arg
 195          200          205

Gly Glu Pro Glu Glu Arg Glu Met Asp Leu Ile Asn Asn Ala Leu Gly
 210          215          220

Arg Asp Ile Gly Glu Arg Phe Ile Ile Asn Gly Asp Glu Thr Gly Ala
 225          230          235          240

Leu Ser Thr Cys Val Ser Met Ala Asn Ile Gly Leu Leu His Thr Leu
      245          250          255

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·Leu

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<210> 161
<211> 894
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(871)
<223> FRXA00256

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<400> 161
aattaatcaa tcagaaaaac atattgaata cttataaatt tctgacatac tcattaatga 60

gatatcgcga gctctttatca aaatgattaa caaaaggagt atg ttt atg tcg cta 115
Met Phe Met Ser Leu
1 5

aaa act cgc cga ata ttc ggc gca ctt gct gtt tcg cta tca atc tct 163
Lys Thr Arg Arg Ile Phe Gly Ala Leu Ala Val Ser Leu Ser Ile Ser
10 15 20

ttc tca gcc att gct aca cct gca gca tcc gca caa gaa cta gtg gtg 211
Phe Ser Ala Ile Ala Thr Pro Ala Ala Ser Ala Gln Glu Leu Val Val
25 30 35

agc aca tca gca gta aac gaa ttt ggt gta gtt acc agt gac atc acg 259
Ser Thr Ser Ala Val Asn Glu Phe Gly Val Val Thr Ser Asp Ile Thr
40 45 50

gct gag caa att ctt cag gcg caa gat cta atc gct gag atg aaa cag 307
Ala Glu Gln Ile Leu Gln Ala Gln Asp Leu Ile Ala Glu Met Lys Gln
55 60 65

tca gag gac ata tat gag tat ttc ggt gcc ttg tct gac gtt gaa cag 355
Ser Glu Asp Ile Tyr Glu Tyr Phe Gly Ala Leu Ser Asp Val Glu Gln
70 75 80 85

aga tcc atc att gca gct gta aag gaa aat cca tat ctc att gag aac 403
Arg Ser Ile Ile Ala Ala Val Lys Glu Asn Pro Tyr Leu Ile Glu Asn
90 95 100

gaa tca ccc cgt atg aga gtc caa agt gaa aca ccc gac gag gaa aca 451
Glu Ser Pro Arg Met Arg Val Gln Ser Glu Thr Pro Asp Glu Glu Thr
105 110 115

cct gat aag aaa aag cag agc aaa acc tac aag ctc tat atg agc att 499
Pro Asp Lys Lys Lys Pro Ser Lys Thr Tyr Lys Leu Tyr Met Ser Ile
120 125 130

ctc gaa atg atg tca tgt atc aat ctt gtt gat gtt cag tca tgt gcc 547
Leu Glu Met Met Ser Cys Ile Asn Leu Val Asp Val Pro Ser Cys Ala
135 140 145

caa gcc ctt aaa gcg gca aat ata gct gaa cgc gag gcc aag gcc cgt 595
Gln Ala Leu Lys Ala Ala Asn Ile Ala Glu Arg Glu Ala Lys Ala Arg
150 155 160 165

tac ccc gat tcg gtc act aat ggt aaa ggc gat gcc ctt cgt cat tgt 643
Tyr Pro Asp Ser Val Thr Asn Gly Lys Gly Asp Ala Leu Arg His Cys
170 175 180

gca tgg agc gct ctc atg act att cga atc gga aaa gat gca gcc gaa 691
Ala Trp Ser Ala Leu Met Thr Ile Arg Ile Gly Lys Asp Ala Ala Glu
185 190 195

aga att ggt aac gct cat gaa acc gtt gtg aga ggt gaa ccc gaa gaa 739
Arg Ile Gly Asn Ala His Glu Thr Val Val Arg Gly Glu Pro Glu Glu
200 205 210

aga gaa atg gat ctc atc aat aac gcg ctg ggt aga gac atc ggc gaa 787

Arg Glu Met Asp Leu Ile Asn Asn Ala Leu Gly Arg Asp Ile Gly Glu
 215 220 225

aga ttc atc atc aat ggc gat gaa acg ggt gcg ctc agt act tgt gta 835
 Arg Phe Ile Ile Asn Gly Asp Glu Thr Gly Ala Leu Ser Thr Cys Val
 230 235 240 245

tcc atg gct aat atc ggg cta ctt cat act ctg ttg taaacaaagg 881
 Ser Met Ala Asn Ile Gly Leu Leu His Thr Leu Leu
 250 255

aagtttctat cat 894

<210> 162
 <211> 257
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 162
 Met Phe Met Ser Leu Lys Thr Arg Arg Ile Phe Gly Ala Leu Ala Val
 1 5 10 15

Ser Leu Ser Ile Ser Phe Ser Ala Ile Ala Thr Pro Ala Ala Ser Ala
 20 25 30

Gln Glu Leu Val Val Ser Thr Ser Ala Val Asn Glu Phe Gly Val Val
 35 40 45

Thr Ser Asp Ile Thr Ala Glu Gln Ile Leu Gln Ala Gln Asp Leu Ile
 50 55 60

Ala Glu Met Lys Gln Ser Glu Asp Ile Tyr Glu Tyr Phe Gly Ala Leu
 65 70 75 80

Ser Asp Val Glu Gln Arg Ser Ile Ile Ala Ala Val Lys Glu Asn Pro
 85 90 95

Tyr Leu Ile Glu Asn Glu Ser Pro Arg Met Arg Val Gln Ser Glu Thr
 100 105 110

Pro Asp Glu Glu Thr Pro Asp Lys Lys Lys Pro Ser Lys Thr Tyr Lys
 115 120 125

Leu Tyr Met Ser Ile Leu Glu Met Met Ser Cys Ile Asn Leu Val Asp
 130 135 140

Val Pro Ser Cys Ala Gln Ala Leu Lys Ala Ala Asn Ile Ala Glu Arg
 145 150 155 160

Glu Ala Lys Ala Arg Tyr Pro Asp Ser Val Thr Asn Gly Lys Gly Asp
 165 170 175

Ala Leu Arg His Cys Ala Trp Ser Ala Leu Met Thr Ile Arg Ile Gly
 180 185 190

Lys Asp Ala Ala Glu Arg Ile Gly Asn Ala His Glu Thr Val Val Arg
 195 200 205

Gly Glu Pro Glu Glu Arg Glu Met Asp Leu Ile Asn Asn Ala Leu Gly
 210 215 220

Arg Asp Ile Gly Glu Arg Phe Ile Ile Asn Gly Asp Glu Thr Gly Ala
225 230 235 240

Leu Ser Thr Cys Val Ser Met Ala Asn Ile Gly Leu Leu His Thr Leu
245 250 255

Leu

<210> 163

<211> 501

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(478)

<223> RXN00264

<400> 163

aaaccggaag ggcccggtta ctccctact tggcgcagaa atccacatca atccaggta 60

agcagtcatc tttgatgttg atcccacggt tgaacacggt ttg ctt gtc gat tcc 115
Leu Leu Val Asp Ser
1 5

ggc gac gtc caa cta gaa ggc gtc acc gtc gag ccc acc cag ctg gcc 163
Gly Asp Val Gln Leu Glu Gly Val Thr Val Glu Pro Thr Gln Leu Ala
10 15 20

tac acc ggc atc aat gaa acc caa ctc cga atc cgt aac atc ggc acc 211
Tyr Thr Gly Ile Asn Glu Thr Gln Leu Arg Ile Arg Asn Ile Gly Thr
25 30 35

aca cgc gcg cgt act gta ctg cta ggt ggc gaa cca ttt acc gaa gac 259
Thr Pro Ala Arg Thr Val Leu Leu Gly Gly Glu Pro Phe Thr Glu Asp
40 45 50

atc gtg atg tgg tgg aac ttc att ggc cgc agc cat gaa gaa att gcc 307
Ile Val Met Trp Trp Asn Phe Ile Gly Arg Ser His Glu Glu Ile Ala
55 60 65

gag tac cgt aaa cag tgg cag gcc gaa gct gat cgt ttt ggt atc acc 355
Glu Tyr Arg Lys Gln Trp Gln Ala Glu Ala Asp Arg Phe Gly Ile Thr
70 75 80 85

cac gga tat atc agc cac cac aaa gat ggg ctg acc agg ctt cca gca 403
His Gly Tyr Ile Ser His His Lys Asp Gly Leu Thr Arg Leu Pro Ala
90 95 100

ccc gag ctt ccc aac gct gct atc aag gca cgt aaa aac cca gca cca 451
Pro Glu Leu Pro Asn Ala Ala Ile Lys Ala Arg Lys Asn Pro Ala Pro
105 110 115

act gca cga cca gaa acg aga att gat taaatgcgct ccgctcacgg 498
Thr Ala Arg Pro Glu Thr Arg Ile Asp
120 125

ccc

501

<210> 164

<211> 126

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 164

Leu Leu Val Asp Ser Gly Asp Val Gln Leu Glu Gly Val Thr Val Glu
 1 5 10 15

Pro Thr Gln Leu Ala Tyr Thr Gly Ile Asn Glu Thr Gln Leu Arg Ile
 20 25 30

Arg Asn Ile Gly Thr Thr Pro Ala Arg Thr Val Leu Leu Gly Gly Glu
 35 40 45

Pro Phe Thr Glu Asp Ile Val Met Trp Trp Asn Phe Ile Gly Arg Ser
 50 55 60

His Glu Glu Ile Ala Glu Tyr Arg Lys Gln Trp Gln Ala Glu Ala Asp
 65 70 75 80

Arg Phe Gly Ile Thr His Gly Tyr Ile Ser His His Lys Asp Gly Leu
 85 90 95

Thr Arg Leu Pro Ala Pro Glu Leu Pro Asn Ala Ala Ile Lys Ala Arg
 100 105 110

Lys Asn Pro Ala Pro Thr Ala Arg Pro Glu Thr Arg Ile Asp
 115 120 125

<210> 165

<211> 501

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(478)

<223> FRXA00264

<400> 165

aaaccggaag ggccsgttaa ctcccctact tggcgcgagaa atccacatca atccagggtga 60

agcagtcattc ttgatgttg atcccacggt tgaacacggt ttg ctt gtc gat tcc 115
 Leu Leu Val Asp Ser 5
 1

ggc gac gtc caa cta gaa ggc gtc acc gtc gag ccc acc cag ctg gcc 163
 Gly Asp Val Gln Leu Glu Gly Val Thr Val Glu Pro Thr Gln Leu Ala 20
 10 15

tac acc ggc atc aat gaa acc caa ctc cga atc cgt aac atc ggc acc 211
 Tyr Thr Gly Ile Asn Glu Thr Gln Leu Arg Ile Arg Asn Ile Gly Thr 35
 25 30

aca ccg gcg cgt act gta ctg cta ggt ggc gaa cca ttt acc gaa gac 259
 Thr Pro Ala Arg Thr Val Leu Leu Gly Gly Glu Pro Phe Thr Glu Asp 40 45 50

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atc gtg atg tgg tgg aac ttc att ggc cgc agc cat gaa gaa att gcc 307
Ile Val Met Trp Trp Asn Phe Ile Gly Arg Ser His Glu Glu Ile Ala
55 60 65

gag tac cgt aaa cag tgg cag gcc gaa gct gat cgt ttt ggt atc acc 355
Glu Tyr Arg Lys Gln Trp Gln Ala Glu Ala Asp Arg Phe Gly Ile Thr
70 75 80 85

cac gga tat atc agc cac cac aaa gat ggg ctc acc agg ctt cca gca 403
His Gly Tyr Ile Ser His His Lys Asp Gly Leu Thr Arg Leu Pro Ala
90 95 100

ccc gag ctt ccc aac gct gct atc aag gca cgt aaa aac cca gca cca 451
Pro Glu Leu Pro Asn Ala Ala Ile Lys Ala Arg Lys Asn Pro Ala Pro
105 110 115

act gca cga cca gaa acg aga att gat taaatgcgct ccgctcacgg 498
Thr Ala Arg Pro Glu Thr Arg Ile Asp
120 125

ccc 501

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<210> 166
<211> 126
<212> PRT
<213> Corynebacterium glutamicum

<400> 166
Leu Leu Val Asp Ser Gly Asp Val Gln Leu Glu Gly Val Thr Val Glu
1 5 10 15

Pro Thr Gln Leu Ala Tyr Thr Gly Ile Asn Glu Thr Gln Leu Arg Ile
20 25 30

Arg Asn Ile Gly Thr Thr Pro Ala Arg Thr Val Leu Leu Gly Gly Glu
35 40 45

Pro Phe Thr Glu Asp Ile Val Met Trp Trp Asn Phe Ile Gly Arg Ser
50 55 60

His Glu Glu Ile Ala Glu Tyr Arg Lys Gln Trp Gln Ala Glu Ala Asp
65 70 75 80

Arg Phe Gly Ile Thr His Gly Tyr Ile Ser His His Lys Asp Gly Leu
85 90 95

Thr Arg Leu Pro Ala Pro Glu Leu Pro Asn Ala Ala Ile Lys Ala Arg
100 105 110

Lys Asn Pro Ala Pro Thr Ala Arg Pro Glu Thr Arg Ile Asp
115 120 125

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<210> 167
<211> 441
<212> DNA
<213> Corynebacterium glutamicum

<220>

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<221> CDS

<222> (101)..(418)

<223> RXN00267

<400> 167

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gtcgtactta tctttttaaag tcatgcctta aagatacagg agatcactcc ggcttggttt 60
gggtggcggt gttatcaaag tagtcgtagc gttgagaact atg cga aac tct aag 115
                                   Met Arg Asn Ser Lys
                                   1 5
tct ggc ctg gcc ttt tcc gca gct gca cta ttt tgt gtc gtc gcg gta 163
Ser Gly Leu Ala Phe Ser Ala Ala Ala Leu Phe Cys Val Val Ala Val
                                   10 15 20
atc act cgt att gca agt tcc cca tca ttt atc gct att gtg gcg atc 211
Ile Thr Arg Ile Ala Ser Ser Pro Ser Phe Ile Ala Ile Val Ala Ile
                                   25 30 35
atc gtg gct gcg atc gca ctt ttt gtg ggt ctg aac agt cgt gtg gga 259
Ile Val Ala Ala Ile Ala Leu Phe Val Gly Leu Asn Ser Arg Val Gly
                                   40 45 50
aca aag ctt gtt gat cag cca gtg gtg ttc acc cag gaa caa att gat 307
Thr Lys Leu Val Asp Gln Pro Val Val Phe Thr Gln Glu Gln Ile Asp
                                   55 60 65
caa ttg aaa gag ttg aaa tcc cgc gac cag gag gcg gca gcg atc cgt 355
Gln Leu Lys Glu Leu Lys Ser Arg Asp Gln Glu Ala Ala Ala Ile Arg
                                   70 75 80 85
cag gcg cag ctg tgg agt agg gga tgg tcc agc gaa gcg gtc gca gag 403
Gln Ala Gln Leu Trp Ser Arg Gly Ser Ser Ser Glu Ala Val Ala Glu
                                   90 95 100
gct gtg agg aag ctc taagtcgact taagtgcgcg aag 441
Ala Val Arg Lys Leu
                                   105

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<210> 168

<211> 106

<212> PRT

<213> Corynebacterium glutamicum

<400> 168

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Met Arg Asn Ser Lys Ser Gly Leu Ala Phe Ser Ala Ala Ala Leu Phe
 1 5 10 15
Cys Val Val Ala Val Ile Thr Arg Ile Ala Ser Ser Pro Ser Phe Ile
 20 25 30
Ala Ile Val Ala Ile Ile Val Ala Ala Ile Ala Leu Phe Val Gly Leu
 35 40 45
Asn Ser Arg Val Gly Thr Lys Leu Val Asp Gln Pro Val Val Phe Thr
 50 55 60
Gln Glu Gln Ile Asp Gln Leu Lys Glu Leu Lys Ser Arg Asp Gln Glu
 65 70 75 80

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Ala Ala Ala Ile Arg Gln Ala Gln Leu Trp Ser Arg Gly Ser Ser Ser
85 90 95

Glu Ala Val Ala Glu Ala Val Arg Lys Leu
100 105

<210> 169

<211> 358

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (66)..(335)

<223> FRXA00267

<400> 169

cgtacgcttg agaactatgc gaaactctaa gtctggcctg gccttttccg cagctgcact 60

atttgtg tct gtc gcg gta atc act cgt att gca agt tcc cca tca ttt 110
Val Ser Val Ala Val Ile Thr Arg Ile Ala Ser Ser Pro Ser Phe
1 5 10 15

atc gct att gtg gcg atc atc gtg gct gcg atc gca ctt ttt gtg ggt 158
Ile Ala Ile Val Ala Ile Ile Val Ala Ala Ile Ala Leu Phe Val Gly
20 25 30

ctg aac agt cgt gtg gga aca aag ctt gtt gat cag cca gtg gtg ttc 206
Leu Asn Ser Arg Val Gly Thr Lys Leu Val Asp Gln Pro Val Val Phe
35 40 45

acc cag gaa caa att gat caa ttg aaa gag ttg aaa tcc cgc gac cag 254
Thr Gln Glu Gln Ile Asp Gln Leu Lys Glu Leu Lys Ser Arg Asp Gln
50 55 60

gag gcg gca gcg atc cgt cag gcg cag ctg tgg agt agg gga tcg tcc 302
Glu Ala Ala Ala Ile Arg Gln Ala Gln Leu Trp Ser Arg Gly Ser Ser
65 70 75

agc gaa gcg gtc gca gag gct gtg agg aag ctc taagtcgact taagtgcgcg 355
Ser Glu Ala Val Ala Glu Ala Val Arg Lys Leu
80 85 90

aag 358

<210> 170

<211> 90

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 170

Val Ser Val Ala Val Ile Thr Arg Ile Ala Ser Ser Pro Ser Phe Ile
1 5 10 15

Ala Ile Val Ala Ile Ile Val Ala Ala Ile Ala Leu Phe Val Gly Leu
20 25 30

Asn Ser Arg Val Gly Thr Lys Leu Val Asp Gln Pro Val Val Phe Thr
35 40 45

Gln Glu Gln Ile Asp Gln Leu Lys Glu Leu Lys Ser Arg Asp Gln Glu
50 55 60

Ala Ala Ala Ile Arg Gln Ala Gln Leu Trp Ser Arg Gly Ser Ser Ser
65 70 75 80

Glu Ala Val Ala Glu Ala Val Arg Lys Leu
85 90

<210> 171

<211> 1113

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1090)

<223> RXN00271

<400> 171

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tctgccctt tttgaaaata acactttaag gagatgtgcc atg ttt tct tcc cgt 115
Met Phe Ser Ser Arg
1 5

tcg aag gta ctc gca agc atc ttt act gtt gcc gcc ttg gcg ttg gct 163
Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly Ala Leu Ala Leu Ala
10 15 20

tcg tgc tca agc gat tcc agt gac agc tcc acc tcc act gat gct gca 211
Ser Cys Ser Ser Asp Ser Ser Asp Ser Ser Thr Ser Thr Asp Ala Ala
25 30 35

ggt gcc gac tct tac cga gtt gcc atc aac cag ctt gtt cag cac cct 259
Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln Leu Val Gln His Pro
40 45 50

gca ctt gat gca gcg acc act ggt ttc aag gaa gct ttt gaa gag gca 307
Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu Ala Phe Glu Glu Ala
55 60 65

ggc gtt gac gtc acc ttt gat gag caa aac gct aac gcc gag cag gcc 355
Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala Asn Gly Glu Gln Gly
70 75 80 85

act gca ctg act att tct cag cag ttc gct tct gac aat ttg gat ctc 403
Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser Asp Asn Leu Asp Leu
90 95 100

gtg ttg gct gtt gca act cca gca gca cag gca act gcg cag aat atc 451
Val Leu Ala Val Ala Thr Pro Ala Ala Gln Ala Thr Ala Gln Asn Ile
105 110 115

act gat atc cca gtc ctg ttc acc gca gtt acc gat gca gtg tcg gca 499
Thr Asp Ile Pro Val Leu Phe Thr Ala Val Thr Asp Ala Val Ser Ala
120 125 130

gag ctg gtg gat tct aat gaa gca cct gcc gga aac gtc acc ggt act 547

Glu	Leu	Val	Asp	Ser	Asn	Glu	Ala	Pro	Gly	Gly	Asn	Val	Thr	Gly	Thr		
135						140					145						
tct	gat	atc	gca	ccg	att	gag	cag	cag	ttg	gag	ctt	ttg	cag	cag	ctg	595	
Ser	Asp	Ile	Ala	Pro	Ile	Glu	Gln	Gln	Leu	Glu	Leu	Leu	Gln	Gln	Leu		
150					155					160					165		
ggt	cct	gac	gca	aag	tcc	atc	ggc	atc	gtc	tac	gcg	tct	ggg	gag	gtc	643	
Val	Pro	Asp	Ala	Lys	Ser	Ile	Gly	Ile	Val	Tyr	Ala	Ser	Gly	Glu	Val		
				170					175					180			
aac	tct	cag	gtg	cag	gtc	gat	gag	gtc	acc	aag	gct	gct	gag	cca	ctg	691	
Asn	Ser	Gln	Val	Gln	Val	Asp	Glu	Val	Thr	Lys	Ala	Ala	Glu	Pro	Leu		
			185					190					195				
ggg	ctg	tcc	ggt	aat	act	cag	act	gtc	act	acc	gtg	aac	gag	att	cag	739	
Gly	Leu	Ser	Val	Asn	Thr	Gln	Thr	Val	Thr	Thr	Val	Asn	Glu	Ile	Gln		
			200				205						210				
cag	gct	ggt	gaa	gct	ctc	ggc	gat	ggt	gat	gtc	atc	tac	ggt	cca	act	787	
Gln	Ala	Val	Glu	Ala	Leu	Gly	Asp	Val	Asp	Val	Ile	Tyr	Val	Pro	Thr		
			215			220						225					
gac	aac	atg	ggt	ggt	tcc	ggt	att	tct	tct	ctg	ggt	cag	ggt	gct	gag	835	
Asp	Asn	Met	Val	Val	Ser	Gly	Ile	Ser	Ser	Leu	Val	Gln	Val	Ala	Glu		
230					235					240				245			
cag	aag	cag	atc	cct	gtg	atc	ggc	gct	gag	tcc	ggc	act	ggt	gag	ggg	883	
Gln	Lys	Gln	Ile	Pro	Val	Ile	Gly	Ala	Glu	Ser	Gly	Thr	Val	Glu	Gly		
				250					255					260			
ggc	gca	ctg	gca	acc	ctg	ggt	atc	gat	tac	acc	gag	ctt	ggc	cgc	cag	931	
Gly	Ala	Leu	Ala	Thr	Leu	Gly	Ile	Asp	Tyr	Thr	Glu	Leu	Gly	Arg	Gln		
			265				270						275				
act	ggt	gag	atg	gct	ctg	cgt	att	ctg	cag	gac	ggc	gaa	gac	cca	gca	979	
Thr	Gly	Glu	Met	Ala	Leu	Arg	Ile	Leu	Gln	Asp	Gly	Glu	Asp	Pro	Ala		
			280				285						290				
acc	atg	cct	gtg	gag	act	gca	act	gag	ttc	acc	tac	gtg	atc	aac	gaa	1027	
Thr	Met	Pro	Val	Glu	Thr	Ala	Thr	Glu	Phe	Thr	Tyr	Val	Ile	Asn	Glu		
			295			300						305					
gat	gca	gca	gag	cgc	cag	ggc	gtg	gag	atc	cct	caa	gag	att	ttg	gat	1075	
Asp	Ala	Ala	Glu	Arg	Gln	Gly	Val	Glu	Ile	Pro	Gln	Glu	Ile	Leu	Asp		
310					315					320				325			
aag	gcc	gaa	cgc	gta	tgatcggcgc	ttttgagttc	gga									1113	
Lys	Ala	Glu	Arg	Val													
				330													

<210> 172

<211> 330

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 172

Met Phe Ser Ser Arg Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly

1

5

10

15

Ala Leu Ala Leu Ala Ser Cys Ser Ser Asp Ser Ser Asp Ser Ser Thr
 20 25 30
 Ser Thr Asp Ala Ala Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln
 35 40 45
 Leu Val Gln His Pro Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu
 50 55 60
 Ala Phe Glu Glu Ala Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala
 65 70 75 80
 Asn Gly Glu Gln Gly Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser
 85 90 95
 Asp Asn Leu Asp Leu Val Leu Ala Val Ala Thr Pro Ala Ala Gln Ala
 100 105 110
 Thr Ala Gln Asn Ile Thr Asp Ile Pro Val Leu Phe Thr Ala Val Thr
 115 120 125
 Asp Ala Val Ser Ala Glu Leu Val Asp Ser Asn Glu Ala Pro Gly Gly
 130 135 140
 Asn Val Thr Gly Thr Ser Asp Ile Ala Pro Ile Glu Gln Gln Leu Glu
 145 150 155 160
 Leu Leu Gln Gln Leu Val Pro Asp Ala Lys Ser Ile Gly Ile Val Tyr
 165 170 175
 Ala Ser Gly Glu Val Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys
 180 185 190
 Ala Ala Glu Pro Leu Gly Leu Ser Val Asn Thr Gln Thr Val Thr Thr
 195 200 205
 Val Asn Glu Ile Gln Gln Ala Val Glu Ala Leu Gly Asp Val Asp Val
 210 215 220
 Ile Tyr Val Pro Thr Asp Asn Met Val Val Ser Gly Ile Ser Ser Leu
 225 230 235 240
 Val Gln Val Ala Glu Gln Lys Gln Ile Pro Val Ile Gly Ala Glu Ser
 245 250 255
 Gly Thr Val Glu Gly Gly Ala Leu Ala Thr Leu Gly Ile Asp Tyr Thr
 260 265 270
 Glu Leu Gly Arg Gln Thr Gly Glu Met Ala Leu Arg Ile Leu Gln Asp
 275 280 285
 Gly Glu Asp Pro Ala Thr Met Pro Val Glu Thr Ala Thr Glu Phe Thr
 290 295 300
 Tyr Val Ile Asn Glu Asp Ala Ala Glu Arg Gln Gly Val Glu Ile Pro
 305 310 315 320
 Gln Glu Ile Leu Asp Lys Ala Glu Arg Val
 325 330

gtt cct gac gca aag tcc atc ggc atc gtc tac gcg tct ggt gag gtc 643
Val Pro Asp Ala Lys Ser Ile Gly Ile Val Tyr Ala Ser Gly Glu Val
170 175 180

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aac tct cag gtg cag gtc gat gag gtc acc aag gct gct gag cca ctg 691
Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys Ala Ala Glu Pro Leu
185 190 195

ggg ctg tcc gtt aat act cag act gtc act acc gtg aac gag att cag 739
Gly Leu Ser Val Asn Thr Gln Thr Val Thr Thr Val Asn Glu Ile Gln
200 205 210

cag gct gtt gaa gct ctc ggc gat gtt gat gtc atc tac gtt cca act 787
Gln Ala Val Glu Ala Leu Gly Asp Val Asp Val Ile Tyr Val Pro Thr
215 220 225

gac aac atg gtt gtt tcc ggt att tct tct ctg gtt cag gtt gct gag 835
Asp Asn Met Val Val Ser Gly Ile Ser Ser Leu Val Gln Val Ala Glu
230 235 240 245

cag aag cag atc cct gtg atc ggc gct gag tcc ggc act gtt gag ggt 883
Gln Lys Gln Ile Pro Val Ile Gly Ala Glu Ser Gly Thr Val Glu Gly
250 255 260

ggc gca ctg gca acc ctg ggt atc gat tac acc gag ctt ggc cgc cag 931
Gly Ala Leu Ala Thr Leu Gly Ile Asp Tyr Thr Glu Leu Gly Arg Gln
265 270 275

act ggt gag atg gct ctg cgt att ctg cag gac ggc gaa gac cca gca 979
Thr Gly Glu Met Ala Leu Arg Ile Leu Gln Asp Gly Glu Asp Pro Ala
280 285 290

acc atg cct gtg gag act gca act gag ttc acc tac gtg atc aac gaa 1027
Thr Met Pro Val Glu Thr Ala Thr Glu Phe Thr Tyr Val Ile Asn Glu
295 300 305

gat gca gca gag cgc cag ggc gtg gag atc cct caa gag att ttg gat 1075
Asp Ala Ala Glu Arg Gln Gly Val Glu Ile Pro Gln Glu Ile Leu Asp
310 315 320 325

aag gcc gaa cgc gta tgatcggcgc ttttgagttc gga 1113
Lys Ala Glu Arg Val
330

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<210> 174

<211> 330

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 174

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Met Phe Ser Ser Arg Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly
1 5 10 15

Ala Leu Ala Leu Ala Ser Cys Ser Ser Asp Ser Ser Asp Ser Ser Thr
20 25 30

Ser Thr Asp Ala Ala Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln
35 40 45

Leu Val Gln His Pro Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu
50 55 60

Ala Phe Glu Glu Ala Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala
65 70 75 80

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Asn Gly Glu Gln Gly Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser
      85                      90                      95

Asp Asn Leu Asp Leu Val Leu Ala Val Ala Thr Pro Ala Ala Gln Ala
      100                      105                      110

Thr Ala Gln Asn Ile Thr Asp Ile Pro Val Leu Phe Thr Ala Val Thr
      115                      120                      125

Asp Ala Val Ser Ala Glu Leu Val Asp Ser Asn Glu Ala Pro Gly Gly
      130                      135                      140

Asn Val Thr Gly Thr Ser Asp Ile Ala Pro Ile Glu Gln Gln Leu Glu
      145                      150                      155                      160

Leu Leu Gln Gln Leu Val Pro Asp Ala Lys Ser Ile Gly Ile Val Tyr
      165                      170                      175

Ala Ser Gly Glu Val Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys
      180                      185                      190

Ala Ala Glu Pro Leu Gly Leu Ser Val Asn Thr Gln Thr Val Thr Thr
      195                      200                      205

Val Asn Glu Ile Gln Gln Ala Val Glu Ala Leu Gly Asp Val Asp Val
      210                      215                      220

Ile Tyr Val Pro Thr Asp Asn Met Val Val Ser Gly Ile Ser Ser Leu
      225                      230                      235                      240

Val Gln Val Ala Glu Gln Lys Gln Ile Pro Val Ile Gly Ala Glu Ser
      245                      250                      255

Gly Thr Val Glu Gly Gly Ala Leu Ala Thr Leu Gly Ile Asp Tyr Thr
      260                      265                      270

Glu Leu Gly Arg Gln Thr Gly Glu Met Ala Leu Arg Ile Leu Gln Asp
      275                      280                      285

Gly Glu Asp Pro Ala Thr Met Pro Val Glu Thr Ala Thr Glu Phe Thr
      290                      295                      300

Tyr Val Ile Asn Glu Asp Ala Ala Glu Arg Gln Gly Val Glu Ile Pro
      305                      310                      315                      320

Gln Glu Ile Leu Asp Lys Ala Glu Arg Val
      325                      330

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<210> 175

<211> 495

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(472)

<223> RXN00272

<400> 175

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tccagtggtt ggccatctgc cacaaccagg tgcagggcac atg ccg gaa cca gaa 115
                                     Met Pro Glu Pro Glu
                                     1 5

acc tcc acg atg ggc tcc atc caa aag tcc ggt gaa tgg ctc gtt cct 163
Thr Ser Thr Met Gly Ser Ile Gln Lys Ser Gly Glu Trp Leu Val Pro
          10          15          20

gca tat tgc gca tac aag ctc aac ggt gct gac ctt ttc tta gat atc 211
Ala Tyr Ser Ala Tyr Lys Leu Asn Gly Ala Asp Leu Phe Leu Asp Ile
          25          30          35

cgc cat gcc acc cgc gct gct cct gtc att acc ttt gat gtc aac atg 259
Arg His Ala Thr Ala Ala Ala Pro Val Ile Thr Phe Asp Val Asn Met
          40          45          50

acc atg ggt tct atg acg etg att gtt cca ccg ggt gtg tat gtg gaa 307
Thr Met Gly Ser Met Thr Leu Ile Val Pro Pro Gly Val Tyr Val Glu
          55          60          65

gtg cag atg gct tcc aag aac tgg tgc gat ttc aag gtt caa aca acc 355
Val Gln Met Ala Ser Lys Asn Trp Ser Asp Phe Lys Val Gln Thr Thr
          70          75          80          85

aat cct ctc ccc ggt gct ccc cga gtg ttc atc act ggt gtt gca cgc 403
Asn Pro Leu Pro Gly Ala Pro Arg Val Phe Ile Thr Gly Val Ala Arg
          90          95          100

gca tca ggg ttg aag gtt ttc acc aag cat cct cat gag cct ttt ggg 451
Ala Ser Gly Leu Lys Val Phe Thr Lys His Pro His Glu Pro Phe Gly
          105          110          115

ttc tgg cag aaa atg ttt gag tagcctcggg ccacgccga acc 495
Phe Trp Gln Lys Met Phe Glu
          120

<210> 176
<211> 124
<212> PRT
<213> Corynebacterium glutamicum

<400> 176
Met Pro Glu Pro Glu Thr Ser Thr Met Gly Ser Ile Gln Lys Ser Gly
 1 5 10 15

Glu Trp Leu Val Pro Ala Tyr Ser Ala Tyr Lys Leu Asn Gly Ala Asp
 20 25 30

Leu Phe Leu Asp Ile Arg His Ala Thr Ala Ala Pro Val Ile Thr
 35 40 45

Phe Asp Val Asn Met Thr Met Gly Ser Met Thr Leu Ile Val Pro Pro
 50 55 60

Gly Val Tyr Val Glu Val Gln Met Ala Ser Lys Asn Trp Ser Asp Phe
 65 70 75 80

Lys Val Gln Thr Thr Asn Pro Leu Pro Gly Ala Pro Arg Val Phe Ile

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85

90

95

Thr Gly Val Ala Arg Ala Ser Gly Leu Lys Val Phe Thr Lys His Pro
 100 105 110

His Glu Pro Phe Gly Phe Trp Gln Lys Met Phe Glu
 115 120

<210> 177

<211> 495

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(472)

<223> FRXA00272

<400> 177

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tccagtggtt ggccatctgc cacaaccagg tgcagggcac atg ccg gaa cca gaa 115
 Met Pro Glu Pro Glu
 1 5

acc tcc acg atg ggc tcc atc caa aag tcc ggt gaa tgg ctc gtt cct 163
 Thr Ser Thr Met Gly Ser Ile Gln Lys Ser Gly Glu Trp Leu Val Pro
 10 15 20

gca tat tgc gca tac aag ctc aac ggt gct gac ctt ttc tta gat atc 211
 Ala Tyr Ser Ala Tyr Lys Leu Asn Gly Ala Asp Leu Phe Leu Asp Ile
 25 30 35

cgc cat gcc acc cgc gct gct cct gtc att acc ttt gat gtc aac atg 259
 Arg His Ala Thr Ala Ala Ala Pro Val Ile Thr Phe Asp Val Asn Met
 40 45 50

acc atg ggt tct atg acg ctg att gtt cca cgc ggt gtg tat gtg gaa 307
 Thr Met Gly Ser Met Thr Leu Ile Val Pro Pro Gly Val Tyr Val Glu
 55 60 65

gtg cag atg gct tcc aag aac tgg tgc gat ttc aag gtt caa aca acc 355
 Val Gln Met Ala Ser Lys Asn Trp Ser Asp Phe Lys Val Gln Thr Thr
 70 75 80 85

aat cct ctc ccc ggt gct ccc cga gtg ttc atc act ggt gtt gca cgc 403
 Asn Pro Leu Pro Gly Ala Pro Arg Val Phe Ile Thr Gly Val Ala Arg
 90 95 100

gca tca ggg ttg aag gtt ttc acc aag cat cct cat gag cct ttt ggg 451
 Ala Ser Gly Leu Lys Val Phe Thr Lys His Pro His Glu Pro Phe Gly
 105 110 115

ttc tgg cag aaa atg ttt gag tagcctcggg ccacgcccga acc 495
 Phe Trp Gln Lys Met Phe Glu
 120

<210> 178

<211> 124

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 178

Met Pro Glu Pro Glu Thr Ser Thr Met Gly Ser Ile Gln Lys Ser Gly
 1 5 10 15

Glu Trp Leu Val Pro Ala Tyr Ser Ala Tyr Lys Leu Asn Gly Ala Asp
 20 25 30

Leu Phe Leu Asp Ile Arg His Ala Thr Ala Ala Ala Pro Val Ile Thr
 35 40 45

Phe Asp Val Asn Met Thr Met Gly Ser Met Thr Leu Ile Val Pro Pro
 50 55 60

Gly Val Tyr Val Glu Val Gln Met Ala Ser Lys Asn Trp Ser Asp Phe
 65 70 75 80

Lys Val Gln Thr Thr Asn Pro Leu Pro Gly Ala Pro Arg Val Phe Ile
 85 90 95

Thr Gly Val Ala Arg Ala Ser Gly Leu Lys Val Phe Thr Lys His Pro
 100 105 110

His Glu Pro Phe Gly Phe Trp Gln Lys Met Phe Glu
 115 120

<210> 179

<211> 1155

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1132)

<223> RXN00283

<400> 179

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tggactgtcg gatttatgac atggcgcgca cgataccgcc gtg gct tcc gcg acc 115
 Val Ala Ser Ala Thr
 1 5

gca tcg gat tcg cac ttg tcg aca tgc tgc tcc tcg tct ggc cga tcg 163
 Ala Ser Asp Ser His Leu Ser Thr Cys Cys Ser Ser Ser Gly Arg Ser
 10 15 20

gct tcg cct tcg tcg cct gga ctg gcg cca agc tgg etc act acc ggc 211
 Ala Ser Pro Ser Ser Pro Gly Leu Ala Pro Ser Trp Leu Thr Thr Gly
 25 30 35

gaa ctc ttt gcc caa ttc acc tcc aca gac ggc aac gct gcg atc atc 259
 Glu Leu Phe Ala Gln Phe Thr Ser Thr Asp Gly Asn Ala Ala Ile Ile
 40 45 50

gca gca tcc ggc ggc ggc gcc ata ggg ccc caa gcg ctt ttc gac gcc 307
 Ala Ala Ser Gly Gly Gly Ala Ile Gly Pro Gln Ala Leu Phe Asp Ala
 55 60 65

tcc gtc cgc acc ttc ctc atc tcc cca gct ctc cta ctc gtc gca gta 355
 Ser Val Arg Thr Phe Leu Ile Ser Pro Ala Leu Leu Val Ala Val
 70 75 80 85

gtt gca gtc ttt ttt gct tat cga cgc cgc gac ccc gaa ccc atc atc 403
 Val Ala Val Phe Phe Ala Tyr Arg Arg Arg Asp Pro Glu Pro Ile Ile
 90 95 100

ccc tta gct ctc atc ggc tct gtg gtg ttc ttc caa atc att acc tac 451
 Pro Leu Ala Leu Ile Gly Ser Val Val Phe Phe Gln Ile Thr Tyr
 105 110 115

tca ctt gga tct acc ttc ggc ctg ctg cgc ttt ttc ctc acc gcc ctg 499
 Ser Leu Gly Ser Thr Phe Gly Leu Leu Arg Phe Phe Leu Thr Ala Leu
 120 125 130

ccg ctc acc att atc ttg ctg ttc caa att atc ccg ccc cgc cac cga 547
 Pro Leu Thr Ile Ile Leu Leu Phe Gln Ile Ile Pro Pro Arg His Arg
 135 140 145

ttc ccc tca ctg cga cca ggt gcg tgc tac cgc gat cgc gtc acc ggc 595
 Phe Pro Ser Leu Arg Pro Gly Ala Cys Tyr Arg Asp Arg Val Thr Gly
 150 155 160 165

aag tac gtg ccc aaa aca atc acc ggt gtt tta gtt ctc gcg atc ttc 643
 Lys Tyr Val Pro Lys Thr Ile Thr Gly Val Leu Val Leu Ala Ile Phe
 170 175 180

ggc ggc acc ggc atc acc ctg tac ggc atg agc agt gct aac tgg gcg 691
 Gly Gly Thr Gly Ile Thr Leu Tyr Gly Met Ser Ser Ala Asn Trp Ala
 185 190 195

ccc cag gaa tat gcc atc caa gaa cta gtt ttc aac atg gga tcg cca 739
 Pro Gln Glu Tyr Ala Ile Gln Glu Leu Val Phe Asn Met Gly Ser Pro
 200 205 210

tcg cag gac gcc gtc cac acc ctg aac acc ttc tcc act gaa atg gat 787
 Ser Gln Asp Ala Val His Thr Leu Asn Thr Phe Ser Thr Glu Met Asp
 215 220 225

gtc gcc gat ttc gtc gac tcc cta aac ctt gga gac ggc gaa gtc ctt 835
 Val Ala Asp Phe Val Asp Ser Leu Asn Leu Gly Asp Gly Glu Val Leu
 230 235 240 245

ctc tcc acc acc tac ggc ttc gcc gtc ctc acc gca tca aac aac caa 883
 Leu Ser Thr Thr Tyr Gly Phe Ala Val Leu Thr Ala Ser Asn Asn Gln
 250 255 260

aag caa ttc atc atc ccc tcc gac gaa gac ttc atc acc acc ctc aac 931
 Lys Gln Phe Ile Ile Pro Ser Asp Glu Asp Phe Ile Thr Leu Asn
 265 270 275

gaa ccc gct gag cac ggc gtt aag tac atc ctc gcc ctc cca cgc gaa 979
 Glu Pro Ala Glu His Gly Val Lys Tyr Ile Leu Ala Leu Pro Arg Glu
 280 285 290

ggt cgc ggc gcc acc gac ccg atc aac ctg cgc tac cca gac atg tat 1027
 Gly Arg Gly Ala Thr Asp Pro Ile Asn Leu Arg Tyr Pro Asp Met Tyr
 295 300 305

gaa acc ggc agc cac atc gcc acg atg gaa atc gaa ttc atc aat caa 1075
 Glu Thr Gly Ser His Ile Ala Thr Met Glu Ile Glu Phe Ile Asn Gln
 310 315 320 325

ggc caa gga caa cca aat tgg cgc ctc tat cgg gtg ctc acc aca cct 1123
 Gly Gln Gly Gln Pro Asn Trp Arg Leu Tyr Arg Val Leu Thr Thr Pro
 330 335 340

gaa cag tcg tagactcttt gtaactaccg ttg 1155
 Glu Gln Ser

<210> 180

<211> 344

<212> ERT

<213> *Corynebacterium glutamicum*

<400> 180

Val Ala Ser Ser Ala Thr Ala Ser Asp Ser His Leu Ser Thr Cys Cys Ser
 1 5 10 15

Ser Ser Gly Arg Ser Ala Ser Pro Ser Ser Pro Gly Leu Ala Pro Ser
 20 25 30

Trp Leu Thr Thr Gly Glu Leu Phe Ala Gln Phe Thr Ser Thr Asp Gly
 35 40 45

Asn Ala Ala Ile Ile Ala Ala Ser Gly Gly Gly Ala Ile Gly Pro Gln
 50 55 60

Ala Leu Phe Asp Ala Ser Val Arg Thr Phe Leu Ile Ser Pro Ala Leu
 65 70 75 80

Leu Leu Val Ala Val Val Ala Val Phe Phe Ala Tyr Arg Arg Arg Asp
 85 90 95

Pro Glu Pro Ile Ile Pro Leu Ala Leu Ile Gly Ser Val Val Phe Phe
 100 105 110

Gln Ile Ile Thr Tyr Ser Leu Gly Ser Thr Phe Gly Leu Leu Arg Phe
 115 120 125

Phe Leu Thr Ala Leu Pro Leu Thr Ile Ile Leu Leu Phe Gln Ile Ile
 130 135 140

Pro Pro Arg His Arg Phe Pro Ser Leu Arg Pro Gly Ala Cys Tyr Arg
 145 150 155 160

Asp Arg Val Thr Gly Lys Tyr Val Pro Lys Thr Ile Thr Gly Val Leu
 165 170 175

Val Leu Ala Ile Phe Gly Gly Thr Gly Ile Thr Leu Tyr Gly Met Ser
 180 185 190

Ser Ala Asn Trp Ala Pro Gln Glu Tyr Ala Ile Gln Glu Leu Val Phe
 195 200

Asn Met Gly Ser Pro Ser Gln Asp Ala Val His Thr Leu Asn Thr Phe
 210 215 220

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Ser Thr Glu Met Asp Val Ala Asp Phe Val Asp Ser Leu Asn Leu Gly
225                230                235                240

Asp Gly Glu Val Leu Leu Ser Thr Thr Tyr Gly Phe Ala Val Leu Thr
                245                250                255

Ala Ser Asn Asn Gln Lys Gln Phe Ile Ile Pro Ser Asp Glu Asp Phe
260                265                270

Ile Thr Thr Leu Asn Glu Pro Ala Glu His Gly Val Lys Tyr Ile Leu
275                280                285

Ala Leu Pro Arg Glu Gly Arg Gly Ala Thr Asp Pro Ile Asn Leu Arg
290                295                300

Tyr Pro Asp Met Tyr Glu Thr Gly Ser His Ile Ala Thr Met Glu Ile
305                310                315                320

Glu Phe Ile Asn Gln Gly Gln Gly Gln Pro Asn Trp Arg Leu Tyr Arg
325                330                335

Val Leu Thr Thr Pro Glu Gln Ser
340

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<210> 181

<211> 1251

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1228)

<223> FRXA00283

<400> 181

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gaagctccgt tcatttacgc cactctctgg gcggtgcgca ggctgattcg gtggagttct 60
acggaaaacg tccacagacc tcattacctg tggttttgcy ttg gca ttg gcg ttt 115
                                         Leu Ala Leu Ala Phe
                                         1                               5

tta gcg cgc tat gac gcc ctc atc atg gcc ttc gta gcc atg tgg act 163
Leu Ala Arg Tyr Asp Ala Leu Ile Met Ala Phe Val Ala Met Trp Thr
                        10                        15                        20

gtc gga ttt atg aca tgg cgc gca cga tac cgc cgt ggc ttc cgc gac 211
Val Gly Phe Met Thr Trp Arg Ala Arg Tyr Arg Arg Gly Phe Arg Asp
                        25                        30                        35

cgc atc gga ttc gca ctt gtc gac atg ctg ctc ctc gtc tgg cag atc 259
Arg Ile Gly Phe Ala Leu Val Asp Met Leu Leu Leu Val Trp Pro Ile
                        40                        45                        50

ggc ttc gcc ttc gtc gcc tgg act ggc gcc agc tgg ctc act acc ggc 307
Gly Phe Ala Phe Val Ala Trp Thr Gly Ala Ser Trp Leu Thr Thr Gly
                        55                        60                        65

gaa ctc ttt gcc caa ttc acc tcc aca gac ggc aac gct gcg atc atc 355
Glu Leu Phe Ala Gln Phe Thr Ser Thr Asp Gly Asn Ala Ala Ile Ile
                        70                        75                        80                        85

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gca gca tcc ggc ggc ggc gcc ata ggg ccc caa gcg ctt ttc gac gcc Ala Ala Ser Gly Gly Gly Ala Ile Gly Pro Gln Ala Leu Phe Asp Ala	403
90 95 100	
tcc gtc cgc acc ttc ctc atc tcc cca gct ctc cta ctc gtc gca gta Ser Val Arg Thr Phe Leu Ile Ser Pro Ala Leu Leu Leu Val Ala Val	451
105 110 115	
gtt gca gtc ttt ttt gct tat cga cgc cgc gac ccc gaa ccc atc atc Val Ala Val Phe Phe Ala Tyr Arg Arg Arg Asp Pro Glu Pro Ile Ile	499
120 125 130	
ccc tta gct ctc atc ggc tct gtg gtg ttc ttc caa atc att acc tac Pro Leu Ala Leu Ile Gly Ser Val Val Phe Phe Gln Ile Ile Thr Tyr	547
135 140 145	
tca ctt gga tct acc ttc ggc ctg ctg cgc ttt ttc ctc acc gcc ctg Ser Leu Gly Ser Thr Phe Gly Leu Leu Arg Phe Phe Leu Thr Ala Leu	595
150 155 160 165	
ccg ctc acc att atc ttg ctg ttc caa att atc ccg ccc cgc cac cga Pro Leu Thr Ile Ile Leu Leu Phe Gln Ile Ile Pro Pro Arg His Arg	643
170 175 180	
ttc ccc tca ctg cga cca ggt gcg tgc tac cgc gat cgc gtc acc gcc Phe Pro Ser Leu Arg Pro Gly Ala Cys Tyr Arg Asp Arg Val Thr Gly	691
185 190 195	
aag tac gtg ccc aaa aca atc acc ggt gtt tta gtt ctc gcg atc ttc Lys Tyr Val Pro Lys Thr Ile Thr Gly Val Leu Val Leu Ala Ile Phe	739
200 205 210	
ggc ggc acc ggc atc acc ctg tac ggc atg agc agt gct aac tgg gcg Gly Gly Thr Gly Ile Thr Leu Tyr Gly Met Ser Ser Ala Asn Trp Ala	787
215 220 225	
ccc cag gaa tat gcc atc caa gaa cta gtt ttc aac atg gga tgg cca Pro Gln Glu Tyr Ala Ile Gln Glu Leu Val Phe Asn Met Gly Ser Pro	835
230 235 240 245	
tcg cag gac gcc gtc cac acc ctg aac acc ttc tcc act gaa atg gat Ser Gln Asp Ala Val His Thr Leu Asn Thr Phe Ser Thr Glu Met Asp	883
250 255 260	
gtc gcc gat ttc gtc gac tcc cta aac ctt gga gac ggc gaa gtc ctt Val Ala Asp Phe Val Asp Ser Leu Asn Leu Gly Asp Gly Glu Val Leu	931
265 270 275	
ctc tcc acc acc tac ggc ttc gcc gtc ctc acc gca tca aac aac caa Leu Ser Thr Thr Tyr Gly Phe Ala Val Leu Thr Ala Ser Asn Asn Gln	979
280 285 290	
aag caa ttc atc atc ccc tcc gac gaa gac ttc atc acc acc ctc aac Lys Gln Phe Ile Ile Pro Ser Asp Glu Asp Phe Ile Thr Thr Leu Asn	1027
295 300 305	
gaa ccc gct gag cac ggc gtt aag tac atc ctc gcc ctc cca cgc gaa Glu Pro Ala Glu His Gly Val Lys Tyr Ile Leu Ala Leu Pro Arg Glu	1075
310 315 320 325	

ggt cgc ggc gcc acc gac cgc atc aac ctg cgc tac cca gac atg tat 1123
 Gly Arg Gly Ala Thr Asp Pro Ile Asn Leu Arg Tyr Pro Asp Met Tyr
 330 335 340

gaa acc ggc agc cac atc gcc acg atg gaa atc gaa ttc atc aat caa 1171
 Glu Thr Gly Ser His Ile Ala Thr Met Glu Ile Glu Phe Ile Asn Gln
 345 350 355

ggc caa gga caa cca aat tgg cgc ctc tat cgg gtg ctc acc aca cct 1219
 Gly Gln Gly Gln Pro Asn Trp Arg Leu Tyr Arg Val Leu Thr Thr Pro
 360 365 370

gaa cag tcg tagactcttt gtaactaccg ttg 1251
 Glu Gln Ser
 375

<210> 182

<211> 376

<212> PRT

<213> Corynebacterium glutamicum

<400> 182

Leu Ala Leu Ala Phe Leu Ala Arg Tyr Asp Ala Leu Ile Met Ala Phe
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Val Ala Met Trp Thr Val Gly Phe Met Thr Trp Arg Ala Arg Tyr Arg
 20 25 30

Arg Gly Phe Arg Asp Arg Ile Gly Phe Ala Leu Val Asp Met Leu Leu
 35 40 45

Leu Val Trp Pro Ile Gly Phe Ala Phe Val Ala Trp Thr Gly Ala Ser
 50 55 60

Trp Leu Thr Thr Gly Glu Leu Phe Ala Gln Phe Thr Ser Thr Asp Gly
 65 70 75 80

Asn Ala Ala Ile Ile Ala Ala Ser Gly Gly Gly Ala Ile Gly Pro Gln
 85 90 95

Ala Leu Phe Asp Ala Ser Val Arg Thr Phe Leu Ile Ser Pro Ala Leu
 100 105 110

Leu Leu Val Ala Val Val Ala Val Phe Phe Ala Tyr Arg Arg Arg Asp
 115 120 125

Pro Glu Pro Ile Ile Pro Leu Ala Leu Ile Gly Ser Val Val Phe Phe
 130 135 140

Gln Ile Ile Thr Tyr Ser Leu Gly Ser Thr Phe Gly Leu Leu Arg Phe
 145 150 155 160

Phe Leu Thr Ala Leu Pro Leu Thr Ile Ile Leu Leu Phe Gln Ile Ile
 165 170 175

Pro Pro Arg His Arg Phe Pro Ser Leu Arg Pro Gly Ala Cys Tyr Arg
 180 185 190

Asp Arg Val Thr Gly Lys Tyr Val Pro Lys Thr Ile Thr Gly Val Leu
 195 200 205

Val Leu Ala Ile Phe Gly Gly Thr Gly Ile Thr Leu Tyr Gly Met Ser
210 215 220

Ser Ala Asn Trp Ala Pro Gln Glu Tyr Ala Ile Gln Glu Leu Val Phe
225 230 235 240

Asn Met Gly Ser Pro Ser Gln Asp Ala Val His Thr Leu Asn Thr Phe
245 250 255

Ser Thr Glu Met Asp Val Ala Asp Phe Val Asp Ser Leu Asn Leu Gly
260 265 270

Asp Gly Glu Val Leu Leu Ser Thr Thr Tyr Gly Phe Ala Val Leu Thr
275 280 285

Ala Ser Asn Asn Gln Lys Gln Phe Ile Ile Pro Ser Asp Glu Asp Phe
290 295 300

Ile Thr Thr Leu Asn Glu Pro Ala Glu His Gly Val Lys Tyr Ile Leu
305 310 315 320

Ala Leu Pro Arg Glu Gly Arg Gly Ala Thr Asp Pro Ile Asn Leu Arg
325 330 335

Tyr Pro Asp Met Tyr Glu Thr Gly Ser His Ile Ala Thr Met Glu Ile
340 345 350

Glu Phe Ile Asn Gln Gly Gln Gly Gln Pro Asn Trp Arg Leu Tyr Arg
355 360 365

Val Leu Thr Thr Pro Glu Gln Ser
370 375

<210> 183

<211> 459

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(436)

<223> RXN00334

<400> 183

ataagccccg catgggatag gagaaaagga atgcacgatg agtattgaat ttccgtagg 60

taatccagcg cctgcacagt ggttttctgg cgagggtccat atg gcc aag ctt gat 115
Met Ala Lys Leu Asp
1 5

gac aac gtg cag att gag act gtg aac gtg tct ttt gag gca ggc ggt 163
Asp Asn Val Gln Ile Glu Thr Val Asn Val Ser Phe Glu Ala Gly Gly
10 15 20

cgc acc aat tgg cac act cac cca gtc ggt caa aac ata att gtg ctg 211
Arg Thr Asn Trp His Thr His Pro Val Gly Gln Asn Ile Ile Val Leu
25 30 35

tcg ggc ttg ggc att tat gag gcg gag ggg gag cct gct cga ctc ctg 259


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Ser Gly Leu Gly Ile Tyr Glu Ala Glu Gly Glu Pro Ala Arg Leu Leu
    40                      45                      50

gag cct ggc gat gtt gtt ttc gca gcc gcc ggg gtt cgc cac tgg cac   307
Glu Pro Gly Asp Val Val Phe Ala Ala Ala Gly Val Arg His Trp His
    55                      60                      65

ggc gcc gtg tct ggt gca ccg atg ttc cac gtg gtg gtt aac ctc aaa   355
Gly Ala Val Ser Gly Ala Pro Met Phe His Val Val Val Asn Leu Lys
    70                      75                      80                      85

ggc atc gac ggc gag acc gtc gat tgg gag gag ccg gtc gac gag gag   403
Gly Ile Asp Gly Glu Thr Val Asp Trp Glu Glu Pro Val Asp Glu Glu
    90                      95                      100

cac tac cgc agc gtg agc gcg gag cta caa aga taaaaatgct tttcgacgtc 456
His Tyr Arg Ser Val Ser Ala Glu Leu Gln Arg
    105                      110

cac                                                                459

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<210> 184
<211> 112
<212> PRT
<213> Corynebacterium glutamicum

<400> 184
Met Ala Lys Leu Asp Asp Asn Val Gln Ile Glu Thr Val Asn Val Ser
  1                      5                      10                      15

Phe Glu Ala Gly Gly Arg Thr Asn Trp His Thr His Pro Val Gly Gln
    20                      25                      30

Asn Ile Ile Val Leu Ser Gly Leu Gly Ile Tyr Glu Ala Glu Gly Glu
    35                      40                      45

Pro Ala Arg Leu Leu Glu Pro Gly Asp Val Val Phe Ala Ala Ala Gly
    50                      55                      60

Val Arg His Trp His Gly Ala Val Ser Gly Ala Pro Met Phe His Val
    65                      70                      75                      80

Val Val Asn Leu Lys Gly Ile Asp Gly Glu Thr Val Asp Trp Glu Glu
    85                      90                      95

Pro Val Asp Glu Glu His Tyr Arg Ser Val Ser Ala Glu Leu Gln Arg
    100                      105                      110

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<210> 185
<211> 459
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(436)

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<400> 185

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taatccagcg cctgcacagt ggttttctgg cgagggtccat atg gcc aag ctt gat 115
                Met Ala Lys Leu Asp
                1                5

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gac aac gtg cag att gag act gtg aac gtg tct ttt gag gca ggc ggt 163
Asp Asn Val Gln Ile Glu Thr Val Asn Val Ser Phe Glu Ala Gly Gly
10 15 20

cgc acc aat tgg cac act cac cca gtc ggt caa aac ata att gtg ctg 211
Arg Thr Asn Trp His Thr His Pro Val Gly Gln Asn Ile Ile Val Leu
25 30 35

tcg ggc ttg ggc att tat gag gcg gag ggg gag cct gct cga ctc ctg 259
Ser Gly Leu Gly Ile Tyr Glu Ala Glu Gly Glu Pro Ala Arg Leu Leu
40 45 50

gag cct ggc gat gtt gtt ttc gca gcc gcc ggg gtt cgc cac tgg cac 307
Glu Pro Gly Asp Val Val Phe Ala Ala Ala Gly Val Arg His Trp His
55 60 65

ggc gcc gtg tct ggt gca ccg atg ttc cac gtg gtg gtt aac ctc aaa 355
Gly Ala Val Ser Gly Ala Pro Met Phe His Val Val Val Asn Leu Lys
70 75 80 85

ggc atc gac ggc gag acc gtc gat tgg gag gag ccg gtc gac gag gag 403
Gly Ile Asp Gly Glu Thr Val Asp Trp Glu Glu Pro Val Asp Glu Glu
90 95 100

cac tac cgc agc gtg agc gcg gag cta caa aga taaaaatgct ttctgacgtc 456
 His Tyr Arg Ser Val Ser Ala Glu Leu Gln Arg
 105 110

cac 459

<210> 186

<211> 112

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 186

Met Ala Lys Leu Asp Asp Asn Val Gln Ile Glu Thr Val Asn Val Ser
1 5 10 15

Phe Glu Ala Gly Gly Arg Thr Asn Trp His Thr His Pro Val Gly Gln
20 25 30

Asn Ile Ile Val Leu Ser Gly Leu Gly Ile Tyr Glu Ala Glu Gly Glu
35 40 45

Pro Ala Arg Leu Leu Glu Pro Gly Asp Val Val Phe Ala Ala Ala Gly
50 55 60

Val Arg His Trp His Gly Ala Val Ser Gly Ala Pro Met Phe His Val
65 70 75 80

ggc ggc atg gac aaa tgg ggc gtg cac gtt ctg ccc aag gat gca gcg 547
Gly Gly Met Asp Lys Trp Gly Val His Val Leu Pro Lys Asp Ala Ala

135	140	145	
tac cta aag aag atg ctt ttc gac gca ggt gcc ggt gcg atc ggc gac Tyr Leu Lys Lys Met Leu Phe Asp Ala Gly Ala Ile Gly Asp 150 155 160 165			595
tac cga gag tgt gcc ttt gag atc gaa gga acc ggg cag ttt agg ccc Tyr Arg Glu Cys Ala Phe Glu Ile Glu Gly Thr Gly Gln Phe Arg Pro 170 175 180			643
gtg gag ggg gcg aat ccg gca gag ggg gac gtc gat aag ctt ttt aaa Val Glu Gly Ala Asn Pro Ala Glu Gly Asp Val Asp Lys Leu Phe Lys 185 190 195			691
tcc ctt gag ctg cgc atc gag ttt gtt gca ccg cgc aac ctg cgc gcc Ser Leu Glu Leu Arg Ile Glu Phe Val Ala Pro Arg Asn Leu Arg Ala 200 205 210			739
ccg ctc acg tcg gtg ctg ccg gag gct cat ccg tat gag gag cct gcc Arg Leu Thr Ser Val Leu Arg Glu Ala His Pro Tyr Glu Glu Pro Ala 215 220 225			787
ttc gat att gtt gaa atg cac agc gct gag agt tta gaa aat gcg acc Phe Asp Ile Val Glu Met His Ser Ala Glu Ser Leu Glu Asn Ala Thr 230 235 240 245			835
gga ttg ggt cgt gtg ggt gaa ttg ccg gag ccg atg cgc ctc gcg gat Gly Leu Gly Arg Val Gly Glu Leu Pro Glu Pro Met Arg Leu Ala Asp 250 255 260			883
ttc gtg caa caa gtg gcc aac aac ctg cct gtc acc gaa tgg ggc gtg Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val Thr Glu Trp Gly Val 265 270 275			931
cgc gct acc ggc gat cct gaa caa atg gtg tcc cgt gtg gcg gtt tca Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser Arg Val Ala Val Ser 280 285 290			979
tca ggg tcg ggt gac agt ttc tta aac gat gtg att aag ctc gga gtg Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val Ile Lys Leu Gly Val 295 300 305			1027
gac gtt tat gtc act tct gat ctg cgc cac cat cca gtt gat gaa tat Asp Val Tyr Val Thr Ser Asp Leu Arg His His Pro Val Asp Glu Tyr 310 315 320 325			1075
ctc cga gaa ggt ggc cct gca gta atc gat act gca cac tgg gcc agc Leu Arg Glu Gly Gly Pro Ala Val Ile Asp Thr Ala His Trp Ala Ser 330 335 340			1123
gaa ttt cca tgg act tcc caa gcc caa gaa att ttg cag gac aaa gcc Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile Leu Gln Asp Lys Ala 345 350 355			1171
cca cag gtt gaa gtt gat gtg att tcg atc cgc aca gac ccc tgg acc Pro Gln Val Glu Val Asp Val Ile Ser Ile Arg Thr Asp Pro Trp Thr 360 365 370			1219
atg tct gcg cga gca gtg aac taaattcttg agaactaaaa aag Met Ser Ala Arg Ala Val Asn 375 380			1263

<210> 188

<211> 380

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 188

Val Ser Asp Val Thr Val Gly Asp Ile Arg Arg Ile Leu Asp Glu Ala
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Tyr Pro Pro Ala Leu Ala Glu Ser Trp Asp Lys Val Gly Leu Ile Cys
 20 25 30

Gly Asp Pro Thr Glu Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys
 35 40 45

Thr Gln Ala Val Ala Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu
 50 55 60

Ile Ile His His Pro Leu Leu Arg Gly Val Thr Ser Val Ala Ala
 65 70 75 80

Asp Glu Pro Lys Gly Lys Val Ile His Thr Leu Ile Arg Gly Gly Val
 85 90 95

Ala Leu Phe Ser Ala His Thr Asn Ala Asp Ser Ala Arg Pro Gly Val
 100 105 110

Asn Asp Lys Leu Ala Glu Leu Val Gly Ile Thr Ala Gly Arg Pro Ile
 115 120 125

Ala Thr Arg Leu Leu Gly Gly Met Asp Lys Trp Gly Val His Val Leu
 130 135 140

Pro Lys Asp Ala Ala Tyr Leu Lys Lys Met Leu Phe Asp Ala Gly Ala
 145 150 155 160

Gly Ala Ile Gly Asp Tyr Arg Glu Cys Ala Phe Glu Ile Glu Gly Thr
 165 170 175

Gly Gln Phe Arg Pro Val Glu Gly Ala Asn Pro Ala Glu Gly Asp Val
 180 185 190

Asp Lys Leu Phe Lys Ser Leu Glu Leu Arg Ile Glu Phe Val Ala Pro
 195 200 205

Arg Asn Leu Arg Ala Arg Leu Thr Ser Val Leu Arg Glu Ala His Pro
 210 215 220

Tyr Glu Glu Pro Ala Phe Asp Ile Val Glu Met His Ser Ala Glu Ser
 225 230 235 240

Leu Glu Asn Ala Thr Gly Leu Gly Arg Val Gly Glu Leu Pro Glu Pro
 245 250 255

Met Arg Leu Ala Asp Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val
 260 265 270

Thr Glu Trp Gly Val Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser
 275 280 285

Arg Val Ala Val Ser Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val
 290 295 300

Ile Lys Leu Gly Val Asp Val Tyr Val Thr Ser Asp Leu Arg His His
 305 310 315 320

Pro Val Asp Glu Tyr Leu Arg Glu Gly Gly Pro Ala Val Ile Asp Thr
 325 330 335

Ala His Trp Ala Ser Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile
 340 345 350

Leu Gln Asp Lys Ala Pro Gln Val Glu Val Asp Val Ile Ser Ile Arg
 355 360 365

Thr Asp Pro Trp Thr Met Ser Ala Arg Ala Val Asn
 370 375 380

<210> 189

<211> 806

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(783)

<223> PRXA00338

<400> 189

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 Val Gly Ile Thr Ala Gly Arg Pro Ile Ala Thr Arg Leu Leu Gly Gly
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atg gac aaa tgg ggc gtg cac gtt ctg ccc aag gat gca gcg tac cta 96
 Met Asp Lys Trp Gly Val His Val Leu Pro Lys Asp Ala Ala Tyr Leu
 20 25 30

aag aag atg ctt ttc gac gca ggt gcc ggt gcg atc ggc gac tac cga 144
 Lys Lys Met Leu Phe Asp Ala Gly Ala Ile Gly Asp Tyr Arg
 35 40 45

gag tgt gcc ttt gag atc gaa gga acc ggg cag ttt agg ccc gtg gag 192
 Glu Cys Ala Phe Glu Ile Glu Gly Thr Gly Gln Phe Arg Pro Val Glu
 50 55 60

ggg gcg aat ccg gca gag ggg gac gtc gat aag ctt ttt aaa tcc ctt 240
 Gly Ala Asn Pro Ala Glu Gly Asp Val Asp Lys Leu Phe Lys Ser Leu
 65 70 75 80

gag ctg cgc atc gag ttt gtt gca ccg cgc aac ctg cgc gcc cgg ctc 288
 Glu Leu Arg Ile Glu Phe Val Ala Pro Arg Asn Leu Arg Ala Arg Leu
 85 90 95

acg tcg gtg ctg cgg gag gct cat ccg tat gag gag cct gcc ttc gat 336
 Thr Ser Val Leu Arg Glu Ala His Pro Tyr Glu Glu Pro Ala Phe Asp
 100 105 110

att gtt gaa atg cac agc gct gag agt tta gaa aat gcg acc gga ttg 384
 Ile Val Glu Met His Ser Ala Glu Ser Leu Glu Asn Ala Thr Gly Leu

115	120	125	
ggt cgt gtg ggt gaa ttg ccg gag ccg atg cgc ctc gcg gat ttc gtg Gly Arg Val Gly Glu Leu Pro Glu Pro Met Arg Leu Ala Asp Phe Val 130 135 140			432
caa caa gtg gcc aac aac ctg cct gtc acc gaa tgg gcc gtg cgc gct Gln Gln Val Ala Asn Asn Leu Pro Val Thr Glu Trp Gly Val Arg Ala 145 150 155 160			480
acc gcc gat cct gaa caa atg gtg tcc cgt gtg gcg gtt tca tca ggg Thr Gly Asp Pro Glu Gln Met Val Ser Arg Val Ala Val Ser Ser Gly 165 170 175			528
tcg ggt gac agt ttc tta aac gat gtg att aag ctc gga gtg gac gtt Ser Gly Asp Ser Phe Leu Asn Asp Val Ile Lys Leu Gly Val Asp Val 180 185 190			576
tat gtc act tct gat ctg cgc cac cat cca gtt gat gaa tat ctc cga Tyr Val Thr Ser Asp Leu Arg His His Pro Val Asp Glu Tyr Leu Arg 195 200 205			624
gaa ggt gcc cct gca gta atc gat act gca cac tgg gcc agc gaa ttt Glu Gly Gly Pro Ala Val Ile Asp Thr Ala His Trp Ala Ser Glu Phe 210 215 220			672
cca tgg act tcc caa gcc caa gaa att ttg cag gac aaa gcc cca cag Pro Trp Thr Ser Gln Ala Gln Glu Ile Leu Gln Asp Lys Ala Pro Gln 225 230 235 240			720
gtt gaa gtt gat gtg att tcg atc cgc aca gac ccc tgg acc atg tct Val Glu Val Asp Val Ile Ser Ile Arg Thr Asp Pro Trp Thr Met Ser 245 250 255			768
gcg cga gca gtg aac taaattcttg agaactaaaa aag Ala Arg Ala Val Asn 260			806
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<211> 261			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 190			
Val Gly Ile Thr Ala Gly Arg Pro Ile Ala Thr Arg Leu Leu Gly Gly 1 5 10 15			
Met Asp Lys Trp Gly Val His Val Leu Pro Lys Asp Ala Ala Tyr Leu 20 25 30			
Lys Lys Met Leu Phe Asp Ala Gly Ala Ile Gly Asp Tyr Arg 35 40 45			
Glu Cys Ala Phe Glu Ile Glu Gly Thr Gly Gln Phe Arg Pro Val Glu 50 55 60			
Gly Ala Asn Pro Ala Glu Gly Asp Val Asp Lys Leu Phe Lys Ser Leu 65 70 75 80			
Glu Leu Arg Ile Glu Phe Val Ala Pro Arg Asn Leu Arg Ala Arg Leu			

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      85              90              95
Thr Ser Val Leu Arg Glu Ala His Pro Tyr Glu Glu Pro Ala Phe Asp
      100              105              110
Ile Val Glu Met His Ser Ala Glu Ser Leu Glu Asn Ala Thr Gly Leu
      115              120              125
Gly Arg Val Gly Glu Leu Pro Glu Pro Met Arg Leu Ala Asp Phe Val
      130              135              140
Gln Gln Val Ala Asn Asn Leu Pro Val Thr Glu Trp Gly Val Arg Ala
      145              150              155              160
Thr Gly Asp Pro Glu Gln Met Val Ser Arg Val Ala Val Ser Ser Gly
      165              170              175
Ser Gly Asp Ser Phe Leu Asn Asp Val Ile Lys Leu Gly Val Asp Val
      180              185              190
Tyr Val Thr Ser Asp Leu Arg His His Pro Val Asp Glu Tyr Leu Arg
      195              200              205
Glu Gly Gly Pro Ala Val Ile Asp Thr Ala His Trp Ala Ser Glu Phe
      210              215              220
Pro Trp Thr Ser Gln Ala Gln Glu Ile Leu Gln Asp Lys Ala Pro Gln
      225              230              235              240
Val Glu Val Asp Val Ile Ser Ile Arg Thr Asp Pro Trp Thr Met Ser
      245              250              255
Ala Arg Ala Val Asn
      260

<210> 191
<211> 310
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(310)
<223> FRXA00318

<400> 191
tcttagaagg cgtagtcaca ccattaacct tgccagaatt ttccaaggct tggcttgact 60
tgggaaacga acatgcggta ccaaccaggg gaggtaatgc gtg agt gat gta acc 115
Val Ser Asp Val Thr
      1 5
gtt ggc gat att ctc cgc att ttg gat gag gct tat ccg ccg gcg ttg 163
Val Gly Asp Ile Leu Arg Ile Leu Asp Glu Ala Tyr Pro Pro Ala Leu
      10 15 20
gcg gaa agc tgg gac aaa gtg gtg ctg atc tgc gtt gat cca aca gag 211
Ala Glu Ser Trp Asp Lys Val Val Leu Ile Cys Val Asp Pro Thr Glu
      25 30 35

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tgc gtg aag cgt gtt ggt tta gca ctc gat tgc acc cag gca ctg gcc 259
 Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys Thr Gln Ala Leu Ala
 40 45 50

gac aag gct gtg gac atg ggt ttg gac atg ctg atc att cac cac cca 307
 Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu Ile Ile His His Pro
 55 60 65

tta 310
 Leu
 70

<210> 192

<211> 70

<212> PRT

<213> Corynebacterium glutamicum

<400> 192

Val Ser Asp Val Thr Val Gly Asp Ile Leu Arg Ile Leu Asp Glu Ala
 1 5 10 15

Tyr Pro Pro Ala Leu Ala Glu Ser Trp Asp Lys Val Val Leu Ile Cys
 20 25 30

Val Asp Pro Thr Glu Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys
 35 40 45

Thr Gln Ala Leu Ala Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu
 50 55 60

Ile Ile His His Pro Leu
 65 70

<210> 193

<211> 552

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(529)

<223> RXN00342

<400> 193

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cgaaaaacac atcggggccc acacgaggag gattattaaa gtg gcc gac gct ccg 115
 Val Ala Asp Ala Pro
 1 5

ggc gca gtc aag caa ggt gcc cag gat tat gct caa cta ctc ggc att 163
 Gly Ala Val Lys Gln Gly Ala Gln Asp Tyr Ala Gln Leu Leu Gly Ile
 10 15 20

caa tcg ggt cat atc gtt caa gaa att gga tgg gat gaa gat tcc gac 211
 Gln Ser Gly His Ile Val Gln Glu Ile Gly Trp Asp Glu Asp Ser Asp
 25 30 35

acg ctg atc agc gag tcc atc gaa gat gca atc ggt gag gaa cta ctc 259

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Thr Leu Ile Ser Glu Ser Ile Glu Asp Ala Ile Gly Glu Glu Leu Leu
      40                      45                      50
gat gaa gaa acc gac gag ctg tgc gat gtc gtg ctg ctc tgg tgg cgc 307
Asp Glu Glu Thr Asp Glu Leu Cys Asp Val Val Leu Leu Trp Trp Arg
      55                      60                      65

gag gat gac ggc gat ctc gtc gac gga ctt gtg gat tcc atc cgc tcc 355
Glu Asp Asp Gly Asp Leu Val Asp Gly Leu Val Asp Ser Ile Arg Ser
      70                      75                      80                      85

ctc gct gag aat ggt cgt atc tgg gtg ttg act cct ggc att ggt aaa 403
Leu Ala Glu Asn Gly Arg Ile Trp Val Leu Thr Pro Gly Ile Gly Lys
      90                      95                      100

gaa gga gcc ctg gct cct gga gtt atc tct gaa tca gct caa ctg gca 451
Glu Gly Ala Leu Ala Pro Gly Val Ile Ser Glu Ser Ala Gln Leu Ala
      105                      110                      115

ggg ctc gtg cag acc aag gca gaa cgt ctc ggt aat tgg caa ggt tct 499
Gly Leu Val Gln Thr Lys Ala Glu Arg Leu Gly Asn Trp Gln Gly Ser
      120                      125                      130

tgc ctc gtc cag cgt gga aac aag aag cct taacaatcgc taatttcac 549
Cys Leu Val Gln Arg Gly Asn Lys Lys Pro
      135                      140

ggc 552

<210> 194
<211> 143
<212> PRT
<213> Corynebacterium glutamicum

<400> 194
Val Ala Asp Ala Pro Gly Ala Val Lys Gln Gly Ala Gln Asp Tyr Ala
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Gln Leu Leu Gly Ile Gln Ser Gly His Ile Val Gln Glu Ile Gly Trp
      20                      25                      30

Asp Glu Asp Ser Asp Thr Leu Ile Ser Glu Ser Ile Glu Asp Ala Ile
      35                      40                      45

Gly Glu Glu Leu Leu Asp Glu Glu Thr Asp Glu Leu Cys Asp Val Val
      50                      55                      60

Leu Leu Trp Trp Arg Glu Asp Asp Gly Asp Leu Val Asp Gly Leu Val
      65                      70                      75                      80

Asp Ser Ile Arg Ser Leu Ala Glu Asn Gly Arg Ile Trp Val Leu Thr
      85                      90                      95

Pro Gly Ile Gly Lys Glu Gly Ala Leu Ala Pro Gly Val Ile Ser Glu
      100                      105                      110

Ser Ala Gln Leu Ala Gly Leu Val Gln Thr Lys Ala Glu Arg Leu Gly
      115                      120                      125

Asn Trp Gln Gly Ser Cys Leu Val Gln Arg Gly Asn Lys Lys Pro

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130

135

140

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<211> 524

<212> DNA

<213> Corynebacterium glutamicum

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<222> (73)..(501)

<223> FRXA00342

<400> 195

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agaattatta aagtg gcc gac gct ccg ggc gca gtc aag caa ggt gcc gag 111
 Val Ala Asp Ala Pro Gly Ala Val Lys Gln Gly Ala Gln
 1 5 10

gat tat gct caa cta ctc ggc att caa tcg ggt cat atc gtt caa gaa 159
 Asp Tyr Ala Gln Leu Leu Gly Ile Gln Ser Gly His Ile Val Gln Glu
 15 20 25

att gga tgg gat gaa gat tcc gac acg ctg atc agc gag tcc atc gaa 207
 Ile Gly Trp Asp Glu Asp Ser Asp Thr Leu Ile Ser Glu Ser Ile Glu
 30 35 40 45

gat gca atc ggt gag gaa cta ctc gat gaa gaa acc gac gag ctg tgc 255
 Asp Ala Ile Gly Glu Glu Leu Leu Asp Glu Glu Thr Asp Glu Leu Cys
 50 55 60

gat gtc gtg ctg ctc tgg tgg cgc gag gat gac ggc gat ctc gtc gac 303
 Asp Val Val Leu Leu Trp Trp Arg Glu Asp Asp Gly Asp Leu Val Asp
 65 70 75

gga ctt gtg gat tcc atc cgc tcc ctc gct gag aat ggt cgt atc tgg 351
 Gly Leu Val Asp Ser Ile Arg Ser Leu Ala Glu Asn Gly Arg Ile Trp
 80 85 90

gtg ttg act cct ggc att ggt aaa gaa gga gcc ctg gct cct gga gtt 399
 Val Leu Thr Pro Gly Ile Gly Lys Glu Gly Ala Leu Ala Pro Gly Val
 95 100 105

atc tct gaa tca gct caa ctg gca ggt ctc gtg cag acc aag gca gaa 447
 Ile Ser Glu Ser Ala Gln Leu Ala Gly Leu Val Gln Thr Lys Ala Glu
 110 115 120 125

cgt ctc ggt aat tgg caa ggt tct tgc ctc gtc cag cgt gga aac aag 495
 Arg Leu Gly Asn Trp Gln Gly Ser Cys Leu Val Gln Arg Gly Asn Lys
 130 135 140

aag cct taacaatgc taatttccac ggc 524
 Lys Pro

<210> 196

<211> 143

<212> PRT

<213> Corynebacterium glutamicum

<400> 196

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Asp Glu Asp Ser Asp Thr Leu Ile Ser Glu Ser Ile Glu Asp Ala Ile
 35 40 45

Gly Glu Glu Leu Leu Asp Glu Glu Thr Asp Glu Leu Cys Asp Val Val
 50 55 60

Leu Leu Trp Trp Arg Glu Asp Asp Gly Asp Leu Val Asp Gly Leu Val
 65 70 75 80

Asp Ser Ile Arg Ser Leu Ala Glu Asn Gly Arg Ile Trp Val Leu Thr
 85 90 95

Pro Gly Ile Gly Lys Glu Gly Ala Leu Ala Pro Gly Val Ile Ser Glu
 100 105 110

Ser Ala Gln Leu Ala Gly Leu Val Gln Thr Lys Ala Glu Arg Leu Gly
 115 120 125

Asn Trp Gln Gly Ser Cys Leu Val Gln Arg Gly Asn Lys Lys Pro
 130 135 140

<210> 197

<211> 1002

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(979)

<223> RXN00344

<400> 197

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cacggtggct cgcatcaacg acagaatcgt ggtgggttaa gtg gat cta tcc acc 115
 Val Asp Leu Ser Thr
 1 5

tgg ctt tcc gac acc caa tat ctc atc agc gtc gat ttc gtc cag cac 163
 Trp Leu Ser Asp Thr Gln Tyr Leu Ile Ser Val Asp Phe Val Gln His
 10 15 20

gca ctc atc gcc tcc gcg ctg ttg gcc ctg ctc tcc ggt gtg atc gcg 211
 Ala Leu Ile Ala Ser Ala Leu Leu Gly Leu Leu Ser Gly Val Ile Ala
 25 30 35

cgg ctc atc gtg gtg cgc caa cag tcc ttc gca gtc cac gcc acc gcc 259
 Pro Leu Ile Val Val Arg Gln Gln Ser Phe Ala Val His Gly Thr Ala
 40 45 50

gaa ctc gcc ctc atg gga gcc gcc gcc gcg ctg ctc ttc gga ttg aat 307
 Glu Leu Ala Leu Met Gly Ala Ala Ala Leu Leu Phe Gly Leu Asn

55	60	65	
gta ggc ggc ggt gca gtg atc ggt tcc gtg gtc gcc gcg atc cta ctg	355		
Val Gly Gly Gly Ala Val Ile Gly Ser Val Val Ala Ala Ile Leu Leu			
70 75 80 85			
gca tta ctc ggc atg aaa caa caa gat tcc gcc gtc ggt gcc gtg atg	403		
Ala Leu Leu Gly Met Lys Gln Gln Asp Ser Ala Val Gly Ala Val Met			
90 95 100			
agt ttc gga ctc ggt ctg tcc gtg ctg ttc att cac ctc tac ccc ggc	451		
Ser Phe Gly Leu Gly Leu Ser Val Leu Phe Ile His Leu Tyr Pro Gly			
105 110 115			
cga agc tcc acc gcg ttc tcc ctg ctc aca ggg caa atc gtt ggt gtt	499		
Arg Ser Ser Thr Ala Phe Ser Leu Leu Thr Gly Gln Ile Val Gly Val			
120 125 130			
tcc tca tca tgg ctg tgg atc ctt gtg gca gtc acc gtg atc gtg gtt	547		
Ser Ser Ser Ser Leu Trp Ile Leu Val Ala Val Thr Val Ile Val Val			
135 140 145			
agc gcc gtg gtg att ttc tgg cgc ccg ctg ctt ttc gcc agc gcc gat	595		
Ser Ala Val Val Ile Phe Trp Arg Pro Leu Leu Phe Ala Ser Ala Asp			
150 155 160 165			
ccg atc atg gcg cag gcc tcc gga gta aac gtc cga ttc atc gcc gtt	643		
Pro Ile Met Ala Gln Ala Ser Gly Val Asn Val Arg Phe Ile Ala Val			
170 175 180			
gcc ttc gca gtt ctg gtt ggc ctc acc acg tcc cag tcc gtg cag att	691		
Ala Phe Ala Val Leu Val Gly Leu Thr Thr Ser Gln Ser Val Gln Ile			
185 190 195			
gtc ggt gcg ctg ctg gtc atg gca ttg ctg atc act ccc gcc gcg gcc	739		
Val Gly Ala Leu Leu Val Met Ala Leu Leu Ile Thr Pro Gly Ala Ala			
200 205 210			
gct gtg gcg gtg acc gcc aat cca gtg aaa gcc gtg gtg ctg gca gtc	787		
Ala Val Ala Val Thr Ala Asn Pro Val Lys Ala Val Val Leu Ala Val			
215 220 225			
atc ttc gcg gaa gta tgc gct gtc ggt ggc ctg cta ttg tgc cta gcg	835		
Ile Phe Ala Glu Val Ser Ala Val Gly Gly Leu Leu Ser Leu Ala			
230 235 240 245			
cct ggt ttg ccg gtg agt gtt ttt gtc acc acc atc tct ttt gtg att	883		
Pro Gly Leu Pro Val Ser Val Phe Val Thr Thr Ile Ser Phe Val Ile			
250 255 260			
tac ctg gtc tgc cgc ctg atc ggt tgg ctc cgc gcc cgt gga gct cag	931		
Tyr Leu Val Cys Arg Leu Ile Gly Trp Leu Arg Gly Arg Gly Ala Gln			
265 270 275			
cgt gac gaa gat gct tat cga cgc cgc cag cac gat cac cac cct cac	979		
Arg Asp Glu Asp Ala Tyr Arg Arg Arg Gln His Asp His His Pro His			
280 285 290			
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<210> 198
 <211> 293
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 198

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Val Asp Leu Ser Thr Trp Leu Ser Asp Thr Gln Tyr Leu Ile Ser Val
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Asp Phe Val Gln His Ala Leu Ile Ala Ser Ala Leu Leu Gly Leu Leu
      20           25           30

Ser Gly Val Ile Ala Pro Leu Ile Val Val Arg Gln Gln Ser Phe Ala
      35           40           45

Val His Gly Thr Ala Glu Leu Ala Leu Met Gly Ala Ala Ala Ala Leu
      50           55           60

Leu Phe Gly Leu Asn Val Gly Gly Gly Ala Val Ile Gly Ser Val Val
      65           70           75           80

Ala Ala Ile Leu Leu Ala Leu Leu Gly Met Lys Gln Gln Asp Ser Ala
      85           90           95

Val Gly Ala Val Met Ser Phe Gly Leu Gly Leu Ser Val Leu Phe Ile
      100          105          110

His Leu Tyr Pro Gly Arg Ser Ser Thr Ala Phe Ser Leu Leu Thr Gly
      115          120          125

Gln Ile Val Gly Val Ser Ser Ser Ser Leu Trp Ile Leu Val Ala Val
      130          135          140

Thr Val Ile Val Val Ser Ala Val Val Ile Phe Trp Arg Pro Leu Leu
      145          150          155          160

Phe Ala Ser Ala Asp Pro Ile Met Ala Gln Ala Ser Gly Val Asn Val
      165          170          175

Arg Phe Ile Ala Val Ala Phe Ala Val Leu Val Gly Leu Thr Thr Ser
      180          185          190

Gln Ser Val Gln Ile Val Gly Ala Leu Leu Val Met Ala Leu Leu Ile
      195          200          205

Thr Pro Gly Ala Ala Ala Val Ala Val Thr Ala Asn Pro Val Lys Ala
      210          215          220

Val Val Leu Ala Val Ile Phe Ala Glu Val Ser Ala Val Gly Gly Leu
      225          230          235          240

Leu Leu Ser Leu Ala Pro Gly Leu Pro Val Ser Val Phe Val Thr Thr
      245          250          255

Ile Ser Phe Val Ile Tyr Leu Val Cys Arg Leu Ile Gly Trp Leu Arg
      260          265          270

Gly Arg Gly Ala Gln Arg Asp Glu Asp Ala Tyr Arg Arg Arg Gln His
      275          280          285

Asp His His Pro His
  
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290

<210> 199
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 <212> DNA
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 <222> (1)..(579)
 <223> FRXA00344

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 ggc cga agc tcc acc gcg ttc tcc ctg ctc aca ggg caa atc gtt ggt 96
 Gly Arg Ser Thr Ala Phe Ser Leu Leu Thr Gly Gln Ile Val Gly
 20 25 30
 gtt tcc tca tca tcg ctg tgg atc ctt gtg gca gtc acc gtg atc gtg 144
 Val Ser Ser Ser Ser Leu Trp Ile Leu Val Ala Val Thr Val Ile Val
 35 40 45
 gtt agc gcc gtg gtg att ttc tgg cgc ccg ctg ctt ttc gcc agc gcc 192
 Val Ser Ala Val Val Ile Phe Trp Arg Pro Leu Leu Phe Ala Ser Ala
 50 55 60
 gat ccg atc atg gcg cag gcc tcc gga gta aac gtc cga ttc atc gcc 240
 Asp Pro Ile Met Ala Gln Ala Ser Gly Val Asn Val Arg Phe Ile Ala
 65 70 75 80
 gtt gcc ttc gca gtt ctg gtt ggc ctc acc acg tcc cag tcc gtg cag 288
 Val Ala Phe Ala Val Leu Val Gly Leu Thr Thr Ser Gln Ser Val Gln
 85 90 95
 att gtc ggt gcg ctg ctg gtc atg gca ttg ctg atc act ccc gcc gcg 336
 Ile Val Gly Ala Leu Leu Val Met Ala Leu Leu Ile Thr Pro Gly Ala
 100 105 110
 gcc gct gtg gcg gtg acc gcc aat cca gtg aaa gcc gtg gtg ctg gca 384
 Ala Ala Val Ala Val Thr Ala Asn Pro Val Lys Ala Val Val Leu Ala
 115 120 125
 gtc atc ttc gcg gaa gta tcg gct gtc ggt gcc ctg cta ttg tcg cta 432
 Val Ile Phe Ala Glu Val Ser Ala Val Gly Gly Leu Leu Ser Leu
 130 135 140
 gcg cct ggt ttg ccg gtg agt gtt ttt gtc acc acc atc tct ttt gtg 480
 Ala Pro Gly Leu Pro Val Ser Val Phe Val Thr Thr Ile Ser Phe Val
 145 150 155 160
 att tac ctg gtc tgc cgc ctg atc ggt tgg ctc cgc gcc cgt gga gct 528
 Ile Tyr Leu Val Cys Arg Leu Ile Gly Trp Leu Arg Gly Arg Gly Val
 165 170 175
 cag cgt gac gaa gat gct tat cga cgc cgc cag cac gat cac cac cct 576
 Gln Arg Asp Glu Asp Ala Tyr Arg Arg Arg Gln His Asp His His Pro
 180 185 190

cac taggcgtttc gaagt
His

594

<210> 200
<211> 193
<212> PRT
<213> Corynebacterium glutamicum

<400> 200
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Gly Arg Ser Ser Thr Ala Phe Ser Leu Leu Thr Gly Gln Ile Val Gly
20 25 30
Val Ser Ser Ser Ser Leu Trp Ile Leu Val Ala Val Thr Val Ile Val
35 40 45
Val Ser Ala Val Val Ile Phe Trp Arg Pro Leu Leu Phe Ala Ser Ala
50 55 60
Asp Pro Ile Met Ala Gln Ala Ser Gly Val Asn Val Arg Phe Ile Ala
65 70 75 80
Val Ala Phe Ala Val Leu Val Gly Leu Thr Thr Ser Gln Ser Val Gln
85 90 95
Ile Val Gly Ala Leu Leu Val Met Ala Leu Leu Ile Thr Pro Gly Ala
100 105 110
Ala Ala Val Ala Val Thr Ala Asn Pro Val Lys Ala Val Val Leu Ala
115 120 125
Val Ile Phe Ala Glu Val Ser Ala Val Gly Gly Leu Leu Leu Ser Leu
130 135 140
Ala Pro Gly Leu Pro Val Ser Val Phe Val Thr Thr Ile Ser Phe Val
145 150 155 160
Ile Tyr Leu Val Cys Arg Leu Ile Gly Trp Leu Arg Gly Arg Gly Ala
165 170 175
Gln Arg Asp Glu Asp Ala Tyr Arg Arg Arg Gln His Asp His His Pro
180 185 190
His

<210> 201
<211> 816
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(793)
<223> RXN00353

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 Val Gly Arg Ser Phe
 1 5
 acc aac agg act ttt gat cgc ttg cgc ttc atg gtg gtt tat cgc gat 163
 Thr Asn Arg Thr Phe Asp Pro Leu Pro Phe Met Val Val Tyr Pro Asp
 10 15 20
 ggg gtg gat cag cat tgg aat gat gcg cgg ttg ggt ttg gat gaa aat 211
 Gly Val Asp Gln His Trp Asn Asp Ala Arg Leu Gly Leu Asp Glu Asn
 25 30 35
 acc cgc cat tta ggc att gat gat gtg ggg ttc ttt gta aaa ctc gcc 259
 Thr Arg His Leu Gly Ile Asp Asp Val Gly Phe Phe Val Lys Leu Ala
 40 45 50
 acg cac ttg ggc aac acg tat ggc atc aag agg atc ttt att gtt ggc 307
 Thr His Leu Gly Asn Thr Tyr Gly Ile Lys Arg Ile Phe Ile Val Gly
 55 60 65
 tat tcc aac ggt ggg cag atg gtg ttg cgg ctc atg cat gag gtt ccc 355
 Tyr Ser Asn Gly Gly Gln Met Val Leu Arg Leu Met His Glu Val Pro
 70 75 80 85
 aag atg ctc agt ggc gct gca acc att gca tcc aac atg cca gtt gca 403
 Lys Met Leu Ser Gly Ala Ala Thr Ile Ala Ser Asn Met Pro Val Ala
 90 95 100
 gag aat acg ctg cgc cag gtg aaa acc ttc aag aca cat cgc gtg cct 451
 Glu Asn Thr Leu Pro Gln Val Lys Thr Phe Lys Thr His Pro Val Pro
 105 110 115
 tat ttg gcg atg gct gga act gcc gat act ttt tca cgc tat gag ggt 499
 Tyr Leu Ala Met Ala Gly Thr Ala Asp Thr Phe Ser Pro Tyr Glu Gly
 120 125 130
 ggc gat gcc ggt att ggt cgc gaa cac cgc cgt ggc gtg ggc atg tcc 547
 Gly Asp Ala Gly Ile Gly Arg Glu His Arg Arg Gly Val Gly Met Ser
 135 140 145
 gcc ttt gat tca gct gcc tat att gcc gcc cga aac gga ctg acc gaa 595
 Ala Phe Asp Ser Ala Ala Tyr Ile Ala Ala Asn Gly Leu Thr Glu
 150 155 160 165
 cac cgc cac gac gtg att gat gat gtg gtg tgc atc gat acc tgg gat 643
 His Arg His Asp Val Ile Asp Asp Val Val Ser Ile Asp Thr Trp Asp
 170 175 180
 gga gaa aat ccc gtt gag ttt tgg aca ctc aac ggg atc ggc cac ttg 691
 Gly Glu Asn Pro Val Glu Phe Trp Thr Leu Asn Gly Ile Gly His Leu
 185 190 195
 gta cca agt ggg aaa act tat cca gaa ttt cta ggc ccc tca acc aca 739
 Val Pro Ser Gly Lys Thr Tyr Pro Glu Phe Leu Gly Pro Ser Thr Thr
 200 205 210
 tca gtg ata gcg gct gag gag att ggg aag ttc ttt gat ggg gtc agg 787

Ser Val Ile Ala Ala Glu Glu Ile Gly Lys Phe Phe Asp Gly Val Arg
 215 220 225

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 Arg Arg
 230

816

<210> 202
 <211> 231
 <212> PRT
 <213> Corynebacterium glutamicum

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Val Val Tyr Pro Asp Gly Val Asp Gln His Trp Asn Asp Ala Arg Leu
 20 25 30

Gly Leu Asp Glu Asn Thr Arg His Leu Gly Ile Asp Asp Val Gly Phe
 35 40 45

Phe Val Lys Leu Ala Thr His Leu Gly Asn Thr Tyr Gly Ile Lys Arg
 50 55 60

Ile Phe Ile Val Gly Tyr Ser Asn Gly Gly Gln Met Val Leu Arg Leu
 65 70 75 80

Met His Glu Val Pro Lys Met Leu Ser Gly Ala Ala Thr Ile Ala Ser
 85 90 95

Asn Met Pro Val Ala Glu Asn Thr Leu Pro Gln Val Lys Thr Phe Lys
 100 105 110

Thr His Pro Val Pro Tyr Leu Ala Met Ala Gly Thr Ala Asp Thr Phe
 115 120 125

Ser Pro Tyr Glu Gly Gly Asp Ala Gly Ile Gly Arg Glu His Arg Arg
 130 135 140

Gly Val Gly Met Ser Ala Phe Asp Ser Ala Ala Tyr Ile Ala Ala Arg
 145 150 155 160

Asn Gly Leu Thr Glu His Arg His Asp Val Ile Asp Asp Val Val Ser
 165 170 175

Ile Asp Thr Trp Asp Gly Glu Asn Pro Val Glu Phe Trp Thr Leu Asn
 180 185 190

Gly Ile Gly His Leu Val Pro Ser Gly Lys Thr Tyr Pro Glu Phe Leu
 195 200 205

Gly Pro Ser Thr Thr Ser Val Ile Ala Ala Glu Glu Ile Gly Lys Phe
 210 215 220

Phe Asp Gly Val Arg Arg Arg
 225 230

<210> 203

<211> 816
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 <213> Corynebacterium glutamicum

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 <223> FRXA00353

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 Val Gly Arg Ser Phe
 1 5
 acc aac agg act ttt gat ccg ttg ccg ttc atg gtg gtt tat ccg gat 163
 Thr Asn Arg Thr Phe Asp Pro Leu Pro Phe Met Val Val Tyr Pro Asp
 10 15 20
 ggg gtg gat cag cat tgg aat gat gcg cgg ttg ggt ttg gat gaa aat 211
 Gly Val Asp Gln His Trp Asn Asp Ala Arg Leu Gly Leu Asp Glu Asn
 25 30 35
 acc cgc cat tta ggc att gat gat gtg ggg ttc ttt gta aaa ctc gcc 259
 Thr Arg His Leu Gly Ile Asp Asp Val Gly Phe Phe Val Lys Leu Ala
 40 45 50
 acg cac ttg ggc aac acg tat ggc atc aag agg atc ttt att gtt ggc 307
 Thr His Leu Gly Asn Thr Tyr Gly Ile Lys Arg Ile Phe Ile Val Gly
 55 60 65
 tat tcc aac ggt ggg cag atg gtg ttg cgg ctc atg cat gag gtt ccc 355
 Tyr Ser Asn Gly Gly Gln Met Val Leu Arg Leu Met His Glu Val Pro
 70 75 80 85
 aag atg ctc agt ggc gct gca acc att gca tcc aac atg cca gtt gca 403
 Lys Met Leu Ser Gly Ala Ala Thr Ile Ala Ser Asn Met Pro Val Ala
 90 95 100
 gag aat acg ctg ccg cag gtg aaa acc ttc aag aca cat ccg gtg cct 451
 Glu Asn Thr Leu Pro Gln Val Lys Thr Phe Lys Thr His Pro Val Pro
 105 110 115
 tat ttg cgc atg gct gga act gcc gat act ttt tca ccg tat gag ggt 499
 Tyr Leu Ala Met Ala Gly Thr Ala Asp Thr Phe Ser Pro Tyr Glu Gly
 120 125 130
 ggc gat gcc ggt att ggt cgc gaa cac cgc cgt ggc gtg ggc atg tcc 547
 Gly Asp Ala Gly Ile Gly Arg Glu His Arg Arg Gly Val Gly Met Ser
 135 140 145
 gcc ttt gat tca gct gcc tat att gcc gcc cga aac gga ctg acc gaa 595
 Ala Phe Asp Ser Ala Ala Tyr Ile Ala Ala Arg Asn Gly Leu Thr Glu
 150 155 160 165
 cac cgc cac gac gtg att gat gat gtg gtg tcg atc gat acc tgg gat 643
 His Arg His Asp Val Ile Asp Asp Val Val Ser Ile Asp Thr Trp Asp
 170 175 180
 gga gaa aat ccc gtt gag ttt tgg aca ctc aac ggg atc ggc cac ttg 691

Gly Glu Asn Pro Val Glu Phe Trp Thr Leu Asn Gly Ile Gly His Leu
 185 190

gta cca agt ggg aaa act tat cca gaa ttt cta ggc ccc tca acc aca 739
 Val Pro Ser Gly Lys Thr Tyr Pro Glu Phe Leu Gly Pro Ser Thr Thr
 200 205 210

tca gtg ata gcg gct gag gag att ggg aag ttc ttt gat ggg gtc agg 787
 Ser Val Ile Ala Ala Glu Glu Ile Gly Lys Phe Phe Asp Gly Val Arg
 215 220 225

cgt cga taagctcaag ctttaaaaaac gca 816
 Arg Arg
 230

<210> 204

<211> 231

<212> PRT

<213> Corynebacterium glutamicum

<400> 204

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 20 25 30

Gly Leu Asp Glu Asn Thr Arg His Leu Gly Ile Asp Asp Val Gly Phe
 35 40 45

Phe Val Lys Leu Ala Thr His Leu Gly Asn Thr Tyr Gly Ile Lys Arg
 50 55 60

Ile Phe Ile Val Gly Tyr Ser Asn Gly Gly Gln Met Val Leu Arg Leu
 65 70 75 80

Met His Glu Val Pro Lys Met Leu Ser Gly Ala Ala Thr Ile Ala Ser
 85 90 95

Asn Met Pro Val Ala Glu Asn Thr Leu Pro Gln Val Lys Thr Phe Lys
 100 105 110

Thr His Pro Val Pro Tyr Leu Ala Met Ala Gly Thr Ala Asp Thr Phe
 115 120 125

Ser Pro Tyr Glu Gly Gly Asp Ala Gly Ile Gly Arg Glu His Arg Arg
 130 135 140

Gly Val Gly Met Ser Ala Phe Asp Ser Ala Ala Tyr Ile Ala Ala Arg
 145 150 155 160

Asn Gly Leu Thr Glu His Arg His Asp Val Ile Asp Asp Val Val Ser
 165 170 175

Ile Asp Thr Trp Asp Gly Glu Asn Pro Val Glu Phe Trp Thr Leu Asn
 180 185 190

Gly Ile Gly His Leu Val Pro Ser Gly Lys Thr Tyr Pro Glu Phe Leu
 195 200 205

Gly Pro Ser Thr Thr Ser Val Ile Ala Ala Glu Glu Ile Gly Lys Phe
 210 215 220

Phe Asp Gly Val Arg Arg Arg
 225 230

<210> 205
 <211> 936
 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <222> (101)..(913)
 <223> RXN00354

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 ttctcgatta tgtacctcat ttacgcgtaa agtttggggc atg gga aag tta ctt 115
 Met Gly Lys Leu Leu
 1 5
 ttc gta gac atc ggt ggc aca ctg ctg gat tac tca aat gaa gtt ccg 163
 Phe Val Asp Ile Gly Gly Thr Leu Leu Asp Tyr Ser Asn Glu Val Pro
 10 15 20
 cgt tcg gcc gtt gac gcg atc cgt aag gca cgc gcc aaa gga cac cgc 211
 Arg Ser Ala Val Asp Ala Ile Arg Lys Ala Arg Ala Lys Gly His Arg
 25 30 35
 gtg tac ttg agc tct ggt cga agc agc gct gag gtg act tct cag ttg 259
 Val Tyr Leu Ser Ser Gly Arg Ser Ser Ala Glu Val Thr Ser Gln Leu
 40 45 50
 tgg gat atc gga gtg gat ggc ctc att ggc gca aat ggt gga tat gtg 307
 Trp Asp Ile Gly Val Asp Gly Leu Ile Gly Ala Asn Gly Gly Tyr Val
 55 60 65
 gaa agc gca cag gag tct gtg ttc cac cgc cgt ttg tcg ggt gag gag 355
 Glu Ser Ala Gln Glu Ser Val Phe His Arg Arg Leu Ser Gly Glu Glu
 70 75 80 85
 acc cgc cac att gtg gag tgg ctc tac aac cgt ggt ttg gag ttt tat 403
 Thr Arg His Ile Val Glu Trp Leu Tyr Asn Arg Gly Leu Glu Phe Tyr
 90 95 100
 ctc gag tcc aac aac ggt ttg tat gca agc cgt ggt ttc cgt gag gct 451
 Leu Glu Ser Asn Asn Gly Leu Tyr Ala Ser Arg Gly Phe Arg Glu Ala
 105 110 115
 tct aag cca gtg ctg tct cgc ctt tcg gag aag acc gac gtg aca gtc 499
 Ser Lys Pro Val Leu Ser Arg Leu Ser Glu Lys Thr Asp Val Thr Val
 120 125 130
 gat agc atg tac ccg gat atg ttc tgg ggc gcg agc ctt gat cgt gac 547
 Asp Ser Met Tyr Pro Asp Met Phe Trp Gly Ala Ser Leu Asp Arg Asp
 135 140 145
 gat gtg aac aag atc agt tac atc ttc aat tct cag gaa gat ttg gac 595

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Asp Val Asn Lys Ile Ser Tyr Ile Phe Asn Ser Gln Glu Asp Leu Asp
150                      155                      160                      165

gca gcg cgt gag gcg ttc cct aac ctg gag cac acc acg tgg ggt ggt      643
Ala Ala Arg Glu Ala Phe Pro Asn Leu Glu His Thr Thr Trp Gly Gly
                      170                      175                      180

cag acg ggt gcg ttg ttc ggc acg atc ggt gtg tct gtc aac aag aag      691
Gln Thr Gly Ala Leu Phe Gly Thr Ile Gly Val Ser Val Asn Lys Lys
                      185                      190                      195

atc ggc gtg gat cgc ctg ctg aag tac ctg aac gca gat cgc gca aac      739
Ile Gly Val Asp Arg Leu Leu Lys Tyr Leu Asn Ala Asp Arg Ala Asn
                      200                      205                      210

acc att gcg ttc ggc gac agc gat gag gat ctc tcc cta ttt gag gcg      787
Thr Ile Ala Phe Gly Asp Ser Asp Glu Asp Leu Ser Leu Phe Glu Ala
                      215                      220                      225

agc gct tac ggc gtc gcg atg ggc gag gcc acc gaa tgg ctc aag gct      835
Ser Ala Tyr Gly Val Ala Met Gly Glu Ala Thr Glu Ser Leu Lys Ala
230                      235                      240                      245

gct gct gac ctg gtc acg gat gct gtt ggg cag gac ggc ttg cgc aat      883
Ala Ala Asp Leu Val Thr Asp Ala Val Gly Gln Asp Gly Leu Arg Asn
250                      255                      260

gcg ttt tta aag ctt gag ctt atc gac gcc tgaccccatc aaagaacttc      933
Ala Phe Leu Lys Leu Glu Leu Ile Asp Ala
265                      270

cca                                                                936

<210> 206
<211> 271
<212> PRT
<213> Corynebacterium glutamicum

<400> 206
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Ser Asn Glu Val Pro Arg Ser Ala Val Asp Ala Ile Arg Lys Ala Arg
20                      25                      30

Ala Lys Gly His Arg Val Tyr Leu Ser Ser Gly Arg Ser Ser Ala Glu
35                      40                      45

Val Thr Ser Gln Leu Trp Asp Ile Gly Val Asp Gly Leu Ile Gly Ala
50                      55                      60

Asn Gly Gly Tyr Val Glu Ser Ala Gln Glu Ser Val Phe His Arg Arg
65                      70                      75                      80

Leu Ser Gly Glu Glu Thr Arg His Ile Val Glu Trp Leu Tyr Asn Arg
85                      90                      95

Gly Leu Glu Phe Tyr Leu Glu Ser Asn Asn Gly Leu Tyr Ala Ser Arg
100                      105                      110

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Gly Phe Arg Glu Ala Ser Lys Pro Val Leu Ser Arg Leu Ser Glu Lys
 115 120
 Thr Asp Val Thr Val Asp Ser Met Tyr Pro Asp Met Phe Trp Gly Ala
 130 135 140
 Ser Leu Asp Arg Asp Asp Val Asn Lys Ile Ser Tyr Ile Phe Asn Ser
 145 150 155 160
 Gln Glu Asp Leu Asp Ala Ala Arg Glu Ala Phe Pro Asn Leu Glu His
 165 170 175
 Thr Thr Trp Gly Gly Gln Thr Gly Ala Leu Phe Gly Thr Ile Gly Val
 180 185 190
 Ser Val Asn Lys Lys Ile Gly Val Asp Arg Leu Leu Lys Tyr Leu Asn
 195 200 205
 Ala Asp Arg Ala Asn Thr Ile Ala Phe Gly Asp Ser Asp Glu Asp Leu
 210 215 220
 Ser Leu Phe Glu Ala Ser Ala Tyr Gly Val Ala Met Gly Glu Ala Thr
 225 230 235 240
 Glu Ser Leu Lys Ala Ala Ala Asp Leu Val Thr Asp Ala Val Gly Gln
 245 250 255
 Asp Gly Leu Arg Asn Ala Phe Leu Lys Leu Glu Leu Ile Asp Ala
 260 265 270

<210> 207

<211> 1470

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}..(1447)

<223> RXN00362

<400> 207

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aacatgctac gggttttttcg gtcacttaaa ggaggcgctt atg gga atc att gct 115
 Met Gly Ile Ile Ala
 1 5

ctg ctc gtt ttt atc gca att gcc gtg ata ttg aat gtg ttt ttg aaa 163
 Leu Leu Val Phe Ile Ala Ile Ala Val Ile Leu Asn Val Phe Leu Lys
 10 15 20

cga gat att tca gaa gca ttg cta gtt gga tta gta gga act gcg ctt 211
 Arg Asp Ile Ser Glu Ala Leu Leu Val Gly Leu Val Gly Thr Ala Leu
 25 30 35

gtc ggc ggt gta aat gca ccg aca tta ctg att gat gct gta gtg gat 259
 Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile Asp Ala Val Val Asp
 40 45 50

gct gct cag tcg gaa gtt act ttc gca ggt atg gcc ttt gtt ttc atg 307

Ala	Ala	Gln	Ser	Glu	Val	Thr	Phe	Ala	Gly	Met	Ala	Phe	Val	Phe	Met	
55						60					65					
ggc	atc	gtt	gtg	caa	tca	act	gga	ttg	att	gat	cga	tta	atc	gca	atc	355
Gly	Ile	Val	Val	Gln	Ser	Thr	Gly	Leu	Ile	Asp	Arg	Leu	Ile	Ala	Ile	
70				75						80					85	
ctt	aac	tcg	att	ttt	ggg	cgg	ctt	cga	ggg	ggc	gca	ggg	tat	gtt	tcc	403
Leu	Asn	Ser	Ile	Phe	Gly	Arg	Leu	Arg	Gly	Gly	Ala	Gly	Tyr	Val	Ser	
				90					95					100		
act	ctt	gga	tct	gcg	ctc	att	gga	ctc	atc	gct	gga	tca	acg	gct	gga	451
Thr	Leu	Gly	Ser	Ala	Leu	Ile	Gly	Leu	Ile	Ala	Gly	Ser	Thr	Ala	Gly	
				105				110					115			
aac	tcc	gcg	acg	gtt	ggc	tca	gtg	acg	atc	cct	tgg	atg	aaa	aag	acg	499
Asn	Ser	Ala	Thr	Val	Gly	Ser	Val	Thr	Ile	Pro	Trp	Met	Lys	Lys	Thr	
				120			125						130			
gga	tgg	act	gct	gaa	agg	tcc	gca	acg	tta	gtc	gcg	ggc	aac	tct	ggc	547
Gly	Trp	Thr	Ala	Glu	Arg	Ser	Ala	Thr	Leu	Val	Ala	Gly	Asn	Ser	Gly	
				135			140					145				
ctt	ggg	gtt	gcg	ttg	cct	ccc	aat	tca	aca	atg	ttc	atc	att	ttg	gca	595
Leu	Gly	Val	Ala	Leu	Pro	Pro	Asn	Ser	Thr	Met	Phe	Ile	Ile	Leu	Ala	
150					155					160					165	
ttg	cca	gct	gca	gca	gct	tct	tcg	gcc	tct	cag	gtg	tac	att	gct	ttg	643
Leu	Pro	Ala	Ala	Ala	Ala	Ser	Ser	Ala	Ser	Gln	Val	Tyr	Ile	Ala	Leu	
				170				175						180		
gct	tgt	ggg	ggg	gcg	tat	gca	gtg	ctc	tac	cgc	tta	gcg	gtc	gtc	ttt	691
Ala	Cys	Gly	Gly	Ala	Tyr	Ala	Val	Leu	Tyr	Arg	Leu	Ala	Val	Val	Phe	
				185				190					195			
tac	tgg	aca	cgt	aaa	gat	aaa	att	cct	gcc	acc	cct	gat	gat	caa	cgg	739
Tyr	Trp	Thr	Arg	Lys	Asp	Lys	Ile	Pro	Ala	Thr	Pro	Asp	Asp	Gln	Arg	
				200			205					210				
gtg	tca	ttc	ggg	gag	gca	atg	aag	act	gga	tgg	cgt	tca	cgg	ttg	atc	787
Val	Ser	Phe	Gly	Glu	Ala	Met	Lys	Thr	Gly	Trp	Arg	Ser	Pro	Leu	Ile	
				215			220					225				
ttc	ctt	gga	att	ttg	atc	ccc	gta	atc	ctc	aca	atc	ggc	cca	ttg	tct	835
Phe	Leu	Gly	Ile	Leu	Ile	Pro	Val	Ile	Leu	Thr	Ile	Gly	Pro	Leu	Ser	
230					235					240					245	
gaa	tgg	tta	aag	aca	cat	gga	gtt	ggg	gag	tct	ggg	gtt	aaa	tcg	atg	883
Glu	Trp	Leu	Lys	Thr	His	Gly	Val	Gly	Glu	Ser	Gly	Val	Lys	Ser	Met	
				250				255						260		
tcg	atc	atc	gtg	tgg	gtg	cca	att	ctg	att	acg	gca	att	gct	ctg	att	931
Ser	Ile	Ile	Val	Trp	Val	Pro	Ile	Leu	Ile	Thr	Ala	Ile	Ala	Leu	Ile	
				265				270					275			
gaa	ggg	cgt	aaa	cga	att	gct	aac	aac	atg	gca	cac	ttt	agg	gtt	cag	979
Glu	Gly	Arg	Lys	Arg	Ile	Ala	Asn	Asn	Met	Ala	His	Thr	Arg	Val	Gln	
				280			285					290				
atc	tcc	aag	gac	ttg	cca	caa	ttt	gcc	acc	gta	gga	att	tcg	ttg	ttt	1027
Ile	Ser	Lys	Asp	Leu	Pro	Gln	Phe	Ala	Thr	Val	Gly	Ile	Ser	Leu	Phe	

295	300	305	
tct gcg ctt gca gca gcg aac atc atg gaa gaa ctg ggt gtt ggc cgg			1075
Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu Leu Gly Val Gly Pro			
310	315	320	325
cag ttg tct aac tgg ctt gat tcc atg gac cta cct aag tct gtc atg			1123
Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu Pro Lys Ser Val Met			
	330	335	340
gtg atc att gtc tgc atc atg tgc att gtg gtg gca acg cca ctg tgc			1171
Val Ile Ile Val Cys Ile Met Cys Ile Val Val Ala Thr Pro Leu Ser			
	345	350	355
tca aca gca acc gcg gct gcg att ggt gct ccc gct gtc gct gcg ttg			1219
Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro Ala Val Ala Ala Leu			
	360	365	370
gct gcg gta ggt att gat cca act gtg gcg atc gta gtg atc ttg ctg			1267
Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile Val Val Ile Leu Leu			
	375	380	385
tgc act tcc act gaa ggt gca tcc cgg ccg gtg ggc gcg ccg att tac			1315
Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val Gly Ala Pro Ile Tyr			
	390	395	400
ctt tct gct gcg atc gcc gat gca aac cca acg aaa atg ttc gta cca			1363
Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr Lys Met Phe Val Pro			
	410	415	420
ctg att acg tac ttt gtt gtc ccc atg att ctg ctt gct tgg cta gtt			1411
Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu Leu Ala Trp Leu Val			
	425	430	435
gga atg gga ttc tta cca gtg att gtt cct acg ggt taaaggggta			1457
Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr Gly			
	440	445	
aaaatgaact caa			1470
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Asn Val Phe Leu Lys Arg Asp Ile Ser Glu Ala Leu Leu Val Gly Leu			
	20	25	30
Val Gly Thr Ala Leu Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile			
	35	40	45
Asp Ala Val Val Asp Ala Ala Gln Ser Glu Val Thr Phe Ala Gly Met			
	50	55	60
Ala Phe Val Phe Met Gly Ile Val Val Gln Ser Thr Gly Leu Ile Asp			
	65	70	75
			80

Arg Leu Ile Ala Ile Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly
 85 90 95
 Ala Gly Tyr Val Ser Thr Leu Gly Ser Ala Leu Ile Gly Leu Ile Ala
 100 105 110
 Gly Ser Thr Ala Gly Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro
 115 120 125
 Trp Met Lys Lys Thr Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val
 130 135 140
 Ala Gly Asn Ser Gly Leu Gly Val Ala Leu Pro Asn Ser Thr Met
 145 150 155 160
 Phe Ile Ile Leu Ala Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln
 165 170 175
 Val Tyr Ile Ala Leu Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg
 180 185 190
 Leu Ala Val Val Phe Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr
 195 200 205
 Pro Asp Asp Gln Arg Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp
 210 215 220
 Arg Ser Pro Leu Ile Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr
 225 230 235 240
 Ile Gly Pro Leu Ser Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser
 245 250 255
 Gly Val Lys Ser Met Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr
 260 265 270
 Ala Ile Ala Leu Ile Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala
 275 280 285
 His Phe Arg Val Gln Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val
 290 295 300
 Gly Ile Ser Leu Phe Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu
 305 310 315 320
 Leu Gly Val Gly Pro Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu
 325 330 335
 Pro Lys Ser Val Met Val Ile Ile Val Cys Ile Met Cys Ile Val Val
 340 345 350
 Ala Thr Pro Leu Ser Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro
 355 360 365
 Ala Val Ala Ala Leu Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile
 370 375 380
 Val Val Ile Leu Leu Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val
 385 390 395 400

Gly Ala Pro Ile Tyr Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr
 405 410 415

Lys Met Phe Val Pro Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu
 420 425 430

Leu Ala Trp Leu Val Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr
 435 440 445

Gly

<210> 209
 <211> 983
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(960)
 <223> FRXA00362

<400> 209
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 Asp Glu Lys Thr Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val Ala
 1 5 10 15

ggc aac tct ggc ctt ggt gtt gcg ttg cct ccc aat tca aca atg ttc 96
 Gly Asn Ser Gly Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met Phe
 20 25 30

atc att ttg gca ttg cca gct gca gca gct tct tcg gcc tct cag gtg 144
 Ile Ile Leu Ala Leu Pro Ala Ala Ala Ser Ser Ala Ser Gln Val
 35 40 45

tac att gct ttg gct tgt ggt ggt gcg tat gca gtg ctc tac cgc tta 192
 Tyr Ile Ala Leu Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg Leu
 50 55 60

gcg gtc gtc ttt tac tgg aca cgt aaa gat aaa att cct gcc acc cct 240
 Ala Val Val Phe Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr Pro
 65 70 75 80

gat gat caa cgg gtg tca ttc ggt gag gca atg aag act gga tgg cgt 288
 Asp Asp Gln Arg Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp Arg
 85 90 95

tca ccg ttg atc ttc ctt gga att ttg atc ccc gta atc ctc aca atc 336
 Ser Pro Leu Ile Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr Ile
 100 105 110

ggc cca ttg tct gaa tgg tta aag aca cat gga gtt ggg gag tct ggt 384
 Gly Pro Leu Ser Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser Gly
 115 120 125

gtt aaa tcg atg tcg atc atc gtg tgg gtg cca att ctg att acg gca 432
 Val Lys Ser Met Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr Ala
 130 135 140

att gct ctg att gaa ggg cgt aaa cga att gct aac aac atg gca cac 480

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Ile Ala Leu Ile Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala His
145          150          155          160

ttt agg gtt cag atc tcc aag gac ttg cca caa ttt gcc acc gta gga    528
Phe Arg Val Gln Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val Gly
          165          170          175

att tcg ttg ttt tct gcg ctt gca gca gcg aac atc atg gaa gaa ctg    576
Ile Ser Leu Phe Ser Ala Leu Ala Ala Asn Ile Met Glu Glu Leu
          180          185          190

ggg gtt ggc ccg cag ttg tct aac tgg ctt gat tcc atg gac cta cct    624
Gly Val Gly Pro Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu Pro
          195          200          205

aag tct gtc atg gtg atc att gtc tgc atc atg tgc att gtg gtg gca    672
Lys Ser Val Met Val Ile Val Val Cys Ile Met Cys Ile Val Val Ala
          210          215          220

acg cca ctg tcg tca aca gca acc gcg gct gcg att ggt gct ccc gct    720
Thr Pro Leu Ser Ser Thr Ala Thr Ala Ala Ile Gly Ala Pro Ala
          225          230          235

gtc gct gcg ttg gct gcg gta ggt att gat cca act gtg gcg atc gta    768
Val Ala Ala Leu Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile Val
          245          250          255

gtg atc ttg ctg tgc act tcc act gaa ggt gca tcc ccg ccg gtg ggc    816
Val Ile Leu Leu Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val Gly
          260          265          270

gcg ccg att tac ctt tct gct gcg atc gcc gat gca aac cca acg aaa    864
Ala Pro Ile Tyr Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr Lys
          275          280          285

atg ttc gta cca ctg att acg tac ttt gtt gtc ccc atg att ctg ctt    912
Met Phe Val Pro Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu Leu
          290          295          300

gct tgg cta gtt gga atg gga ttc tta cca gtg att gtt cct acg ggt    960
Ala Trp Leu Val Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr Gly
          305          310          315

taaaggggta aaaatgaact caa    983

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<210> 210

<211> 320

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 210

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Asp Glu Lys Thr Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val Ala
  1              5              10              15

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Gly Asn Ser Gly Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met Phe
  20              25              30

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Ile Ile Leu Ala Leu Pro Ala Ala Ala Ser Ser Ala Ser Gln Val
  35              40              45

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Tyr Ile Ala Leu Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg Leu
  50                      55                      60

Ala Val Val Phe Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr Pro
  65                      70                      75                      80

Asp Asp Gln Arg Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp Arg
  85                      90                      95

Ser Pro Leu Ile Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr Ile
 100                      105                      110

Gly Pro Leu Ser Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser Gly
 115                      120                      125

Val Lys Ser Met Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr Ala
 130                      135                      140

Ile Ala Leu Ile Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala His
 145                      150                      155                      160

Phe Arg Val Gln Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val Gly
 165                      170                      175

Ile Ser Leu Phe Ser Ala Leu Ala Ala Asn Ile Met Glu Glu Leu
 180                      185                      190

Gly Val Gly Pro Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu Pro
 195                      200                      205

Lys Ser Val Met Val Ile Ile Val Cys Ile Met Cys Ile Val Val Ala
 210                      215                      220

Thr Pro Leu Ser Ser Thr Ala Thr Ala Ala Ile Gly Ala Pro Ala
 225                      230                      235                      240

Val Ala Ala Leu Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile Val
 245                      250                      255

Val Ile Leu Leu Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val Gly
 260                      265                      270

Ala Pro Ile Tyr Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr Lys
 275                      280                      285

Met Phe Val Pro Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu Leu
 290                      295                      300

Ala Trp Leu Val Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr Gly
 305                      310                      315                      320

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<210> 211

<211> 439

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(439)

<223> RXN00373

<400> 211

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cgaaaagcgt cttaaaaggt ttttactag ggtgtgtcc atg gac atc cag cag 115
 Met Asp Ile Gln Gln
 1 5

cta gac gcc gaa aca aca gca tgg aaa gac agc ctc ctg cgc gcc gca 163
 Leu Asp Ala Gly Phe His Thr Ala Trp Lys Asp Ser Leu Leu Arg Ala Ala
 10 15 20

cag gag gct ggt ttt cat ttt gag cca ccg aaa ctc ttc gag gat ttt 211
 Gln Glu Ala Gly Phe His Phe Glu Pro Pro Lys Leu Phe Glu Asp Phe
 25 30 35

gag acc atg gtg gag cag tac aag cag gca gct gcg agc gac ccg gac 259
 Glu Thr Met Val Glu Gln Tyr Lys Gln Ala Ala Ala Ser Asp Pro Asp
 40 45 50

att gat gtc act gat att cag caa atg tgg ggc atc gtg gtg ggg gag 307
 Ile Asp Val Thr Asp Ile Gln Gln Met Trp Gly Ile Val Val Gly Glu
 55 60 65

tac ctg cgc gaa aaa atg ggc atg gaa tgg gtc gtc atc acc gat gac 355
 Tyr Leu Arg Glu Lys Met Gly Met Glu Trp Val Val Ile Thr Asp Asp
 70 75 80 85

tac ggc act gac ctc gcg att cta gcc acg gca ccc aac ggg gac cac 403
 Tyr Gly Thr Asp Leu Ala Ile Leu Ala Thr Ala Pro Asn Gly Asp His
 90 95 100

gta tat tcc tgc ccc atc atc gtg gtg ggc aag cgc 439
 Val Tyr Ser Cys Pro Ile Ile Val Val Gly Lys Arg
 105 110

<210> 212

<211> 113

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 212

Met Asp Ile Gln Gln Leu Asp Ala Glu Thr Thr Ala Trp Lys Asp Ser

1

5

10

15

Leu Leu Arg Ala Ala Gln Glu Ala Gly Phe His Phe Glu Pro Pro Lys

20

25

30

Leu Phe Glu Asp Phe Glu Thr Met Val Glu Gln Tyr Lys Gln Ala Ala

35

40

45

Ala Ser Asp Pro Asp Ile Asp Val Thr Asp Ile Gln Gln Met Trp Gly

50

55

60

Ile Val Val Gly Glu Tyr Leu Arg Glu Lys Met Gly Met Glu Trp Val

65

70

75

80

Val Ile Thr Asp Asp Tyr Gly Thr Asp Leu Ala Ile Leu Ala Thr Ala
85 95

Pro Asn Gly Asp His Val Tyr Ser Cys Pro Ile Ile Val Val Gly Lys
100 105 110

Arg

<210> 213

<211> 439

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(439)

<223> FRXA00373

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cgaaaaagcgt cttaaaaggt ttttactag ggtgttgtcc atg gac atc cag cag 115
Met Asp Ile Gln Gln
1 5

cta gac gcc gaa aca aca gca tgg aaa gac agc ctc ctg cgc gcc gca 163
Leu Asp Ala Glu Thr Thr Ala Trp Lys Asp Ser Leu Leu Arg Ala Ala
10 15 20

cag gag gct ggt ttt cat ttt gag cca ccg aaa ctc ttc gag gat ttt 211
Gln Glu Ala Gly Phe His Phe Glu Pro Pro Lys Leu Phe Glu Asp Phe
25 30 35

gag acc atg gtg gag cag tac aag cag gca gct gcg agc gac ccg gac 259
Glu Thr Met Val Glu Gln Tyr Lys Gln Ala Ala Ala Ser Asp Pro Asp
40 45 50

att gat gtc act gat att cag caa atg tgg ggc atc gtg gtg ggg gag 307
Ile Asp Val Thr Asp Ile Gln Gln Met Trp Gly Ile Val Val Gly Glu
55 60 65

tac ctg cgc gaa aaa atg ggc atg gaa tgg gtc gtc atc acc gat gac 355
Tyr Leu Arg Glu Lys Met Gly Met Glu Trp Val Val Ile Thr Asp Asp
70 75 80 85

tac ggc act gac ctc gcg att cta gcc acg gca ccc aac ggg gac cac 403
Tyr Gly Thr Asp Leu Ala Ile Leu Ala Thr Ala Pro Asn Gly Asp His
90 95 100

gta tat tcc tgc ccc atc atc gtg gtg ggc aag cgc 439
Val Tyr Ser Cys Pro Ile Ile Val Val Gly Lys Arg
105 110

<210> 214

<211> 113

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 214

Met Asp Ile Gln Gln Leu Asp Ala Glu Thr Thr Ala Trp Lys Asp Ser
 1 5 10 15

Leu Leu Arg Ala Ala Gln Glu Ala Gly Phe His Phe Glu Pro Pro Lys
 20 25 30

Leu Phe Glu Asp Phe Glu Thr Met Val Glu Gln Tyr Lys Gln Ala Ala
 35 40 45

Ala Ser Asp Pro Asp Ile Asp Val Thr Asp Ile Gln Gln Met Trp Gly
 50 55 60

Ile Val Val Gly Glu Tyr Leu Arg Glu Lys Met Gly Met Glu Trp Val
 65 70 75 80

Val Ile Thr Asp Asp Tyr Gly Thr Asp Leu Ala Ile Leu Ala Thr Ala
 85 90 95

Pro Asn Gly Asp His Val Tyr Ser Cys Pro Ile Ile Val Val Gly Lys
 100 105 110

Arg

<210> 215

<211> 528

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(505)

<223> RXN00390

<400> 215

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tagttgacac ggaaactaat tcattctagc tttagtgacc atg tca act acc agg 115
 Met Ser Thr Thr Arg
 1 5

gaa att gca ttc ctc atc gca cgt atc ctc ttg ggc gtc atc ctc atc 163
 Glu Ile Ala Phe Leu Ile Ala Arg Ile Leu Leu Gly Val Ile Leu Ile
 10 15 20

gcc cac ggc tgg gac aag ttc gcc atc aca gga ctt gaa ggc gtc acc 211
 Ala His Gly Trp Asp Lys Phe Ala Ile Thr Gly Leu Glu Gly Val Thr
 25 30 35

ggc ttc ttc gat tca ctc ggc atc cca gca gcc ggc atc gcc gca ata 259
 Gly Phe Phe Asp Ser Leu Gly Ile Pro Ala Ala Gly Ile Ala Ala Ile
 40 45 50

gct gct gca gtc gtc gag ctc cta gga gga atc ctt atc atc cta gga 307
 Ala Ala Ala Val Val Glu Leu Leu Gly Gly Ile Leu Ile Leu Gly
 55 60 65

gta ttt acc cgc atc gtt gcc gcc ttc gtt gcc ata gac atg ctc ttc 355
 Val Phe Thr Arg Ile Val Ala Ala Phe Val Ala Ile Asp Met Leu Phe

70	75	80	85	
gca gca ctg ttt gcg cac gtc tcc tcc ggc atc ttt gtc acc aac aat				403
Ala Ala Leu Phe Ala His Val Ser Ser Gly Ile Phe Val Thr Asn Asn	90	95	100	
ggt tgg gaa ctc acc ggc gca atc ggc gct ggc gcg ctg ctt ctc atc				451
Gly Trp Glu Leu Thr Gly Ala Ile Gly Ala Gly Ala Leu Leu Leu Ile	105	110	115	
gca gtt ggc gca agt gca tgg agc atc gac ggg gtt ctg gca aaa cgc				499
Ala Val Gly Ala Ser Ala Trp Ser Ile Asp Gly Val Leu Ala Lys Arg	120	125	130	
aag gcc taaatctagc gccacaactc cga				528
Lys Ala				
135				

<210> 216

<211> 135

<212> PRT

<213> Corynebacterium glutamicum

<400> 216

Met Ser Thr Thr Arg Glu Ile Ala Phe Leu Ile Ala Arg Ile Leu Leu			
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Gly Val Ile Leu Ile Ala His Gly Trp Asp Lys Phe Ala Ile Thr Gly			
20 25 30			

Leu Glu Gly Val Thr Gly Phe Phe Asp Ser Leu Gly Ile Pro Ala Ala			
35 40 45			

Gly Ile Ala Ala Ile Ala Ala Val Val Glu Leu Leu Gly Gly Ile			
50 55 60			

Leu Ile Ile Leu Gly Val Phe Thr Arg Ile Val Ala Ala Phe Val Ala			
65 70 75 80			

Ile Asp Met Leu Phe Ala Ala Leu Phe Ala His Val Ser Ser Gly Ile			
85 90 95			

Phe Val Thr Asn Asn Gly Trp Glu Leu Thr Gly Ala Ile Gly Ala Gly			
100 105 110			

Ala Leu Leu Leu Ile Ala Val Gly Ala Ser Ala Trp Ser Ile Asp Gly			
115 120 125			

Val Leu Ala Lys Arg Lys Ala	
130 135	

<210> 217

<211> 528

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> {101}..(505)

Leu Glu Gly Val Thr Gly Phe Phe Asp Ser Leu Gly Ile Pro Ala Ala
35 40 45

Gly Ile Ala Ala Ile Ala Ala Ala Val Val Glu Leu Leu Gly Gly Ile
 50 55 60
 Leu Ile Ile Leu Gly Val Phe Thr Arg Ile Val Ala Ala Phe Val Ala
 65 70 75 80
 Ile Asp Met Leu Phe Ala Ala Leu Phe Ala His Val Ser Ser Gly Ile
 85 90 95
 Phe Val Thr Asn Asn Gly Trp Glu Leu Thr Gly Ala Ile Gly Ala Gly
 100 105 110
 Ala Leu Leu Leu Ile Ala Val Gly Ala Ser Ala Trp Ser Ile Asp Gly
 115 120 125
 Val Leu Ala Lys Arg Lys Ala
 130 135

<210> 219
 <211> 438
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(415)
 <223> RXN00399

<400> 219
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 attcaatgat tttcttttcc cacaggccta aacttaaatc atg agc cac aac gac 115
 Met Ser His Asn Asp
 1 5
 agc cca aac ttt gct cgc cga gcg ctc aat tgg ctc cgc caa ggt tat 163
 Ser Pro Asn Phe Ala Arg Arg Ala Leu Asn Trp Leu Arg Gln Gly Tyr
 10 15 20
 cca acc ggt gtt ccg cgg cac gat act ttc gct ctg ttt tac gtt ttg 211
 Pro Thr Gly Val Pro Arg His Asp Thr Phe Ala Leu Phe Tyr Val Leu
 25 30 35
 gag cgc gaa ctt act gag gaa gat ctc aat gag ctc gca gag ctt ctc 259
 Glu Arg Glu Leu Thr Glu Glu Asp Leu Asn Glu Leu Ala Glu Leu Leu
 40 45 50
 atc gcg gaa ggt gag aac aat ggg ctg cac gat aat ccc att acg cgt 307
 Ile Ala Glu Gly Glu Asn Asn Gly Leu His Asp Asn Pro Ile Thr Arg
 55 60 65
 gaa aaa atc ggc aag ctg atc acg cat gtt cac agt cag cca cct gag 355
 Glu Lys Ile Gly Lys Leu Ile Thr His Val His Ser Gln Pro Pro Glu
 70 75 80 85
 gat gaa gac atc gat cga att cag aaa aag ctg cag gct gag ggc ttc 403
 Asp Glu Asp Ile Asp Arg Ile Gln Lys Lys Leu Gln Ala Glu Gly Phe
 90 95 100
 ccc acc cgc aat taattaattg gagttttgtt gtt 438

Pro Thr Arg Asn
105

<210> 220

<211> 105

<212> PRT

<213> Corynebacterium glutamicum

<400> 220

Met Ser His Asn Asp Ser Pro Asn Phe Ala Arg Arg Ala Leu Asn Trp
1 5 10 15

Leu Arg Gln Gly Tyr Pro Thr Gly Val Pro Arg His Asp Thr Phe Ala
20 25 30

Leu Phe Tyr Val Leu Glu Arg Glu Leu Thr Glu Glu Asp Leu Asn Glu
35 40 45

Leu Ala Glu Leu Leu Ile Ala Glu Gly Glu Asn Asn Gly Leu His Asp
50 55 60

Asn Pro Ile Thr Arg Glu Lys Ile Gly Lys Leu Ile Thr His Val His
65 70 75 80

Ser Gln Pro Pro Glu Asp Glu Asp Ile Asp Arg Ile Gln Lys Lys Leu
85 90 95

Gln Ala Glu Gly Phe Pro Thr Arg Asn
100 105

<210> 221

<211> 438

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(415)

<223> FRXA00399

<400> 221

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attcaatgat tttcttttcc cacaggccta aacttaaatc atg agc cac aac gac 115
Met Ser His Asn Asp
1 5

agc cca aac ttt get cgc cga gcg ctc aat tgg ctc cgc caa ggt tat 163
Ser Pro Asn Phe Ala Arg Arg Ala Leu Asn Trp Leu Arg Gln Gly Tyr
10 15 20

cca acc ggt gtt ccg cgg cac gat act ttc gct ctg ttt tac gtt ttg 211
Pro Thr Gly Val Pro Arg His Asp Thr Phe Ala Leu Phe Tyr Val Leu
25 30 35

gag cgc gaa ctt act gag gaa gat ctc aat gag ctc gca gag ctt ctc 259
Glu Arg Glu Leu Thr Glu Glu Asp Leu Asn Glu Leu Ala Glu Leu Leu
40 45 50

atc gcg gaa ggt gag aac aat ggg ctg cac gat aat ccc att acg cgt 307
 ile ala glu gly glu asn asn gly leu his asp asn pro ile thr arg
 55 60 65

gaa aaa atc ggc aag ctg atc acg cat gtt cac agt cag cca cct gag 355
 glu lys ile gly lys leu ile thr his val his ser gln pro pro glu
 70 75 80 85

gat gaa gac atc gat cga att cag aaa aag ctg cag gct gag ggc ttc 403
 asp glu asp ile asp arg ile gln lys lys leu gln ala glu gly phe
 90 95 100

ccc acc cgc aat taattaattg gagttttgtt gtt 438
 pro thr arg asn
 105

<210> 222

<211> 105

<212> PRT

<213> Corynebacterium glutamicum

<400> 222

Met Ser His Asn Asp Ser Pro Asn Phe Ala Arg Arg Ala Leu Asn Trp
 1 5 10 15

Leu Arg Gln Gly Tyr Pro Thr Gly Val Pro Arg His Asp Thr Phe Ala
 20 25 30

Leu Phe Tyr Val Leu Glu Arg Glu Leu Thr Glu Glu Asp Leu Asn Glu
 35 40 45

Leu Ala Glu Leu Leu Ile Ala Glu Gly Glu Asn Asn Gly Leu His Asp
 50 55 60

Asn Pro Ile Thr Arg Glu Lys Ile Gly Lys Leu Ile Thr His Val His
 65 70 75 80

Ser Gln Pro Pro Glu Asp Glu Asp Ile Asp Arg Ile Gln Lys Lys Leu
 85 90 95

Gln Ala Glu Gly Phe Pro Thr Arg Asn
 100 105

<210> 223

<211> 1673

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1650)

<223> RXN00416

<400> 223
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 leu ala ser tyr leu ser pro thr ala leu val val ala val leu ala
 1 5 10 15

att ccg ctg tct gcg acc cgc ctg tat ttg gac gga atc agc gtt gac 96

Ile	Pro	Leu	Ser	Ala	Thr	Arg	Leu	Tyr	Leu	Asp	Gly	Ile	Ser	Val	Asp		
			20					25					30				
cag	ggc	ttt	aga	act	cag	ttt	tta	acc	cgc	atg	gct	gac	gat	atc	ggc	144	
Gln	Gly	Phe	Arg	Thr	Gln	Phe	Leu	Thr	Arg	Met	Ala	Asp	Asp	Ile	Gly		
		35					40					45					
ttg	tcg	gac	atg	aac	tac	atc	gat	atg	oct	acc	ttc	tac	oct	gct	gga	192	
Leu	Ser	Asp	Met	Asn	Tyr	Ile	Asp	Met	Pro	Thr	Phe	Tyr	Pro	Ala	Gly		
		50				55					60						
tgg	ttc	tgg	ctc	ggg	ggg	cgc	ttg	gcc	aat	ctt	ttg	ggg	ctg	ccc	ggg	240	
Trp	Phe	Trp	Leu	Gly	Gly	Arg	Leu	Ala	Asn	Leu	Gly	Leu	Pro	Gly			
					70					75				80			
tgg	gaa	gct	ttc	cag	cca	tgg	gca	att	gtg	tcc	atg	gca	ggt	gct	gct	288	
Trp	Glu	Ala	Phe		Pro	Trp	Ala	Ile	Val	Ser	Met	Ala	Val	Ala	Ala		
				85					90					95			
tct	gtg	tta	gtt	cca	gtg	tgg	cag	cgc	atc	acc	ggg	tcc	ctg	ccg	gtg	336	
Ser	Val	Leu	Val	Pro	Val	Trp	Gln	Arg	Ile	Thr	Gly	Ser	Leu	Pro	Val		
			100					105					110				
gca	aca	ggc	att	gcg	ttg	gtg	aca	acc	tgc	att	atc	ttg	gcg	atg	aat	384	
Ala	Thr	Gly	Ile	Ala	Leu	Val	Thr	Thr	Cys	Ile	Ile	Leu	Ala	Met	Asn		
			115				120					125					
tcc	gaa	gag	ccc	tac	gct	gca	atc	ggt	gcg	atg	ggg	att	cca	gcg	atg	432	
Ser	Glu	Glu	Pro	Tyr	Ala	Ala	Ile	Val	Ala	Met	Gly	Ile	Pro	Ala	Met		
			130			135					140						
ctc	gtg	ctg	gct	tcc	cgc	att	gcc	aag	ggc	gat	aag	ttt	gcg	ctt	gcc	480	
Leu	Val	Leu	Ala	Ser	Arg	Ile	Ala	Lys	Gly	Asp	Lys	Phe	Ala	Leu	Ala		
					150					155				160			
ggc	ggc	att	att	tac	ttg	ggg	gtt	tcg	gct	act	ttc	tat	act	ttg	ttc	528	
Gly	Gly	Ile	Ile	Tyr	Leu	Gly	Val	Ser	Ala	Thr	Phe	Tyr	Thr	Leu	Phe		
				165				170						175			
acc	ggg	gct	atc	gcg	ctt	tct	gcg	gtc	gcg	gtg	tgc	atc	gtg	gtg	gcg	576	
Thr	Gly	Ala	Ile	Ala	Leu	Ser	Ala	Val	Ala	Val	Cys	Ile	Val	Val	Ala		
			180					185					190				
gct	att	gtg	cag	cgc	tcc	atc	aaa	cca	ctg	ctg	tgg	ctt	gca	gtg	ctg	624	
Ala	Ile	Val	Gln	Arg	Ser	Ile	Lys	Pro	Leu	Leu	Trp	Leu	Ala	Val	Leu		
			195			200						205					
ggg	ggg	gga	tcc	att	gtc	att	gcg	ttg	att	tct	tgg	ggg	oct	tac	ctt	672	
Gly	Gly	Gly	Ser	Ile	Val	Ile	Ala	Leu	Ile	Ser	Trp	Gly	Pro	Tyr	Leu		
			210			215					220						
ctg	gcc	tcc	atc	aac	gga	gcg	gag	cgc	tct	ggc	gat	tcc	gca	aca	cac	720	
Leu	Ala	Ser	Ile	Asn	Gly	Ala	Glu	Arg	Ser	Gly	Asp	Ser	Ala	Thr	His		
					230					235				240			
tac	ctg	cct	ctt	gaa	ggc	acc	caa	ttc	ccg	gtt	oct	ttc	ttg	gca	tca	768	
Tyr	Leu	Pro	Leu	Glu	Gly	Thr	Gln	Phe	Pro	Val	Pro	Phe	Leu	Ala	Ser		
				245				250						255			
agc	gtt	gtg	gga	ctg	ttg	tgt	ctt	gtt	ggc	ctg	atc	tat	ttg	gtg	gtg	816	
Ser	Val	Val	Gly	Leu	Leu	Cys	Leu	Val	Gly	Leu	Ile	Tyr	Leu	Val	Val		

260										265										270										
cgt	ttc	cac	aac	aat	gag	gtg	cgc	gcg	atg	tgg	gtc	ggc	atc	gca	gtg	864														
Arg	Phe	His	Asn	Asn	Glu	Val	Arg	Ala	Met	Trp	Val	Gly	Ile	Ala	Val															
		275					280					285																		
ttt	tat	gcc	tgg	atg	ggc	atg	tcc	atg	gcg	atc	acg	ctt	ttg	ggc	aac	912														
Phe	Tyr	Ala	Trp	Met	Gly	Met	Ser	Met	Ala	Ile	Thr	Leu	Leu	Gly	Asn															
		290				295					300																			
acg	ttg	ctt	gga	ttc	cgt	ctt	gat	acg	gtg	ctg	gtg	ctt	att	ttt	gcc	960														
Thr	Leu	Leu	Gly	Phe	Arg	Leu	Asp	Thr	Val	Leu	Val	Leu	Ile	Phe	Ala															
		305				310					315				320															
acg	gct	gga	gtg	ttg	ggc	att	gca	gat	ttc	cgc	ctt	gcc	agt	gtg	tat	1008														
Thr	Ala	Gly	Val	Leu	Gly	Ile	Ala	Asp	Phe	Arg	Leu	Ala	Ser	Val	Tyr															
				325					330					335																
cag	ctc	tac	ccc	acc	caa	atc	aca	gag	cgc	acg	gcc	acc	cat	ctg	acc	1056														
Gln	Leu	Tyr	Pro	Thr	Gln	Ile	Thr	Glu	Arg	Thr	Ala	Thr	His	Leu	Thr															
			340						345					350																
aat	cta	att	gtg	gtc	ctc	gtg	ctg	ctt	ggc	ggc	ctc	tac	tac	gcg	caa	1104														
Asn	Leu	Ile	Val	Val	Leu	Val	Leu	Leu	Gly	Gly	Leu	Tyr	Tyr	Ala	Gln															
			355				360							365																
gat	ctg	ccg	cag	aag	aac	gca	cga	gct	atc	gat	ctg	gcc	tat	acc	gat	1152														
Asp	Leu	Pro	Gln	Lys	Asn	Ala	Arg	Ala	Ile	Asp	Leu	Ala	Tyr	Thr	Asp															
			370				375						380																	
act	gat	ggc	tac	ggc	gag	cgc	gcg	gat	ctg	tat	ccg	gcc	gga	gct	gca	1200														
Thr	Asp	Gly	Tyr	Gly	Glu	Arg	Ala	Asp	Leu	Tyr	Pro	Ala	Gly	Ala	Ala															
		385				390					395				400															
cgt	tat	tac	aag	gac	atc	aac	gat	cat	ctg	ctt	gat	caa	gga	ttc	gag	1248														
Arg	Tyr	Tyr	Lys	Asp	Ile	Asn	Asp	His	Leu	Leu	Asp	Gln	Gly	Phe	Glu															
			405						410					415																
cct	tcc	gaa	act	gtc	gtg	ctg	aca	gac	gaa	ctc	gat	ttc	atg	tcc	tac	1296														
Pro	Ser	Glu	Thr	Val	Val	Leu	Thr	Asp	Glu	Leu	Asp	Phe	Met	Ser	Tyr															
			420						425					430																
tac	cct	tat	cgc	gga	tac	caa	gct	ttt	act	tcc	cac	tac	gcc	aac	ccg	1344														
Tyr	Pro	Tyr	Arg	Gly	Tyr	Gln	Ala	Phe	Thr	Ser	His	Tyr	Ala	Asn	Pro															
			435				440						445																	
ctt	ggt	gag	ttc	gga	aac	agg	aac	gca	ttc	atc	gaa	gat	ctc	gcg	atc	1392														
Leu	Gly	Glu	Phe	Gly	Asn	Arg	Asn	Ala	Phe	Ile	Glu	Asp	Leu	Ala	Ile															
			450				455					460																		
cga	agc	tgg	gat	gag	ttg	gct	gat	cct	caa	caa	ttc	agc	gac	gcc	ttg	1440														
Arg	Ser	Trp	Asp	Glu	Leu	Ala	Asp	Pro	Gln	Gln	Phe	Ser	Asp	Ala	Leu															
		465				470					475				480															
aac	acc	tct	cca	tgg	acg	atc	cct	gag	gtg	ttc	atc	ttc	cgt	ggc	tcc	1488														
Asn	Thr	Ser	Pro	Trp	Thr	Ile	Pro	Glu	Val	Phe	Ile	Phe	Arg	Gly	Ser															
			485						490					495																
atc	gat	gat	cct	gac	gcc	ggt	tgg	aaa	tac	gac	gtg	gct	gaa	gat	ctg	1536														
Ile	Asp	Asp	Pro	Asp	Ala	Gly	Trp	Lys	Tyr	Asp	Val	Ala	Glu	Asp	Leu															
			500					505					510																	

tac ccg aac aat cca aac gtg cgc ttc cgc ggc gtg tac ttt aac ccg 1584
 Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro
 515 520 525
 gag tca ttt gat cag atg tgg cag acc aag caa gtg gga cct ttc gtg 1632
 Glu Ser Phe Asp Gln Met Trp Gln Thr Lys Gln Val Gly Pro Phe Val
 530 535 540
 gtg gta acg cac aat gag taattcctca ccaaacgacc caa 1673
 Val Val Thr His Asn Glu
 545 550

<210> 224

<211> 550

<212> PRT

<213> Corynebacterium glutamicum

<400> 224

Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala
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Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp
 20 25 30

Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly
 35 40 45

Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly
 50 55 60

Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly
 65 70 75 80

Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala
 85 90 95

Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val
 100 105 110

Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn
 115 120 125

Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met
 130 135 140

Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala
 145 150 155 160

Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe
 165 170 175

Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala
 180 185 190

Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu
 195 200 205

Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu
 210 215 220

Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His
 225 230 235 240
 Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser
 245 250 255
 Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val
 260 265 270
 Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val
 275 280 285
 Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn
 290 295 300
 Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala
 305 310 315 320
 Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr
 325 330 335
 Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr
 340 345 350
 Asn Leu Ile Val Val Leu Val Leu Leu Gly Gly Leu Tyr Tyr Ala Gln
 355 360 365
 Asp Leu Pro Gln Lys Asn Ala Arg Ala Ile Asp Leu Ala Tyr Thr Asp
 370 375 380
 Thr Asp Gly Tyr Gly Glu Arg Ala Asp Leu Tyr Pro Ala Gly Ala Ala
 385 390 395 400
 Arg Tyr Tyr Lys Asp Ile Asn Asp His Leu Leu Asp Gln Gly Phe Glu
 405 410 415
 Pro Ser Glu Thr Val Val Leu Thr Asp Glu Leu Asp Phe Met Ser Tyr
 420 425 430
 Tyr Pro Tyr Arg Gly Tyr Gln Ala Phe Thr Ser His Tyr Ala Asn Pro
 435 440 445
 Leu Gly Glu Phe Gly Asn Arg Asn Ala Phe Ile Glu Asp Leu Ala Ile
 450 455 460
 Arg Ser Trp Asp Glu Leu Ala Asp Pro Gln Gln Phe Ser Asp Ala Leu
 465 470 475 480
 Asn Thr Ser Pro Trp Thr Ile Pro Glu Val Phe Ile Phe Arg Gly Ser
 485 490 495
 Ile Asp Asp Pro Asp Ala Gly Trp Lys Tyr Asp Val Ala Glu Asp Leu
 500 505 510
 Tyr Pro Asn Asn Pro Asn Val Arg Phe Arg Gly Val Tyr Phe Asn Pro
 515 520 525
 Glu Ser Phe Asp Gln Met Trp Gln Thr Lys Gln Val Gly Pro Phe Val
 530 535 540

Val Val Thr His Asn Glu
545 550

<210> 225

<211> 350

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(327)

<223> FRXA00416

<400> 225

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Thr Ser His Tyr Ala Asn Pro Leu Gly Glu Phe Gly Asn Arg Asn Ala
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ttc atc gaa gat ctc gcg atc cga agc tgg aat gag ttg gct gat cct 96
Phe Ile Glu Asp Leu Ala Ile Arg Ser Trp Asn Glu Leu Ala Asp Pro
20 25 30

caa caa ttc agc gac gcc ttg aac acc tct cca tgg acg atc cct gag 144
Gln Gln Phe Ser Asp Ala Leu Asn Thr Ser Pro Trp Thr Ile Pro Glu
35 40 45

gtg ttc atc ttc cgt ggc tcc atc gat gat cct gac gcc ggt tgg aaa 192
Val Phe Ile Phe Arg Gly Ser Ile Asp Asp Pro Asp Ala Gly Trp Lys
50 55 60

tac gat gtg gct gaa gat ctg tac ccg aac aat cca aac gtg cgc ttc 240
Tyr Asp Val Ala Glu Asp Leu Tyr Pro Asn Asn Pro Asn Val Arg Phe
65 70 75 80

cgc ggc gtg tac ttt aac ccg gag tca ttt gat cag atg tgg cag acc 288
Arg Gly Val Tyr Phe Asn Pro Glu Ser Phe Asp Gln Met Trp Gln Thr
85 90 95

aag caa gtg gga cct ttc gtg gtg gta acg cac aat gag taattcctca 337
Lys Gln Val Gly Pro Phe Val Val Val Thr His Asn Glu
100 105

ccaaacgacc caa 350

<210> 226

<211> 109

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 226

Thr Ser His Tyr Ala Asn Pro Leu Gly Glu Phe Gly Asn Arg Asn Ala
1 5 10 15

Phe Ile Glu Asp Leu Ala Ile Arg Ser Trp Asn Glu Leu Ala Asp Pro
20 25 30

Gln Gln Phe Ser Asp Ala Leu Asn Thr Ser Pro Trp Thr Ile Pro Glu
35 40 45

Val Phe Ile Phe Arg Gly Ser Ile Asp Asp Pro Asp Ala Gly Trp Lys
 50 55 60
 Tyr Asp Val Ala Glu Asp Leu Tyr Pro Asn Asn Pro Asn Val Arg Phe
 65 70 75 80
 Arg Gly Val Tyr Phe Asn Pro Glu Ser Phe Asp Gln Met Trp Gln Thr
 85 90 95
 Lys Gln Val Gly Pro Phe Val Val Val Thr His Asn Glu
 100 105

<210> 227

<211> 1065

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1065)

<223> FRXA00418

<400> 227

ctg gcg tct tac tta agc cca act gcg ctg gtg gtt gcg gtg ttg gct 48
 Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala
 1 5 10 15
 att ccg ctg tct gcg acc cgc ctg tat ttg gac gga atc agc gtt gac 96
 Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp
 20 25 30
 cag ggc ttt aga act cag ttt tta acc cgc atg gct gac gat atc ggc 144
 Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly
 35 40 45
 ttg tcg gac atg aac tac atc gat atg cct acc ttc tac cct gct gga 192
 Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly
 50 55 60
 tgg ttc tgg ctc ggt ggt cgc ttg gcc aat ctt ttg ggg ctg ccc ggt 240
 Trp Phe Trp Leu Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly
 65 70 75 80
 tgg gaa gct ttc cag cca tgg gca att gtg tcc atg gca gtt gct gct 288
 Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala
 85 90 95
 tct gtg tta gtt cca gtg tgg cag cgc atc acc ggt tcc ctg ccg gtg 336
 Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val
 100 105 110
 gca aca ggc att gcg ttg gtg aca acc tgc att atc ttg gcg atg aat 384
 Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn
 115 120 125
 tcc gaa gag ccc tac gct gca atc gtt gcg atg ggt att cca gcg atg 432
 Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met
 130 135 140
 ctc gtg ctg gct tcc cgc att gcc aag ggc gat aag ttt gcg ctt gcc 480

Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala
 145 150 155 160
 ggc ggc att att tac ttg ggt gtt tcg gct act ttc tat act ttg ttc 528
 Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe
 165 170 175
 acc ggt gct atc gcg ctt tct gcg gtc gcg gtg tgc atc gtg gtg gcg 576
 Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala
 180 185 190
 gct att gtg cag cgc tcc atc aaa cca ctg ctg tgg ctt gca gtg ctg 624
 Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Trp Gly Ala Val Leu
 195 200 205
 ggt ggt gga tcc att gtc att gcg ttg att tct tgg ggt cct tac ctt 672
 Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu
 210 215 220
 ctg gcc tcc atc aac gga gcg gag cgc tct ggc gat tcc gca aca cac 720
 Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His
 225 230 235 240
 tac ctg cct ctt gaa ggc acc caa ttc ccg gtt cct ttc ttg gca tca 768
 Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser
 245 250 255
 agc gtt gtg gga ctg ttg tgt ctt gtt ggc ctg atc tat ttg gtg gtg 816
 Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val
 260 265 270
 cgt ttc cac aac aat gag gtg gcg gcg atg tgg gtc ggc atc gca gtg 864
 Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val
 275 280 285
 ttt tat gcc tgg atg ggc atg tcc atg gcg atc acg ctt ttg ggc aac 912
 Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn
 290 295 300
 acg ttg ctt gga ttc cgt ctt gat acg gtg ctg gtg ctt att ttt gcc 960
 Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala
 305 310 315 320
 acg gct gga gtg ttg ggc att gca gat ttc gcg ctt gcc agt gtg tat 1008
 Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr
 325 330 335
 cag ctc tac ccc acc caa atc aca gag gcg acc gcc cat ctg acc 1056
 Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr
 340 345 350
 aat cta att 1065
 Asn Leu Ile
 355

<210> 228

<211> 355

<212> PRT

<213> Corynebacterium glutamicum

<400> 228

Leu Ala Ser Tyr Leu Ser Pro Thr Ala Leu Val Val Ala Val Leu Ala
 1 5 10 15

Ile Pro Leu Ser Ala Thr Arg Leu Tyr Leu Asp Gly Ile Ser Val Asp
 20 25 30

Gln Gly Phe Arg Thr Gln Phe Leu Thr Arg Met Ala Asp Asp Ile Gly
 35 40 45

Leu Ser Asp Met Asn Tyr Ile Asp Met Pro Thr Phe Tyr Pro Ala Gly
 50 55 60

Trp Phe Trp Leu Gly Gly Arg Leu Ala Asn Leu Leu Gly Leu Pro Gly
 65 70 75 80

Trp Glu Ala Phe Gln Pro Trp Ala Ile Val Ser Met Ala Val Ala Ala
 85 90 95

Ser Val Leu Val Pro Val Trp Gln Arg Ile Thr Gly Ser Leu Pro Val
 100 105 110

Ala Thr Gly Ile Ala Leu Val Thr Thr Cys Ile Ile Leu Ala Met Asn
 115 120 125

Ser Glu Glu Pro Tyr Ala Ala Ile Val Ala Met Gly Ile Pro Ala Met
 130 135 140

Leu Val Leu Ala Ser Arg Ile Ala Lys Gly Asp Lys Phe Ala Leu Ala
 145 150 155 160

Gly Gly Ile Ile Tyr Leu Gly Val Ser Ala Thr Phe Tyr Thr Leu Phe
 165 170 175

Thr Gly Ala Ile Ala Leu Ser Ala Val Ala Val Cys Ile Val Val Ala
 180 185 190

Ala Ile Val Gln Arg Ser Ile Lys Pro Leu Leu Trp Leu Ala Val Leu
 195 200 205

Gly Gly Gly Ser Ile Val Ile Ala Leu Ile Ser Trp Gly Pro Tyr Leu
 210 215 220

Leu Ala Ser Ile Asn Gly Ala Glu Arg Ser Gly Asp Ser Ala Thr His
 225 230 235 240

Tyr Leu Pro Leu Glu Gly Thr Gln Phe Pro Val Pro Phe Leu Ala Ser
 245 250 255

Ser Val Val Gly Leu Leu Cys Leu Val Gly Leu Ile Tyr Leu Val Val
 260 265 270

Arg Phe His Asn Asn Glu Val Arg Ala Met Trp Val Gly Ile Ala Val
 275 280 285

Phe Tyr Ala Trp Met Gly Met Ser Met Ala Ile Thr Leu Leu Gly Asn
 290 295 300

Thr Leu Leu Gly Phe Arg Leu Asp Thr Val Leu Val Leu Ile Phe Ala
 305 310 315 320

Thr Ala Gly Val Leu Gly Ile Ala Asp Phe Arg Leu Ala Ser Val Tyr
 325 330 335

Gln Leu Tyr Pro Thr Gln Ile Thr Glu Arg Thr Ala Thr His Leu Thr
 340 345 350

Asn Leu Ile
 355

<210> 229

<211> 1017

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(994)

<223> RXN00422

<400> 229

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cttgacaccg aataggacaa atgggtctat cctggggcgc atg ccc acg aat tat 115
 Met Pro Thr Asn Tyr
 1 5

gca cgc gac aac gtc att tcc ttg gcg tct gcc cgc gag cag cgt tcc 163
 Ala Arg Asp Asn Val Ile Ser Leu Ala Ser Ala Arg Glu Gln Arg Ser
 10 15 20

ggg aaa ccc gag ccc aaa ccc gaa cta aca ctc atc gtc cgc gcc acc 211
 Gly Lys Pro Glu Pro Lys Pro Glu Leu Thr Leu Ile Val Arg Ala Thr
 25 30 35

aac gtg caa gcg gac ggc gag gtc cac agg caa att ggg ttg aac tcg 259
 Asn Val Gln Ala Asp Gly Glu Val His Arg Gln Ile Gly Leu Asn Ser
 40 45 50

gcg atg agc ctg gac gag ctg cac aat gta ctc aac atc gtt ttc ggt 307
 Ala Met Ser Leu Asp Glu Leu His Asn Val Leu Asn Ile Val Phe Gly
 55 60 65

gtt ggc ggc gag cag tca ccc tgg cgt ttc gaa gac caa ttc cac caa 355
 Val Gly Gly Glu Gln Ser Pro Trp Arg Phe Glu Asp Gln Phe His Gln
 70 75 80 85

ccc agc gcc ccc gac acc aac ctc ggc gaa ctc ctg ccc gaa ccc gcc 403
 Pro Ser Ala Pro Asp Thr Asn Leu Gly Glu Leu Leu Pro Glu Pro Gly
 90 95 100

gac ttc ctg ttt tac ttc tgg ggc ctg tgg caa ttc aac ctg caa tgc 451
 Asp Phe Leu Phe Tyr Phe Trp Gly Leu Trp Gln Phe Asn Leu Gln Cys
 105 110 115

gtg gaa atg tac ccg cgc gac aac ggc acc ccg cgc gcg ctg tgc atc 499
 Val Glu Met Tyr Pro Arg Asp Asn Gly Thr Pro Arg Ala Leu Cys Ile
 120 125 130

ggc ggc tcc ggc ggc ctc ggc gac gac ttc gac caa gcc acc atc aac 547
 Gly Gly Ser Gly Gly Leu Gly Asp Asp Phe Asp Gln Ala Thr Ile Asn

135 140 145

gcc gaa ctc acc ggc acc gac acc atc cgc gac gtc ctc tcc ggc gtc 595
Ala Glu Leu Thr Gly Thr Asp Thr Ile Arg Asp Val Leu Ser Gly Val
150 155 160 165

cgc ccc gaa gtc atc gac ctc gtc gac cgc acc ggc gtc ttc gac ttc 643
Arg Pro Glu Val Ile Asp Leu Val Asp Arg Thr Gly Val Phe Asp Phe
170 175 180

atc cca ctg ctc caa gcg ctc gac ctc aaa aga gaa cgc ctt atc gac 691
Ile Pro Leu Leu Gln Ala Leu Asp Leu Lys Arg Glu Pro Leu Ile Asp
185 190 195

gcc acc cgc tac cac acc tgc cgc acg ctg cca gtg gaa aac agc gcc 739
Ala Thr Arg Tyr His Thr Cys Arg Thr Leu Pro Val Glu Asn Ser Ala
200 205 210

gaa gcc tcc gac gca ttc tgg tcc tgc gta ctc gcc ctg tcc tgc ctc 787
Glu Ala Ser Asp Ala Phe Trp Ser Cys Val Leu Ala Leu Ser Cys Leu
215 220 225

gga aac gac gaa ctt ttc atc gaa gtg atc gaa tcc aca atg agc acc 835
Gly Asn Asp Glu Leu Phe Ile Glu Val Ile Glu Ser Thr Met Ser Thr
230 235 240 245

ctc ggc tgg gtc gcc gac gac ggc tcc cca cta cgt gca cca gag atc 883
Leu Gly Trp Val Ala Asp Asp Gly Ser Pro Leu Arg Ala Pro Glu Ile
250 255 260

acc agc gcc tgc gaa gcc tcc ctg aag ata ctc gcg gaa ctc ggt ggc 931
Thr Ser Ala Cys Glu Ala Ser Leu Lys Ile Leu Ala Glu Leu Gly Gly
265 270 275

tac ggc cca gag cgg ctt gcc ccc gtg gat cgc ctg gac att tat agg 979
Tyr Gly Pro Glu Arg Leu Ala Pro Val Asp Arg Leu Asp Ile Tyr Arg
280 285 290

gag ctg ctg tgt ttc taggtattgt gtaacctcgt gtc 1017
Glu Leu Leu Cys Phe
295

<210> 230

<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 230

Met Pro Thr Asn Tyr Ala Arg Asp Asn Val Ile Ser Leu Ala Ser Ala
1 5 10 15

Arg Glu Gln Arg Ser Gly Lys Pro Glu Pro Lys Pro Glu Leu Thr Leu
20 25 30

Ile Val Arg Ala Thr Asn Val Gln Ala Asp Gly Glu Val His Arg Gln
35 40 45

Ile Gly Leu Asn Ser Ala Met Ser Leu Asp Glu Leu His Asn Val Leu
50 55 60

Asn Ile Val Phe Gly Val Gly Gly Glu Gln Ser Pro Trp Arg Phe Glu
 65 70 75 80
 Asp Gln Phe His Gln Pro Ser Ala Pro Asp Thr Asn Leu Gly Glu Leu
 85 90 95
 Leu Pro Glu Pro Gly Asp Phe Leu Phe Tyr Phe Trp Gly Leu Trp Gln
 100 105 110
 Phe Asn Leu Gln Cys Val Glu Met Tyr Pro Arg Asp Asn Gly Thr Pro
 115 120 125
 Arg Ala Leu Cys Ile Gly Gly Ser Gly Gly Leu Gly Asp Asp Phe Asp
 130 135 140
 Gln Ala Thr Ile Asn Ala Glu Leu Thr Gly Thr Asp Thr Ile Arg Asp
 145 150 155 160
 Val Leu Ser Gly Val Arg Pro Glu Val Ile Asp Leu Val Asp Arg Thr
 165 170 175
 Gly Val Phe Asp Phe Ile Pro Leu Leu Gln Ala Leu Asp Leu Lys Arg
 180 185 190
 Glu Pro Leu Ile Asp Ala Thr Arg Tyr His Thr Cys Arg Thr Leu Pro
 195 200 205
 Val Glu Asn Ser Ala Glu Ala Ser Asp Ala Phe Trp Ser Cys Val Leu
 210 215 220
 Ala Leu Ser Cys Leu Gly Asn Asp Glu Leu Phe Ile Glu Val Ile Glu
 225 230 235 240
 Ser Thr Met Ser Thr Leu Gly Trp Val Ala Asp Asp Gly Ser Pro Leu
 245 250 255
 Arg Ala Pro Glu Ile Thr Ser Ala Cys Glu Ala Ser Leu Lys Ile Leu
 260 265 270
 Ala Glu Leu Gly Gly Tyr Gly Pro Glu Arg Leu Ala Pro Val Asp Arg
 275 280 285
 Leu Asp Ile Tyr Arg Glu Leu Leu Cys Phe
 290 295

<210> 231

<211> 523

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(523)

<223> FRXA00422

<400> 231

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 cttgacaccg aataggacaa atgggtctat cctggggcgc atg ccc acg aat tat 115
 Met Pro Thr Asn Tyr

1

5

gca cgc gac aac gtc att tcc ttg gcg tct gcc cgc gag cag cgt tcc 163
 Ala Arg Asp Asn Val Ile Ser Leu Ala Ser Ala Arg Glu Gln Arg Ser
 10 15 20

ggg aaa ccc gag ccc aaa ccc gaa cta aca ctc atc gtc cgc gcc acc 211
 Gly Lys Pro Glu Pro Lys Pro Glu Leu Thr Leu Ile Val Arg Ala Thr
 25 30 35

aac gtg caa gcg gac ggc gag gtc cac agg caa att ggg ttg aac tcg 259
 Asn Val Gln Ala Asp Gly Glu Val His Arg Gln Ile Gly Leu Asn Ser
 40 45 50

gcg atg agc ctg gac gag ctg cac aat gta ctc aac atc gtt ttc ggt 307
 Ala Met Ser Leu Asp Glu Leu His Asn Val Leu Asn Ile Val Phe Gly
 55 60 65

gtt ggc ggc gag cag tca ccc tgg cgt ttc gaa gac caa ttc cac caa 355
 Val Gly Gly Glu Gln Ser Pro Trp Arg Phe Glu Asp Gln Phe His Gln
 70 75 80 85

ccc agc gcc ccc gac acc aac ctc ggc gaa ctc ctg ccc gaa ccc gcc 403
 Pro Ser Ala Pro Asp Thr Asn Leu Gly Glu Leu Leu Pro Glu Pro Gly
 90 95 100

gac ttc ctg ttt tac ttc tgg ggc ctg tgg caa ttc aac ctg caa tgc 451
 Asp Phe Leu Phe Tyr Phe Trp Gly Leu Trp Gln Phe Asn Leu Gln Cys
 105 110 115

gtg gaa atg tac ccg cgc gac aac ggc acc ccg cgc gcg ctg tgc atc 499
 Val Glu Met Tyr Pro Arg Asp Asn Gly Thr Pro Arg Ala Leu Cys Ile
 120 125 130

ggc ggc tcc ggc ggc ctc ggc gac
 Gly Gly Ser Gly Gly Leu Gly Asp 523
 135 140

<210> 232

<211> 141

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 232

Met Pro Thr Asn Tyr Ala Arg Asp Asn Val Ile Ser Leu Ala Ser Ala
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Arg Glu Gln Arg Ser Gly Lys Pro Glu Pro Lys Pro Glu Leu Thr Leu
 20 25 30

Ile Val Arg Ala Thr Asn Val Gln Ala Asp Gly Glu Val His Arg Gln
 35 40 45

Ile Gly Leu Asn Ser Ala Met Ser Leu Asp Glu Leu His Asn Val Leu
 50 55 60

Asn Ile Val Phe Gly Val Gly Gly Glu Gln Ser Pro Trp Arg Phe Glu
 65 70 75 80

Asp Gln Phe His Gln Pro Ser Ala Pro Asp Thr Asn Leu Gly Glu Leu

85 90 95

Leu Pro Glu Pro Gly Asp Phe Leu Phe Tyr Phe Trp Gly Leu Trp Gln
100 105 110

Phe Asn Leu Gln Cys Val Glu Met Tyr Pro Arg Asp Asn Gly Thr Pro
115 120 125

Arg Ala Leu Cys Ile Gly Gly Ser Gly Gly Leu Gly Asp
130 135 140

<210> 233
<211> 543
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(520)
<223> RXN00447

<400> 233
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gaggaactcg acaagctgct gcgcgcgtgg gaggccatca atg ctg ggt agt ctt 115
Met Leu Gly Ser Leu
1 5

tgg cgt ttt gcg gtg cgc acc gca gca ggc gcg gtg gcg ttg tgg gtg 163
Trp Arg Phe Ala Val Arg Thr Ala Ala Gly Ala Val Ala Leu Trp Val
10 15 20

gtt att aag ctt atc gac gcc atc tcc ctg agt ttt ccc acc aca cct 211
Val Ile Lys Leu Ile Asp Gly Ile Ser Leu Ser Phe Pro Thr Thr Pro
25 30 35

ctc tat cag gac ggt cag cac gac aat ctg ctg aca ttc ctg gcg gtg 259
Leu Tyr Gln Asp Gly Gln His Asp Asn Leu Leu Thr Phe Leu Ala Val
40 45 50

gca gca atc att gtc gtg ttg aat gcc acg gtg aaa ccc gtc ttg aag 307
Ala Ala Ile Ile Val Val Leu Asn Ala Thr Val Lys Pro Val Leu Lys
55 60 65

ctg ctt ggt ttg ccg ttg aca atc atc acc ttg ggt ctg ttc tcg ctg 355
Leu Leu Gly Leu Pro Leu Thr Ile Ile Thr Leu Gly Leu Phe Ser Leu
70 75 80 85

gtc atc aac gcg gta atc atg ctg ctg gcg gag tat gtg tca gat ttg 403
Val Ile Asn Ala Val Ile Met Leu Leu Ala Glu Tyr Val Ser Asp Leu
90 95 100

atc ggt ttc ggt cta cgc att gaa acc ttc ggt gcg gcc ttc tgg ggt 451
Ile Gly Phe Gly Leu Arg Ile Glu Thr Phe Gly Ala Ala Phe Trp Gly
105 110 115

gcg att gtg ctg gcg tta gtg aac tgg gtt ctt ggc ccc att acc gcc 499
Ala Ile Val Leu Ala Leu Val Asn Trp Val Leu Gly Pro Ile Thr Gly
120 125 130

ctc ctc ggt gca aaa aag gac taaccatggc ggatctgagc att 543
 Leu Leu Gly Ala Lys Lys Asp
 135 140

<210> 234
 <211> 140
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 234
 Met Leu Gly Ser Leu Trp Arg Phe Ala Val Arg Thr Ala Ala Gly Ala
 1 5 10 15
 Val Ala Leu Trp Val Val Ile Lys Leu Ile Asp Gly Ile Ser Leu Ser
 20 25 30
 Phe Pro Thr Thr Pro Leu Tyr Gln Asp Gly Gln His Asp Asn Leu Leu
 35 40 45
 Thr Phe Leu Ala Val Ala Ala Ile Ile Val Val Leu Asn Ala Thr Val
 50 55 60
 Lys Pro Val Leu Lys Leu Leu Gly Leu Pro Leu Thr Ile Ile Thr Leu
 65 70 75 80
 Gly Leu Phe Ser Leu Val Ile Asn Ala Val Ile Met Leu Leu Ala Glu
 85 90 95
 Tyr Val Ser Asp Leu Ile Gly Phe Gly Leu Arg Ile Glu Thr Phe Gly
 100 105 110
 Ala Ala Phe Trp Gly Ala Ile Val Leu Ala Leu Val Asn Trp Val Leu
 115 120 125
 Gly Pro Ile Thr Gly Leu Leu Gly Ala Lys Lys Asp
 130 135 140

<210> 235
 <211> 400
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(400)
 <223> FRXA00447

<400> 235
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 gaggaactg acaagctgct gcgcgcgtgg gaggccatca atg ctg ggt agt ctt 115
 Met Leu Gly Ser Leu
 1 5
 tgg cgt ttt gcg gtg cgc acc gca gca ggc gcg gtg gcg ttg tgg gtg 163
 Trp Arg Phe Ala Val Arg Thr Ala Ala Gly Ala Val Ala Leu Trp Val
 10 15 20
 gtt att aag ctt atc gac ggc atc tcc ctg agt ttt ccc acc aca cct 211

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Val Ile Lys Leu Ile Asp Gly Ile Ser Leu Ser Phe Pro Thr Thr Pro
      25                      30                      35

ctc tat cag gac ggt cag cac gac aat ctg ctg aca ttc ctg gcg gtg 259
Leu Tyr Gln Asp Gly Gln His Asp Asn Leu Leu Thr Phe Leu Ala Val
      40                      45                      50

gca gca atc att gtc gtg ttg aat gcc acg gtg aaa ccc gtc ttg aag 307
Ala Ala Ile Ile Val Val Leu Asn Ala Thr Val Lys Pro Val Leu Lys
      55                      60                      65

ctg ctt ggt ttg ccg ttg aca atc atc acc ttg ggt ctg ttc tcg ctg 355
Leu Leu Gly Leu Pro Leu Thr Thr Ile Ile Thr Leu Gly Leu Phe Ser Leu
      70                      75                      80                      85

gtc atc aac gcg gta atc atg ctg ctg gcg gag tat gtg tca gat 400
Val Ile Asn Ala Val Ile Met Leu Leu Ala Glu Tyr Val Ser Asp
      90                      95                      100

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<210> 236

<211> 100

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 236

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Met Leu Gly Ser Leu Trp Arg Phe Ala Val Arg Thr Ala Ala Gly Ala
  1           5           10          15

Val Ala Leu Trp Val Val Ile Lys Leu Ile Asp Gly Ile Ser Leu Ser
      20           25           30

Phe Pro Thr Thr Pro Leu Tyr Gln Asp Gly Gln His Asp Asn Leu Leu
      35           40           45

Thr Phe Leu Ala Val Ala Ala Ile Ile Val Val Leu Asn Ala Thr Val
      50           55           60

Lys Pro Val Leu Lys Leu Leu Gly Leu Pro Leu Thr Ile Ile Thr Leu
      65           70           75           80

Gly Leu Phe Ser Leu Val Ile Asn Ala Val Ile Met Leu Leu Ala Glu
      85           90           95

Tyr Val Ser Asp
      100

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<210> 237

<211> 873

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(850)

<223> RXN00455

<400> 237

gaagtgtctg gccgattggc taacaatctc tagttaaatc ccgcctcatg aaaccacgat 60

gaaaccaaca tgagagtttt ttcattccacg tttctctggct	atg gtt gtg gac gtg	115
	Met Val Val Asp Val	
	1 5	
caa aat caa tca cac acc cca gaa acc cag cct caa cct ggg cag ggc		163
Gln Asn Gln Ser His Thr Pro Glu Thr Gln Pro Gln Pro Gly Gln Gly		
	10 15 20	
gca gcc aag aaa acc ccc gtt gcg tcc gga aac tcc acg ttc att cac		211
Ala Ala Lys Lys Thr Pro Val Ala Ser Gly Asn Ser Thr Phe Ile His		
	25 30 35	
att cag cca agc ttg tac ccc att ttg ctg gcg ctg ttt gtt gca gtc		259
Ile Gln Pro Ser Leu Tyr Pro Ile Leu Leu Ala Leu Phe Val Ala Val		
	40 45 50	
ttt cta att tca aat atc acc gca acc aag ggc gta gaa atc ggc ccg		307
Phe Leu Ile Ser Asn Ile Thr Ala Thr Lys Gly Val Glu Ile Gly Pro		
	55 60 65	
ttg gtg aca gac ggt gcg ttc ttc ctc ttc ccc atc tca tat gtg ttg		355
Leu Val Thr Asp Gly Ala Phe Phe Leu Phe Pro Ile Ser Tyr Val Leu		
	70 75 80 85	
ggc gat gtt cta gcc gaa tgt tac ggc ttc aaa tcc act cgt cgt gcc		403
Gly Asp Val Leu Ala Glu Cys Tyr Gly Phe Lys Ser Thr Arg Ala Ala		
	90 95 100	
att ctt act ggt ttt ggc atc acg atg ctc gcg gcg ctg tct ttc tac		451
Ile Leu Thr Gly Phe Gly Ile Thr Met Leu Ala Ala Leu Ser Phe Tyr		
	105 110 115	
att tcc atc tgg ctg cct ggc gca agt ttc tgg gaa ggc caa gaa gct		499
Ile Ser Ile Trp Leu Pro Gly Ala Ser Phe Trp Glu Gly Gln Glu Ala		
	120 125 130	
ttc gaa gca acg ctc ggc ctt gtt cca cag atc atc gtg gca tca ctg		547
Phe Glu Ala Thr Leu Gly Leu Val Pro Gln Ile Ile Val Ala Ser Leu		
	135 140 145	
gcg ggc tat att gtg ggt cag ctg ctc aac gcc aaa gtt ctg gtg gct		595
Ala Gly Tyr Ile Val Gly Gln Leu Leu Asn Ala Lys Val Leu Val Ala		
	150 155 160 165	
atc aaa aag cgc acg ggt gaa aag tcc ctg tgg gcg cgc ctg att ggt		643
Ile Lys Lys Arg Thr Gly Glu Lys Ser Leu Trp Ala Arg Leu Ile Gly		
	170 175 180	
tcc acc gtt gtc gga gaa ttt gtc gat acc ctg ctg ttt tgc gcc atc		691
Ser Thr Val Val Gly Glu Phe Val Asp Thr Leu Leu Phe Cys Ala Ile		
	185 190 195	
gca gcg cca gtg atc ggt att gcc acc gcc ccg gat ttc atc aac tac		739
Ala Ala Pro Val Ile Gly Ile Ala Thr Ala Pro Asp Phe Ile Asn Tyr		
	200 205 210	
gtt gtg gtg ggc ttc gtg tgg aaa acc ctt cta gag gtc atc ctc atg		787
Val Val Val Gly Phe Val Trp Lys Thr Leu Leu Glu Val Ile Leu Met		
	215 220 225	
ccc atc acc tac gca gtc att agg tgg gtg aaa cgc cgc gaa ggt tat		835

Pro Ile Thr Tyr Ala Val Ile Arg Trp Val Lys Arg Arg Glu Gly Tyr
 230 235 240 245

gaa acc ttc gac gcg tagtaccggc ctaagaattc ttc
 Glu Thr Phe Asp Ala
 250

873

<210> 238

<211> 250

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 238

Met Val Val Asp Val Gln Asn Gln Ser His Thr Pro Glu Thr Gln Pro
 1 5 10 15

Gln Pro Gly Gln Gly Ala Ala Lys Lys Thr Pro Val Ala Ser Gly Asn
 20 25 30

Ser Thr Phe Ile His Ile Gln Pro Ser Leu Tyr Pro Ile Leu Leu Ala
 35 40 45

Leu Phe Val Ala Val Phe Leu Ile Ser Asn Ile Thr Ala Thr Lys Gly
 50 55 60

Val Glu Ile Gly Pro Leu Val Thr Asp Gly Ala Phe Phe Leu Phe Pro
 65 70 75 80

Ile Ser Tyr Val Leu Gly Asp Val Leu Ala Glu Cys Tyr Gly Phe Lys
 85 90 95

Ser Thr Arg Arg Ala Ile Leu Thr Gly Phe Gly Ile Thr Met Leu Ala
 100 105 110

Ala Leu Ser Phe Tyr Ile Ser Ile Trp Leu Pro Gly Ala Ser Phe Trp
 115 120 125

Glu Gly Gln Glu Ala Phe Glu Ala Thr Leu Gly Leu Val Pro Gln Ile
 130 135 140

Ile Val Ala Ser Leu Ala Gly Tyr Ile Val Gly Gln Leu Leu Asn Ala
 145 150 155 160

Lys Val Leu Val Ala Ile Lys Lys Arg Thr Gly Glu Lys Ser Leu Trp
 165 170 175

Ala Arg Leu Ile Gly Ser Thr Val Val Gly Glu Phe Val Asp Thr Leu
 180 185 190

Leu Phe Cys Ala Ile Ala Ala Pro Val Ile Gly Ile Ala Thr Ala Pro
 195 200 205

Asp Phe Ile Asn Tyr Val Val Val Gly Phe Val Trp Lys Thr Leu Leu
 210 215 220

Glu Val Ile Leu Met Pro Ile Thr Tyr Ala Val Ile Arg Trp Val Lys
 225 230 235 240

Arg Arg Glu Gly Tyr Glu Thr Phe Asp Ala
 245 250

<210> 239

<211> 641

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(618)

<223> FRXA00455

<400> 239

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gca	acc	aag	ggc	gta	gaa	atc	ggc	cgc	ttg	gtg	aca	gac	ggg	gcg	ttc	96
Ala	Thr	Lys	Gly	Val	Glu	Ile	Gly	Pro	Leu	Val	Thr	Asp	Gly	Ala	Phe	
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ttc	ctc	ttc	ccc	atc	tca	tat	gtg	ttg	ggc	gat	gtt	cta	gcc	gaa	tgt	144
Phe	Leu	Phe	Pro	Ile	Ser	Tyr	Val	Leu	Gly	Asp	Val	Leu	Ala	Glu	Cys	
		35					40					45				

tac	ggc	ttc	aaa	tcc	act	cgt	cgt	gcc	att	ctt	act	ggg	ttt	ggc	atc	192
Tyr	Gly	Phe	Lys	Ser	Thr	Arg	Arg	Ala	Ile	Leu	Thr	Gly	Phe	Gly	Ile	
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Thr	Met	Leu	Ala	Ala	Leu	Ser	Phe	Tyr	Ile	Ser	Ile	Trp	Leu	Pro	Gly	
65					70					75					80	

gca	agt	ttc	tgg	gaa	ggc	caa	gaa	gct	ttc	gaa	gca	acg	ctc	ggc	ctt	288
Ala	Ser	Phe	Trp	Glu	Gly	Gln	Glu	Ala	Phe	Glu	Ala	Thr	Leu	Gly	Leu	
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gtt	cca	cag	atc	atc	gtg	gca	tca	ctg	gcg	ggc	tat	att	gtg	ggg	cag	336
Val	Pro	Gln	Ile	Ile	Val	Ala	Ser	Leu	Ala	Gly	Tyr	Ile	Val	Gly	Gln	
		100						105					110			

ctg	ctc	aac	gcc	aaa	gtt	ctg	gtg	gct	atc	aaa	aag	cgc	acg	ggg	gaa	384
Leu	Leu	Asn	Ala	Lys	Val	Leu	Val	Ala	Ile	Lys	Lys	Arg	Thr	Gly	Glu	
		115					120					125				

aag	tcc	ctg	tgg	gcg	cgc	ctg	att	ggg	tcc	acc	gtt	gtc	gga	gaa	ttt	432
Lys	Ser	Leu	Trp	Ala	Arg	Leu	Ile	Gly	Ser	Thr	Val	Val	Gly	Glu	Phe	
		130				135					140					

gtc	gat	acc	ctg	ctg	ttt	tgc	gcc	atc	gca	gcg	cca	gtg	atc	ggg	att	480
Val	Asp	Thr	Leu	Leu	Phe	Cys	Ala	Ile	Ala	Ala	Pro	Val	Ile	Gly	Ile	
145					150					155				160		

gcc	acc	gcc	cgc	gat	ttc	atc	aac	tac	gtt	gtg	gtg	ggc	ttc	gtg	tgg	528
Ala	Thr	Ala	Pro	Asp	Phe	Ile	Asn	Tyr	Val	Val	Val	Gly	Phe	Val	Trp	
				165				170					175			

aaa	acc	ctt	cta	gag	gtc	atc	ctc	atg	ccc	atc	acc	tac	gca	gtc	att	576
Lys	Thr	Leu	Leu	Glu	Val	Ile	Leu	Met	Pro	Ile	Thr	Tyr	Ala	Val	Ile	
			180					185					190			

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<210> 240

<211> 206

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 240

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Phe Leu Phe Pro Ile Ser Tyr Val Leu Gly Asp Val Leu Ala Glu Cys
 35 40 45

Tyr Gly Phe Lys Ser Thr Arg Ala Ile Leu Thr Gly Phe Gly Ile
 50 55 60

Thr Met Leu Ala Ala Leu Ser Phe Tyr Ile Ser Ile Trp Leu Pro Gly
 65 70 75 80

Ala Ser Phe Trp Glu Gly Gln Glu Ala Phe Glu Ala Thr Leu Gly Leu
 85 90 95

Val Pro Gln Ile Ile Val Ala Ser Leu Ala Gly Tyr Ile Val Gly Gln
 100 105 110

Leu Leu Asn Ala Lys Val Leu Val Ala Ile Lys Lys Arg Thr Gly Glu
 115 120 125

Lys Ser Leu Trp Ala Arg Leu Ile Gly Ser Thr Val Val Gly Glu Phe
 130 135 140

Val Asp Thr Leu Leu Phe Cys Ala Ile Ala Ala Pro Val Ile Gly Ile
 145 150 155 160

Ala Thr Ala Pro Asp Phe Ile Asn Tyr Val Val Val Gly Phe Val Trp
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Lys Thr Leu Leu Glu Val Ile Leu Met Pro Ile Thr Tyr Ala Val Ile
 180 185 190

Arg Trp Val Lys Arg Arg Glu Gly Tyr Glu Thr Phe Asp Ala
 195 200 205

<210> 241

<211> 912

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(889)

<223> RXN00473

<400> 241

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Met Ser Gly Thr Gly
1 5

gtt cga aag ttg tgg gga gat ggc act ccg gtg tgc ctc cct gac ctt 163
Val Arg Lys Leu Trp Gly Asp Gly Thr Pro Val Ser Leu Pro Asp Leu
10 15 20

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Ser Gly Leu Ser Arg Ala Glu Arg Ile Asp Ala Leu Arg Ser Arg Met
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Ser Thr Met Gly Ala Ala Val Pro Lys Phe Glu Pro Ser Val Glu Glu
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agt gct gaa caa aag cag gat tct ctc gcc gaa aaa cag gac ata gtt 307
Ser Ala Glu Gln Lys Gln Asp Ser Leu Ala Glu Lys Lys Gln Asp Ile Val
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gca gtt cct tcc gct ttt tct gat ctt ttc cct ggg gat ggt ttg ccg 355
Ala Val Pro Ser Ala Phe Ser Asp Leu Phe Pro Gly Asp Gly Leu Pro
70 75 80 85

cgt cgt gcg gtt act caa ttg gtt gaa cag cca ctt gtg gtg gtg gac 403
Arg Arg Ala Val Thr Gln Leu Val Glu Gln Pro Leu Val Val Val Asp
90 95 100

ttc ctg gct cat att act gcc cag ggt gga cac gct gcg gtg att ggg 451
Phe Leu Ala His Ile Thr Ala Gln Gly Gly His Ala Ala Val Ile Gly
105 110 115

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Trp Lys Asp Leu Ala Tyr Ala Gly Val Ile Asp Ser Gly Gly Val Cys
120 125 130

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Glu Asn Ile Ile Ala Ile Pro Asn Pro Gly Thr Glu Pro Leu Asn Val
135 140 145

gca gcg gtg ctg tgt gag ggg ttg gat gtg gtc gtg tac aaa ggc ccg 595
Ala Ala Val Leu Cys Glu Gly Leu Asp Val Val Val Tyr Lys Gly Pro
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Glu Ile Ser Leu Ser Pro Thr Arg Ala Arg Pro Leu Leu Gly Lys Leu
170 175 180

agg cag ggg act gct gcc ttg gtg atg gtt gcc acg aaa gta agc tca 691
Arg Gln Gly Thr Ala Ala Leu Val Met Val Gly Thr Lys Val Ser Ser
185 190 195

ccg gcg ctg tgc gtg gat gca gag atc act gat tat gtt gcc att ggt 739
Pro Ala Leu Ser Val Asp Ala Glu Ile Thr Asp Tyr Val Gly Ile Gly
200 205 210

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gca ggt agt ggg cgt att cgt ggc gtt gag atg cag gtg cgg gct gtg 787
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 215 220 225

tcg aaa act cac ggt gtg cgc agc gga aaa gtc ctg atc agt agg cct 835
 Ser Lys Thr His Gly Val Arg Ser Gly Lys Val Leu Ile Ser Arg Pro
 230 235 240 245

cag gat gca gca ttg ctt gag cct gaa cag cca aca acg ttg cgg gcg 883
 Gln Asp Ala Ala Leu Leu Glu Pro Glu Gln Pro Thr Thr Leu Arg Ala
 250 255 260

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 Val Pro

<210> 242

<211> 263

<212> PRT

<213> Corynebacterium glutamicum

<400> 242

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 20 25 30

Leu Arg Ser Arg Met Ser Thr Met Gly Ala Ala Val Pro Lys Phe Glu
 35 40 45

Pro Ser Val Glu Glu Ser Ala Glu Gln Lys Gln Asp Ser Leu Ala Glu
 50 55 60

Lys Gln Asp Ile Val Ala Val Pro Ser Ala Phe Ser Asp Leu Phe Pro
 65 70 75 80

Gly Asp Gly Leu Pro Arg Arg Ala Val Thr Gln Leu Val Glu Gln Pro
 85 90 95

Leu Val Val Val Asp Phe Leu Ala His Ile Thr Ala Gln Gly Gly His
 100 105 110

Ala Ala Val Ile Gly Trp Lys Asp Leu Ala Tyr Ala Gly Val Ile Asp
 115 120 125

Ser Gly Gly Val Cys Glu Asn Ile Ile Ala Ile Pro Asn Pro Gly Thr
 130 135 140

Glu Pro Leu Asn Val Ala Ala Val Leu Cys Glu Gly Leu Asp Val Val
 145 150 155 160

Val Tyr Lys Gly Pro Glu Ile Ser Leu Ser Pro Thr Arg Ala Arg Pro
 165 170 175

Leu Leu Gly Lys Leu Arg Gln Gly Thr Ala Ala Leu Val Met Val Gly
 180 185 190

Thr Lys Val Ser Ser Pro Ala Leu Ser Val Asp Ala Glu Ile Thr Asp
 195 200 205

Tyr Val Gly Ile Gly Ala Gly Ser Gly Arg Ile Arg Gly Val Glu Met
 210 215 220
 Gln Val Arg Ala Val Ser Lys Thr His Gly Val Arg Ser Gly Lys Val
 225 230 235 240
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 245 250 255
 Thr Thr Leu Arg Ala Val Pro
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 <213> Corynebacterium glutamicum

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 <222> (101)..(865)
 <223> FRXA00473

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 Leu Trp Gly Asp Gly
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 Thr Pro Val Ser Leu Pro Asp Leu Ser Gly Leu Ser Arg Ala Glu Arg
 10 15 20
 att gat gcg ttg cgt tca cgc atg tcc acc atg ggt gct gcg gtg cca 211
 Ile Asp Ala Leu Arg Ser Arg Met Ser Thr Met Gly Ala Ala Val Pro
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 aag ttt gag ccg tcg gtg gaa gaa agt gct gaa caa aag cag gat tct 259
 Lys Phe Glu Pro Ser Val Glu Glu Ser Ala Glu Gln Lys Gln Asp Ser
 40 45 50
 ctc gcc gaa aaa cag gac ata gtt gca gtt cct tcc gct ttt tct gat 307
 Leu Ala Glu Lys Gln Asp Ile Val Ala Val Pro Ser Ala Phe Ser Asp
 55 60 65
 ctt ttc cct ggg gat ggt ttg ccg cgt cgt gcg gtt act caa ttg gtt 355
 Leu Phe Pro Gly Asp Gly Leu Pro Arg Arg Ala Val Thr Gln Leu Val
 70 75 80 85
 gaa cag cca ctt gtg gtg gtg gac ttc ctg gct cat att act gcc cag 403
 Glu Gln Pro Leu Val Val Val Asp Phe Leu Ala His Ile Thr Ala Gln
 90 95 100
 ggt gga cac gct gcg gtg att ggg tgg aag gat tta gcc tac gcc ggg 451
 Gly Gly His Ala Ala Val Ile Gly Trp Lys Asp Leu Ala Tyr Ala Gly
 105 110 115
 gtg att gat tcc gga ggt gtg tgc gag aac atc att gct att cca aat 499
 Val Ile Asp Ser Gly Gly Val Cys Glu Asn Ile Ile Ala Ile Pro Asn

120	125	130	
cct ggt acg gag cca ctg aat gtg gca gcg gtg ctg tgt gag ggg ttg			547
Pro Gly Thr Glu Pro Leu Asn Val Ala Val Leu Cys Glu Gly Leu			
135	140	145	
gat gtg gtc gtg tac aaa ggc ccg gag att tcc ctg tcg cca acc aga			595
Asp Val Val Val Tyr Lys Gly Pro Glu Ile Ser Leu Ser Pro Thr Arg			
150	155	160	165
gcg agg ccg ttg ctg gga aag ctg agg cag ggg act gct gcc ttg gtg			643
Ala Arg Pro Leu Leu Gly Lys Leu Arg Gln Gly Thr Ala Ala Leu Val			
170	175	180	
atg gtt ggc acg aaa gta agc tca ccg gcg ctg tcg gtg gat gca gag			691
Met Val Gly Thr Lys Val Ser Ser Pro Ala Leu Ser Val Asp Ala Glu			
185	190	195	
atc act gat tat gtt ggc att ggt gca ggt agt ggg cgt att cgt ggc			739
Ile Thr Asp Tyr Val Gly Ile Gly Ala Gly Ser Gly Arg Ile Arg Gly			
200	205	210	
ggt gag atg cag gtg cgg gct gtg tcg aaa act cac ggt gtg cgc agc			787
Val Glu Met Gln Val Arg Ala Val Ser Lys Thr His Gly Val Arg Ser			
215	220	225	
gga aaa gtc ctg atc agt agg cct cag gat gca gca ttg ctt gag cct			835
Gly Lys Val Leu Ile Ser Arg Pro Gln Asp Ala Ala Leu Leu Glu Pro			
230	235	240	245
gaa cag cca aca acg ttg cgg gcg gtc cca tgacgcgggt gatggcattg			885
Glu Gln Pro Thr Thr Leu Arg Ala Val Pro			
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Gln Lys Gln Asp Ser Leu Ala Glu Lys Gln Asp Ile Val Ala Val Pro			
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Ser Ala Phe Ser Asp Leu Phe Pro Gly Asp Gly Leu Pro Arg Arg Ala			
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Val Thr Gln Leu Val Glu Gln Pro Leu Val Val Val Asp Phe Leu Ala			
85	90	95	

His Ile Thr Ala Gln Gly Gly His Ala Ala Val Ile Gly Trp Lys Asp
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 Leu Ala Tyr Ala Gly Val Ile Asp Ser Gly Gly Val Cys Glu Asn Ile
 115 120 125
 Ile Ala Ile Pro Asn Pro Gly Thr Glu Pro Leu Asn Val Ala Ala Val
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 Leu Cys Glu Gly Leu Asp Val Val Val Tyr Lys Gly Pro Glu Ile Ser
 145 150 155 160
 Leu Ser Pro Thr Arg Ala Arg Pro Leu Leu Gly Lys Leu Arg Gln Gly
 165 170 175
 Thr Ala Ala Leu Val Met Val Gly Thr Lys Val Ser Ser Pro Ala Leu
 180 185 190
 Ser Val Asp Ala Glu Ile Thr Asp Tyr Val Gly Ile Gly Ala Gly Ser
 195 200 205
 Gly Arg Ile Arg Gly Val Glu Met Gln Val Arg Ala Val Ser Lys Thr
 210 215 220
 His Gly Val Arg Ser Gly Lys Val Leu Ile Ser Arg Pro Gln Asp Ala
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 245 250 255

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<211> 2418

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(2395)

<223> RXN00485

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 Val Ser Ser Val Asn 5
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gat ctt ttt gcc aag cgg tat gaa aac gct gat ctt gtg gtc acg gtg 163
 Asp Leu Phe Ala Lys Pro Tyr Glu Asn Ala Asp Leu Val Val Thr Val 10 15 20

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 Ser Ala Lys Asn Glu Asp Ser Phe Ala Ala Phe Glu Gln Gln Leu Ala 25 30 35

acg aca cct ggt gtt gaa gct ctg gct ttt gat caa aat ttt gca gcc 259
 Thr Thr Pro Gly Val Glu Ala Leu Ala Phe Asp Gln Asn Phe Ala Ala 40 45 50

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Ile	Ser	Glu	Gly	Pro	Leu	Gln	Trp	Arg	Pro	Ile	Leu	Glu	Gly	Arg	Leu	
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Pro	Gln	Gly	Pro	Gly	Glu	Ile	Ala	Val	Thr	Thr	Ala	Pro	Gly	Ala	Pro	
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gaa	gtt	ggt	gag	cac	gta	tcc	att	cgc	ctg	tcc	caa	aac	act	gag	gac	451
Glu	Val	Gly	Glu	His	Val	Ser	Ile	Arg	Leu	Ser	Gln	Asn	Thr	Glu	Asp	
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act	gag	gtt	ctt	gtg	gtt	ggc	gtg	gtg	gag	cca	gcg	gcg	cag	gaa	act	499
Thr	Glu	Val	Leu	Val	Val	Gly	Val	Val	Glu	Pro	Ala	Ala	Gln	Glu	Thr	
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Leu	Gly	Gly	Ala	Pro	Phe	Val	Val	Ala	Ser	Pro	Asp	Ala	Leu	Met	Glu	
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Trp	Asn	Ser	Ser	Gly	Val	Arg	Gly	Glu	Phe	Arg	Val	Ala	Thr	Ser	Asp	
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cct	gcc	tcg	cta	gag	gct	gca	agc	ttt	agc	gac	gct	acg	gtg	gtg	gtt	643
Pro	Ala	Ser	Leu	Glu	Ala	Ala	Ser	Phe	Ser	Asp	Ala	Thr	Val	Val	Val	
				170					175					180		
gct	tcg	gcg	gag	ggg	cac	gtc	gat	aag	ctt	gct	gat	tct	tat	ttg	ggc	691
Ala	Ser	Ala	Glu	Gly	His	Val	Asp	Lys	Leu	Ala	Asp	Ser	Tyr	Leu	Gly	
			185					190					195			
cag	cga	gat	cgc	tat	ttc	ttg	ctg	ctc	gca	gcg	ttt	gtg	gca	gtg	gct	739
Gln	Arg	Asp	Arg	Tyr	Phe	Leu	Leu	Leu	Ala	Ala	Phe	Val	Ala	Val	Ala	
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gct	gcc	gtg	gcg	ttt	ttg	gtg	gtc	ttt	tct	gca	tat	tcg	gtg	ctc	act	787
Ala	Ala	Val	Ala	Phe	Leu	Val	Val	Phe	Ser	Ala	Tyr	Ser	Val	Leu	Thr	
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Thr	Pro	Gln	Ile	Leu	Gly	Ser	Val	Ile	Phe	Glu	Ala	Gly	Ile	Leu	Gly	
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Val	Val	Ala	Ala	Gly	Phe	Gly	Ala	Pro	Ala	Gly	Leu	Met	Ala	Ala	Arg	
			265				270						275			
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Leu	Leu	Ala	Asp	Asn	Ala	Ala	Arg	Phe	Gly	Ile	Arg	Val	Pro	Ile	Asp	
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gtg	att	gat	ctg	cca	agt	agc	acg	atg	tgg	ctc	atc	gct	ggc	gtc	ggc	1027
Val	Ile	Asp	Leu	Pro	Ser	Ser	Thr	Met	Trp	Leu	Ile	Ala	Gly	Val	Gly	

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gaa atc tct agc atc gac gcc gtg aaa act gcc atc gcg cca gcc acc Glu Ile Ser Ser Ile Asp Gly Val Lys Thr Ala Ile Ala Pro Ala Thr 490 495 500			1603
acc gct gtg gaa ttg gaa gat tcc gcc aat ttc tct gtg ctc atg ctc Thr Ala Val Glu Leu Glu Asp Ser Gly Asn Phe Ser Val Leu Met Leu 505 510 515			1651
gct gaa gaa gac gga gcc tcc gtg atg cgc gca ggc gat act ggt gca Ala Glu Glu Asp Gly Ala Ser Val Met Arg Ala Gly Asp Thr Gly Ala 520 525 530			1699
cca gct ggt ggc ctt gtt ttg ggc aga aac tct cct gac cag gat gct Pro Ala Gly Gly Leu Val Leu Gly Arg Asn Ser Pro Asp Gln Asp Ala 535 540 545			1747

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Tyr Pro Ala Gly Gln Ala Ala Asn Ile Ile Val Ala Asp Thr Pro Thr	
550 555 560	
cag gcg gaa atc ttc cac agc gac aac tac ttc tcc atg atc gac cca	1843
Gln Ala Glu Ile Phe His Ser Asp Asn Tyr Phe Ser Met Ile Asp Pro	
570 575 580	
gca ctc gcc acc ggc ccc agc acc aca cgc aac gta ctg atc ctg ctc	1891
Ala Leu Ala Thr Gly Pro Ser Thr Thr Arg Asn Val Leu Ile Leu Leu	
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gac ggc gac tcc aac cag gcc ccc gac aac gcc acg gcg cag gcg gta	1939
Asp Gly Asp Ser Asn Gln Ala Pro Asp Asn Ala Thr Ala Gln Ala Val	
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cgc aag acc att tcg ctt ttc gac gga cga tac tcc atc acc gag ggt	1987
Arg Lys Thr Ile Ser Leu Phe Asp Gly Arg Tyr Ser Ile Thr Glu Gly	
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Phe Ser Ala Arg Gln Asn Thr Phe Glu Leu Val Ser Arg Ile Thr Thr	
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atg tcc aca ctg ctt gcc atc gtg gcc tta gcg atc gct gcc gtt ggc	2083
Met Ser Thr Leu Leu Ala Ile Val Ala Leu Ala Ile Ala Ala Val Gly	
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Leu Ile Asn Thr Val Ala Leu Thr Ile Ser Glu Arg Ala Arg Asp Arg	
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Tyr Leu Leu Arg Thr Ile Gly Leu Thr Ser Thr Gly Gln Ile Leu Val	
680 685 690	
atg gct att gaa atg atc gcg ctc tca ttg cgg gct gcc att gtt ggt	2227
Met Ala Ile Glu Met Ile Ala Leu Ser Leu Pro Ala Ala Ile Val Gly	
695 700 705	
gca gtt tcg gga gga ttc tta ggc aga ttc gtt gcc agt tct gcc acc	2275
Ala Val Ser Gly Gly Phe Leu Gly Arg Phe Val Ala Ser Ser Ala Thr	
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aac acc gct gcg acg gca cca ctt caa gta gac att ctc ggc gga acg	2323
Asn Thr Ala Ala Thr Ala Pro Leu Gln Val Asp Ile Leu Gly Gly Thr	
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gtt ctc gcg atg gtc gca gga tct gta ctg tgc gcg ctc atc gtg ctg	2371
Val Leu Ala Met Val Ala Gly Ser Val Leu Cys Ala Leu Ile Val Leu	
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Ala Asn Lys Arg Arg Arg Val Val	
760 765	

<210> 246

<211> 765

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 246

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			20					25					30		
Glu	Gln	Gln	Leu	Ala	Thr	Thr	Pro	Gly	Val	Glu	Ala	Leu	Ala	Phe	Asp
		35					40					45			
Gln	Asn	Phe	Ala	Ala	Ser	Val	Lys	Gln	Ser	Asp	Gly	Ile	Tyr	Ala	Ser
	50						55				60				
Thr	Ser	Val	Gln	Ser	Ile	Ser	Glu	Gly	Pro	Leu	Gln	Trp	Arg	Pro	Ile
	65				70				75					80	
Leu	Glu	Gly	Arg	Leu	Pro	Gln	Gly	Pro	Gly	Glu	Ile	Ala	Val	Thr	Thr
				85				90						95	
Ala	Pro	Gly	Ala	Pro	Glu	Val	Gly	Glu	His	Val	Ser	Ile	Arg	Leu	Ser
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Gln	Asn	Thr	Glu	Asp	Thr	Glu	Val	Leu	Val	Val	Gly	Val	Val	Glu	Pro
		115					120					125			
Ala	Ala	Gln	Glu	Thr	Leu	Gly	Gly	Ala	Pro	Phe	Val	Val	Ala	Ser	Pro
		130				135					140				
Asp	Ala	Leu	Met	Glu	Trp	Asn	Ser	Ser	Gly	Val	Arg	Gly	Glu	Phe	Arg
	145				150					155				160	
Val	Ala	Thr	Ser	Asp	Pro	Ala	Ser	Leu	Glu	Ala	Ala	Ser	Phe	Ser	Asp
			165					170						175	
Ala	Thr	Val	Val	Val	Ala	Ser	Ala	Glu	Gly	His	Val	Asp	Lys	Leu	Ala
		180						185					190		
Asp	Ser	Tyr	Leu	Gly	Gln	Arg	Asp	Arg	Tyr	Phe	Leu	Leu	Leu	Ala	Ala
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Phe	Val	Ala	Val	Ala	Ala	Ala	Val	Ala	Phe	Leu	Val	Val	Phe	Ser	Ala
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Tyr	Ser	Val	Leu	Thr	Gly	Glu	Arg	Val	Arg	Glu	Phe	Gly	Leu	Ile	Arg
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Ser	Val	Gly	Ala	Ser	Thr	Pro	Gln	Ile	Leu	Gly	Ser	Val	Ile	Phe	Glu
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Ala	Gly	Ile	Leu	Gly	Val	Val	Ala	Ala	Gly	Phe	Gly	Ala	Pro	Ala	Gly
		260					265						270		
Leu	Met	Ala	Ala	Arg	Leu	Leu	Ala	Asp	Asn	Ala	Ala	Arg	Phe	Gly	Ile
		275					280						285		
Arg	Val	Pro	Ile	Asp	Val	Ile	Asp	Leu	Pro	Ser	Ser	Thr	Met	Trp	Leu
	290					295				300					
Ile	Ala	Gly	Val	Gly	Val	Val	Met	Ser	Val	Ile	Ala	Ala	Leu	Pro	Ala

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Val Phe Ser	Val Cys Arg Lys Ser	Ala Val Glu Ser	Leu Ser Thr	Pro		
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Ala Ile Ser	Arg Thr Ser Pro Trp	Phe Gly Ala Leu Trp	Leu Leu Leu			
	340	345	350			
Ala Gly Ile	Val Gly Ala Gly Gly Met	Trp Ala Tyr Glu Ala Thr Ser				
	355	360	365			
Asp Tyr Arg	Gly Met Arg Ser Val Ala Leu Ser	Ile Ala Gly Ser Gly				
	370	375	380			
Ala Leu Val	Cys Ala Leu Leu Ile Ala Thr	Ala Val Leu Val Pro Trp				
	385	390	395		400	
Leu Leu His	Val Phe Ser Arg Ile Val Gly Gly Thr Val Pro Thr Leu					
	405		410		415	
Gln Leu Gly	Leu Ala Phe Ala Ala Lys Gln Lys Ser Arg Ser Ala Ala					
	420		425		430	
Leu Ile Ala	Val Ile Leu Ala Gly Ser Ala Leu Ser Ser Ala Val Leu					
	435		440		445	
His Gly Gln	Ala His Ile Gly Thr His Leu Val Ala Val Ala Lys Gly					
	450		455		460	
Met Gly Gly	Thr Asp Met Met Val Thr Ala Leu Asp Gly Glu Ile Pro					
	465		470		475	480
Ala Gly Met	Leu Glu Glu Ile Ser Ser Ile Asp Gly Val Lys Thr Ala					
	485		490		495	
Ile Ala Pro	Ala Thr Thr Ala Val Glu Leu Glu Asp Ser Gly Asn Phe					
	500		505		510	
Ser Val Leu	Met Leu Ala Glu Glu Asp Gly Ala Ser Val Met Arg Ala					
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Gly Asp Thr	Gly Ala Pro Ala Gly Gly Leu Val Leu Gly Arg Asn Ser					
	530		535		540	
Pro Asp Gln	Asp Ala Tyr Pro Ala Gly Gln Ala Ala Asn Ile Ile Val					
	545		550		555	560
Ala Asp Thr	Pro Thr Gln Ala Glu Ile Phe His Ser Asp Asn Tyr Phe					
	565		570		575	
Ser Met Ile	Asp Pro Ala Leu Ala Thr Gly Pro Ser Thr Thr Arg Asn					
	580		585		590	
Val Leu Ile	Leu Leu Asp Gly Asp Ser Asn Gln Ala Pro Asp Asn Ala					
	595		600		605	
Thr Ala Gln	Ala Val Arg Lys Thr Ile Ser Leu Phe Asp Gly Arg Tyr					
	610		615		620	
Ser Ile Thr	Glu Gly Phe Ser Ala Arg Gln Asn Thr Phe Glu Leu Val					
	625		630		635	640

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Ser Arg Ile Thr Thr Met Ser Thr Leu Leu Ala Ile Val Ala Leu Ala
      645                      650                      655

Ile Ala Ala Val Gly Leu Ile Asn Thr Val Ala Leu Thr Ile Ser Glu
      660                      665                      670

Arg Ala Arg Asp Arg Tyr Leu Leu Arg Thr Ile Gly Leu Thr Ser Thr
      675                      680                      685

Gly Gln Ile Leu Val Met Ala Ile Glu Met Ile Ala Leu Ser Leu Pro
      690                      695                      700

Ala Ala Ile Val Gly Ala Val Ser Gly Gly Phe Leu Gly Arg Phe Val
      705                      710                      715                      720

Ala Ser Ser Ala Thr Asn Thr Ala Ala Thr Ala Pro Leu Gln Val Asp
      725                      730                      735

Ile Leu Gly Gly Thr Val Leu Ala Met Val Ala Gly Ser Val Leu Cys
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Ala Leu Ile Val Leu Ala Asn Lys Arg Arg Arg Val Val
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<211> 2166

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2143)

<223> FRXA00485

<400> 247

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      Leu Pro Gln Gly Pro
      1                      5

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Gly Glu Ile Ala Val Thr Thr Ala Pro Gly Ala Pro Glu Val Gly Glu
      10                      15                      20

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cac gta tcc att cgc ctg tcc caa aac act gag gac act gag gtt ctt 211
His Val Ser Ile Arg Leu Ser Gln Asn Thr Glu Asp Thr Glu Val Leu
      25                      30                      35

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gtg gtt ggc gtg gtg gag cca gcg gcg cag gaa act tta ggt ggc gca 259
Val Val Gly Val Val Glu Pro Ala Ala Gln Glu Thr Leu Gly Gly Ala
      40                      45                      50

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ccg ttc gtt gtg gcg tct cct gat gcg ctg atg gag tgg aat tct tcc 307
Pro Phe Val Val Ala Ser Pro Asp Ala Leu Met Glu Trp Asn Ser Ser
      55                      60                      65

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ggt gtg cgg ggt gaa ttc cga gtg gca act tcc gat cct gcc tcg cta 355
Gly Val Arg Gly Glu Phe Arg Val Ala Thr Ser Asp Pro Ala Ser Leu

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ggg cac gtc gat aag ctt gct gat tct tat ttg ggc cag cga gat cgc	451			
Gly His Val Asp Lys Leu Ala Asp Ser Tyr Leu Gly Gln Arg Asp Arg				
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tat ttc ttg ctg ctc gca gcg ttt gtg gca gtg gct gct gcc gtg gcg	499			
Tyr Phe Leu Leu Leu Ala Ala Phe Val Ala Val Ala Ala Val Ala				
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ttt ttg gtg gtc ttt tct gca tat tcg gtg ctc act ggt gag cga gtt	547			
Phe Leu Val Val Phe Ser Ala Tyr Ser Val Leu Thr Gly Glu Arg Val				
135 140 145				
cgc gag ttc ggg ctg att cgt tca gtg ggc gca tcg acg ccg cag att	595			
Arg Glu Phe Gly Leu Ile Arg Ser Val Gly Ala Ser Thr Pro Gln Ile				
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Leu Gly Ser Val Ile Phe Glu Ala Gly Ile Leu Gly Val Val Ala Ala				
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Gly Phe Gly Ala Pro Ala Gly Leu Met Ala Ala Arg Leu Leu Ala Asp				
185 190 195				
aat gcc gca cgt ttt ggc att cgt gtg ccc att gat gtg att gat ctg	739			
Asn Ala Ala Arg Phe Gly Ile Arg Val Pro Ile Asp Val Ile Asp Leu				
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cca agt agc acg atg ttg ctc atc gct ggc gtc ggc gtg gtg atg tcc	787			
Pro Ser Ser Thr Met Trp Leu Ile Ala Gly Val Gly Val Val Met Ser				
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Val Ile Ala Ala Leu Pro Ala Val Phe Ser Val Cys Arg Lys Ser Ala				
230 235 240 245				
gtg gaa tca ctg agt acg cct gct att tcg agg act tcc ccc tgg ttc	883			
Val Glu Ser Leu Ser Thr Pro Ala Ile Ser Arg Thr Ser Pro Trp Phe				
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Gly Ala Leu Trp Leu Leu Leu Ala Gly Ile Val Gly Ala Gly Met				
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tgg gcg tat gag gca acc tcg gac tac cgc ggc atg cgt tca gtg gct	979			
Trp Ala Tyr Glu Ala Thr Ser Asp Tyr Arg Gly Met Arg Ser Val Ala				
280 285 290				
tta tcc atc gcc ggt tca gcc gct ttg gtg tgt gcg ttg ttg att gcc	1027			
Leu Ser Ile Ala Gly Ser Gly Ala Leu Val Cys Ala Leu Leu Ile Ala				
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acg gcg gtg ctc gtg ccc tgg tta ttg cac gta ttc tcc agg att gtg	1075			
Thr Ala Val Leu Val Pro Trp Leu Leu His Val Phe Ser Arg Ile Val				
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Gly Gly Thr Val Pro Thr Leu Gln Leu Gly Leu Ala Phe Ala Ala Lys	
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Gln Lys Ser Arg Ser Ala Ala Leu Ile Ala Val Ile Leu Ala Gly Ser	
345 350 355	
gca tta agc tcc gct gtt ctg cat ggc cag gca cat atc ggc acg cat	1219
Ala Leu Ser Ser Ala Val Leu His Gly Gln Ala His Ile Gly Thr His	
360 365 370	
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Leu Val Ala Val Ala Lys Gly Met Gly Gly Thr Asp Met Met Val Thr	
375 380 385	
gcg ctt gat ggg gaa atc ccc gcc gga atg ctg gag gaa atc tct agc	1315
Ala Leu Asp Gly Glu Ile Pro Ala Gly Met Leu Glu Glu Ile Ser Ser	
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atc gac ggc gtg aaa act gcc atc gcg cca gcc acc acc gct gtg gaa	1363
Ile Asp Gly Val Lys Thr Ala Ile Ala Pro Ala Thr Thr Ala Val Glu	
410 415 420	
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Leu Glu Asp Ser Gly Asn Phe Ser Val Leu Met Leu Ala Glu Glu Asp	
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gga gcc tcc gtg atg cgc gca ggc gat act ggt gca cca gct ggt ggc	1459
Gly Ala Ser Val Met Arg Ala Gly Asp Thr Gly Ala Pro Ala Gly Gly	
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Leu Val Leu Gly Arg Asn Ser Pro Asp Gln Asp Ala Tyr Pro Ala Gly	
455 460 465	
cag gct gca aac atc att gtc gcg gat acc cca acg cag gcg gaa atc	1555
Gln Ala Ala Asn Ile Ile Val Ala Asp Thr Pro Thr Gln Ala Glu Ile	
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Phe His Ser Asp Asn Tyr Phe Ser Met Ile Asp Pro Ala Leu Ala Thr	
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Gly Pro Ser Thr Thr Arg Asn Val Leu Ile Leu Leu Asp Gly Asp Ser	
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Asn Gln Ala Pro Asp Asn Ala Thr Ala Gln Ala Val Arg Lys Thr Ile	
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tcg ctt ttc gac gga cga tac tcc atc acc gag ggt ttc tcc gcc cgc	1747
Ser Leu Phe Asp Gly Arg Tyr Ser Ile Thr Glu Gly Phe Ser Ala Arg	
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caa aac act ttt gaa ctg gtt tcc cgc atc acc acc atg tcc aca ctg	1795
Gln Asn Thr Phe Glu Leu Val Ser Arg Ile Thr Thr Met Ser Thr Leu	
550 555 560 565	

ctt gcc atc gtg gcc tta gcg atc gct gcc gtt ggc ctg atc aac aca 1843
 Leu Ala Ile Val Ala Leu Ala Ile Ala Val Gly Leu Ile Asn Thr 570 575 580

 gtg gca ctc acc att tct gag cgt gcc cgc gat cgt tat ttg ctg cgc 1891
 Val Ala Leu Thr Ile Ser Glu Arg Ala Arg Asp Arg Tyr Leu Leu Arg 585 590 595

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 Thr Ile Gly Leu Thr Ser Thr Gly Gln Ile Leu Val Met Ala Ile Glu 600 605 610

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 acg gca cca ctt caa gta gac att ctc ggc gga acg gtt ctc gcg atg 2083
 Thr Ala Pro Leu Gln Val Asp Ile Leu Gly Gly Thr Val Leu Ala Met 650 655 660

 gtc gca gga tct gta ctg tgc gcg ctc atc gtg ctg gcg aac aaa cga 2131
 Val Ala Gly Ser Val Leu Cys Ala Leu Ile Val Leu Ala Asn Lys Arg 665 670 675

 cgt cgg gtg gtt tgattataaa atccaaaaat cga 2166
 Arg Arg Val Val 680

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 <211> 681
 <212> PRT
 <213> *Corynebacterium glutamicum*

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 Asp Thr Glu Val Leu Val Val Gly Val Val Glu Pro Ala Ala Gln Glu
 35 40 45
 Thr Leu Gly Gly Ala Pro Phe Val Val Ala Ser Pro Asp Ala Leu Met
 50 55 60
 Glu Trp Asn Ser Ser Gly Val Arg Gly Glu Phe Arg Val Ala Thr Ser
 65 70 75 80
 Asp Pro Ala Ser Leu Glu Ala Ala Ser Phe Ser Asp Ala Thr Val Val
 85 90 95
 Val Ala Ser Ala Glu Gly His Val Asp Lys Leu Ala Asp Ser Tyr Leu
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 Gly Gln Arg Asp Arg Tyr Phe Leu Leu Leu Ala Ala Phe Val Ala Val

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Thr	Gly	Glu	Arg	Val	Arg	Glu	Phe	Gly	Leu	Ile	Arg	Ser	Val	Gly	Ala	
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Ser	Thr	Pro	Gln	Ile	Leu	Gly	Ser	Val	Ile	Phe	Glu	Ala	Gly	Ile	Leu	
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Cys	Arg	Lys	Ser	Ala	Val	Glu	Ser	Leu	Ser	Thr	Pro	Ala	Ile	Ser	Arg	
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Met	Arg	Ser	Val	Ala	Leu	Ser	Ile	Ala	Gly	Ser	Gly	Ala	Leu	Val	Cys	
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Phe	Ser	Arg	Ile	Val	Gly	Gly	Thr	Val	Pro	Thr	Leu	Gln	Leu	Gly	Leu	
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His	Ile	Gly	Thr	His	Leu	Val	Ala	Val	Ala	Lys	Gly	Met	Gly	Gly	Thr	
370					375					380						
Asp	Met	Met	Val	Thr	Ala	Leu	Asp	Gly	Glu	Ile	Pro	Ala	Gly	Met	Leu	
385					390					395					400	
Glu	Glu	Ile	Ser	Ser	Ile	Asp	Gly	Val	Lys	Thr	Ala	Ile	Ala	Pro	Ala	
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Leu	Ala	Glu	Glu	Asp	Gly	Ala	Ser	Val	Met	Arg	Ala	Gly	Asp	Thr	Gly	
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Ala Pro Ala Gly Gly Leu Val Leu Gly Arg Asn Ser Pro Asp Gln Asp
450 455 460

Ala Tyr Pro Ala Gly Gln Ala Ala Asn Ile Ile Val Ala Asp Thr Pro
465 470 475 480

Thr Gln Ala Glu Ile Phe His Ser Asp Asn Tyr Phe Ser Met Ile Asp
485 490 495

Pro Ala Leu Ala Thr Gly Pro Ser Thr Thr Arg Asn Val Leu Ile Leu
500 505 510

Leu Asp Gly Asp Ser Asn Gln Ala Pro Asp Asn Ala Thr Ala Gln Ala
515 520 525

Val Arg Lys Thr Ile Ser Leu Phe Asp Gly Arg Tyr Ser Ile Thr Glu
530 535 540

Gly Phe Ser Ala Arg Gln Asn Thr Phe Glu Leu Val Ser Arg Ile Thr
545 550 555 560

Thr Met Ser Thr Leu Leu Ala Ile Val Ala Leu Ala Ile Ala Ala Val
565 570 575

Gly Leu Ile Asn Thr Val Ala Leu Thr Ile Ser Glu Arg Ala Arg Asp
580 585 590

Arg Tyr Leu Leu Arg Thr Ile Gly Leu Thr Ser Thr Gly Gln Ile Leu
595 600 605

Val Met Ala Ile Glu Met Ile Ala Leu Ser Leu Pro Ala Ala Ile Val
610 615 620

Gly Ala Val Ser Gly Gly Phe Leu Gly Arg Phe Val Ala Ser Ser Ala
625 630 635 640

Thr Asn Thr Ala Ala Thr Ala Pro Leu Gln Val Asp Ile Leu Gly Gly
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Thr Val Leu Ala Met Val Ala Gly Ser Val Leu Cys Ala Leu Ile Val
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Leu Ala Asn Lys Arg Arg Arg Val Val
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<210> 249

<211> 1149

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1126)

<223> RXN00496

<400> 249

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cat ggt ggt gag cag gat ggc cag gaa cac gtt aaa gga cag cta aag						163
His Gly Gly Glu Gln Asp Gly Gln Glu His Val Lys Gly Gln Leu Lys						
	10				20	
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Gln Leu Phe Asp Asp Ala Phe Leu Thr Asp Leu Ser Arg Gly Val						
	25				35	
gat ccc tca gag ggc gat gac gcc ctc gct ggc ctc ctc ctc gat tta						259
Asp Pro Ser Glu Gly Asp Asp Ala Leu Ala Gly Leu Leu Leu Asp Leu						
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Thr Lys Glu Ala Gln Glu Pro Pro Ala Thr Met Pro Asp Trp Ser Thr						
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Leu Leu Pro Gly Ile Leu Asp Gln Asp Gln Asp Leu Pro Val Glu Ser						
	70				80	85
act tcg gac acc acg gtt atg cag gca tca aac cct gca acc caa gaa						403
Thr Ser Asp Thr Thr Val Met Gln Ala Ser Asn Pro Ala Thr Gln Glu						
	90				95	100
ttc gca cct gtt tct att tct gat acc ccc aac act gca act aat tca						451
Phe Ala Pro Val Ser Ile Ser Asp Thr Pro Asn Thr Ala Thr Asn Ser						
	105				110	115
gct gat gca gat gag tcc gca act gtt gtt cca ctt gca gca cgc cgt						499
Ala Asp Ala Asp Glu Ser Ala Thr Val Val Pro Leu Ala Ala Arg Arg						
	120				125	130
gag aag cgt gcc aag agc gga tca agc ggg gtt cat tca ctg gat gct						547
Glu Lys Arg Ala Lys Ser Gly Ser Ser Gly Val His Ser Leu Asp Ala						
	135				140	145
tcg gca acc cag cgc aaa tct cac cca ttc ctt agc ggt ttg gtg ggt						595
Ser Ala Thr Gln Arg Lys Ser His Pro Phe Leu Ser Gly Leu Val Gly						
	150				155	160
gct gca gct gca act cta gtc atc gca ggc ggt gga gca gca gtg tac						643
Ala Ala Ala Ala Thr Leu Val Ile Ala Gly Gly Gly Ala Ala Val Tyr						
	170				175	180
aac gct gat gaa aac tcc ccg ttg tat ggc atg aat cag cag ctg ttt						691
Asn Ala Asp Glu Asn Ser Pro Leu Tyr Gly Met Asn Gln Gln Leu Phe						
	185				190	195
ggc aat caa gat tct cca agc gtg gtg gag ctt gcc tcc acg ctg gaa						739
Gly Asn Gln Asp Ser Pro Ser Val Val Glu Leu Ala Ser Thr Leu Glu						
	200				205	210
gaa gtt gat agt cgt aca gct agt ggc gat gtg gaa ggg gca cgt gct						787
Glu Val Asp Ser Arg Thr Ala Ser Gly Asp Val Glu Gly Ala Arg Ala						
	215				220	225
cta ctc gag cag gct cga gca atg ctg gat ggc atg gca cct cct cga						835
Leu Leu Glu Gln Ala Arg Ala Met Leu Asp Gly Met Ala Pro Pro Arg						

230	235	240	245	
aag gcg ccg tcg gag gca acc cga acg gtt gaa tct gaa cca ggt act				883
Lys Ala Pro Ser Glu Ala Thr Arg Thr Val Glu Ser Glu Pro Gly Thr	250	255	260	
cag acg ttg act gca acg gtt act gaa tcc gca agt ccg gaa cca ccg				931
Gln Thr Leu Thr Ala Thr Val Thr Glu Ser Ala Ser Pro Glu Pro Pro	265	270	275	
gtc acg gaa act caa act gtt acc tcc acc gag gta cag aca gtg aca				979
Val Thr Glu Thr Gln Thr Val Thr Ser Thr Glu Val Gln Thr Val Thr	280	285	290	
acc act gcg gtt gct cca ccg gtc tgg act cct aat cca gag cca aca				1027
Thr Thr Glu Val Ala Pro Pro Val Trp Thr Pro Asn Pro Glu Pro Thr	295	300	305	
acc aca gct gcc ccg act tot acg cct tca act ggt ggc ggt gag gga				1075
Thr Thr Ala Ala Pro Thr Ser Thr Pro Ser Thr Gly Gly Gly Glu Gly	310	315	320	
acc ggc aat gat ggt gac tct gga ctt gtg cca cct cag act cct gga				1123
Thr Gly Asn Asp Gly Asp Ser Gly Leu Val Pro Pro Gln Thr Pro Gly	330	335	340	
aac taggtaaaaa tataaaaact gct				1149
Asn				
<210> 250				
<211> 342				
<212> FRT				
<213> Corynebacterium glutamicum				
<400> 250				
Met Thr Arg Arg Leu His Gly Gly Glu Gln Asp Gly Gln Glu His Val	1	5	10	15
Lys Gly Gln Leu Lys Gln Leu Phe Asp Asp Ala Phe Leu Thr Asp	20	25	30	
Leu Ser Arg Gly Val Asp Pro Ser Glu Gly Asp Asp Ala Leu Ala Gly	35	40	45	
Leu Leu Leu Asp Leu Thr Lys Glu Ala Gln Glu Pro Pro Ala Thr Met	50	55	60	
Pro Asp Trp Ser Thr Leu Leu Pro Gly Ile Leu Asp Gln Asp Gln Asp	65	70	75	80
Leu Pro Val Glu Ser Thr Ser Asp Thr Thr Val Met Gln Ala Ser Asn	85	90	95	
Pro Ala Thr Gln Glu Phe Ala Pro Val Ser Ile Ser Asp Thr Pro Asn	100	105	110	
Thr Ala Thr Asn Ser Ala Asp Ala Asp Glu Ser Ala Thr Val Val Pro	115	120	125	

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Leu Ala Ala Arg Arg Glu Lys Arg Ala Lys Ser Gly Ser Ser Gly Val
130                      135                      140

His Ser Leu Asp Ala Ser Ala Thr Gln Arg Lys Ser His Pro Phe Leu
145                      150                      155                      160

Ser Gly Leu Val Gly Ala Ala Ala Ala Thr Leu Val Ile Ala Gly Gly
165                      170                      175

Gly Ala Ala Val Tyr Asn Ala Asp Glu Asn Ser Pro Leu Tyr Gly Met
180                      185                      190

Asn Gln Gln Leu Phe Gly Asn Gln Asp Ser Pro Ser Val Val Glu Leu
195                      200                      205

Ala Ser Thr Leu Glu Glu Val Asp Ser Arg Thr Ala Ser Gly Asp Val
210                      215                      220

Glu Gly Ala Arg Ala Leu Leu Glu Gln Ala Arg Ala Met Leu Asp Gly
225                      230                      235                      240

Met Ala Pro Pro Arg Lys Ala Pro Ser Glu Ala Thr Arg Thr Val Glu
245                      250                      255

Ser Glu Pro Gly Thr Gln Thr Leu Thr Ala Thr Val Thr Glu Ser Ala
260                      265                      270

Ser Pro Glu Pro Pro Val Thr Glu Thr Gln Thr Val Thr Ser Thr Glu
275                      280                      285

Val Gln Thr Val Thr Thr Thr Ala Val Ala Pro Pro Val Trp Thr Pro
290                      295                      300

Asn Pro Glu Pro Thr Thr Thr Ala Ala Pro Thr Ser Thr Pro Ser Thr
305                      310                      315                      320

Gly Gly Gly Glu Gly Thr Gly Asn Asp Gly Asp Ser Gly Leu Val Pro
325                      330                      335

Pro Gln Thr Pro Gly Asn
340

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<210> 251

<211> 502

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(502)

<223> FRXA00496

<400> 251

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cgacacttcg aagcacactt gagcagcagg agaacaagta atg act cga cgt cta 115
              Met Thr Arg Arg Leu
              1              5

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cat ggt ggt gag cag gat ggc cag gaa cac gtt aaa gga cag cta aag 163

His Gly Gly Glu Gln Asp Gly Gln Glu His Val Lys Gly Gln Leu Lys
 10 15 20
 cag ctg ttc gac gac gac gcg ttc ttg act gac ctg tcc cgc ggc gtt 211
 Gln Leu Phe Asp Asp Ala Phe Leu Thr Asp Leu Ser Arg Gly Val
 25 30 35
 gat ccc tca gag ggc gat gac gcc ctc gct ggc ctc ctc gat tta 259
 Asp Pro Ser Ser Glu Gly Asp Asp Ala Leu Ala Gly Leu Leu Asp Leu
 40 45 50
 aca aag gaa gct cag gag ccg ccg gca aca atg ccg gat tgg tct act 307
 Thr Lys Glu Ala Gln Glu Pro Pro Ala Thr Met Pro Asp Trp Ser Thr
 55 60 65
 ttg ctc cct gga att ttg gat cag gat cag gat ttg cca gtg gaa tcc 355
 Leu Leu Pro Gly Ile Leu Asp Gln Asp Gln Asp Leu Pro Val Glu Ser
 70 75 80 85
 act tcg gac acc acg gtt atg cag gca tca aac cct gca acc caa gaa 403
 Thr Ser Asp Thr Thr Val Met Gln Ala Ser Asn Pro Ala Thr Gln Glu
 90 95 100
 ttc gca cct gtt tct att tct gat acc ccc aac act gca act aat tca 451
 Phe Ala Pro Val Ser Ile Ser Asp Thr Pro Asn Thr Ala Thr Asn Ser
 105 110 115
 gct gat gca gat gag tcc gca act gtt gtt cca ctt gca gca cgc cgt 499
 Ala Asp Ala Asp Glu Ser Ala Thr Val Val Pro Leu Ala Ala Arg Arg
 120 125 130
 gag 502
 Glu
 <210> 252
 <211> 134
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 252
 Met Thr Arg Arg Leu His Gly Gly Glu Gln Asp Gly Gln Glu His Val
 1 5 10 15
 Lys Gly Gln Leu Lys Gln Leu Phe Asp Asp Ala Phe Leu Thr Asp
 20 25 30
 Leu Ser Arg Gly Val Asp Pro Ser Glu Gly Asp Asp Ala Leu Ala Gly
 35 40 45
 Leu Leu Leu Asp Leu Thr Lys Glu Ala Gln Glu Pro Pro Ala Thr Met
 50 55 60
 Pro Asp Trp Ser Thr Leu Leu Pro Gly Ile Leu Asp Gln Asp Gln Asp
 65 70 75 80
 Leu Pro Val Glu Ser Thr Ser Asp Thr Thr Val Met Gln Ala Ser Asn
 85 90 95
 Pro Ala Thr Gln Glu Phe Ala Pro Val Ser Ile Ser Asp Thr Pro Asn

100

105

110

Thr Ala Thr Asn Ser Ala Asp Ala Asp Glu Ser Ala Thr Val Val Pro
 115 120 125

Leu Ala Ala Arg Arg Glu
 130

<210> 253

<211> 1845

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}...(1822)

<223> RXN00503

<400> 253

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tgagacccca cagggtgtttt aaacattttag tattagtctcc atg aaa cca gtc ttc 115
 Met Lys Pro Val Phe
 1 5

tcc gtt gac caa atc cga cgc gca gaa aac acc ctt ttt gag ctt cag 163
 Ser Val Asp Gln Ile Arg Ala Glu Asn Thr Leu Phe Glu Leu Gln
 10 15 20

gca gat ccg gat gag ctg atg atc tcc gcg gca tcg gcg gtg gcc gat 211
 Ala Asp Pro Asp Glu Leu Met Ile Ser Ala Ala Ser Ala Val Ala Asp
 25 30 35

gtc gcg ttg gca atg gtg gac ggc ccc gct cca gcg gtc tcc agt gag 259
 Val Ala Leu Ala Met Val Asp Gly Pro Ala Pro Ala Val Ser Ser Glu
 40 45 50

gag tca atc ctg ctg ctg gtc ggc ccc ggt ggc aac ggt ggc gac gcc 307
 Glu Ser Ile Leu Leu Leu Val Gly Pro Gly Gly Asn Gly Gly Asp Ala
 55 60 65

ttg tat gca ggc gcg ttc ctt gca gaa gaa ggc cac cac gtt gat gct 355
 Leu Tyr Ala Gly Ala Phe Leu Ala Glu Glu Gly His His Val Asp Ala
 70 75 80 85

ttg ctg ttg gga aac ggc aaa gtc cat caa tca gca ttg gca tat tat 403
 Leu Leu Leu Gly Asn Gly Lys Val His Gln Ser Ala Leu Ala Tyr Tyr
 90 95 100

gag tct ttg ggc ggg cag atc att tcc gat ttt ccc cct cac tac ctc 451
 Glu Ser Leu Gly Gly Gln Ile Ile Ser Asp Phe Pro Pro His Tyr Leu
 105 110 115

tac cgc ctg gtg att gat ggt ttg ttt ggc atc ggt ggt cgg gga ggg 499
 Tyr Arg Leu Val Ile Asp Gly Leu Phe Gly Ile Gly Gly Arg Gly Gly
 120 125 130

ctc acc cca gag ctg gcc agt ttg gtg gag tct ttt tcc gct tca ggt 547
 Leu Thr Pro Glu Leu Ala Ser Leu Val Glu Ser Phe Ser Ala Ser Gly
 135 140 145

115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

atc ccc att ttg gcg att gat gtg ccg tct ggc gtg cat gcc gat agt 595
 ile Pro ile Leu Ala ile Asp Val Pro Ser Gly Val His Ala Asp Ser
 150 155 160

ggt gaa ctg ccg ccc ggc gtg atg gtg acg gtg gaa gga ttt gat aat 643
 Gly Glu Leu Pro Pro Gly Val Met Val Thr Val Glu Gly Phe Asp Asn
 170 175 180

gat gca ccg atg gcg cgt cag aaa att ccg gca cac att gac gct gat 691
 Asp Ala Pro Met Ala Arg Gln Lys ile Pro Ala His ile Asp Ala Asp
 185 190 195

gtc acg atc acg ttt ggc ggt ttg aga cgc gcc cac gcg gtc agt cct 739
 Val Thr ile Thr Phe Gly Gly Leu Arg Arg Ala His Ala Val Ser Pro
 200 205 210

gcg tgt ggt gaa gtg ctc tgt gct gat atc aac atc gct ggt ggc gcc 787
 Ala Cys Gly Glu Val Leu Cys Ala Asp ile Asn ile Ala Gly Gly Gly
 215 220 225

gga aaa tcg ctg tcc gct gag ttg agt cag gtg cag gca gaa gac gcg 835
 Gly Lys Ser Leu Ser Ala Glu Leu Ser Gln Val Gln Ala Glu Asp Ala
 230 235 240 245

acc ccg cag atg ttt gcc tcc aag gcg tat caa cgg aaa gat tcg ctt 883
 Thr Pro Gln Met Phe Ala Ser Lys Ala Tyr Gln Arg Lys Asp Ser Leu
 250 255 260

ttt gag cgc gcg aat ctc aaa gct acg gcg cca cat atc cat agg atc 931
 Phe Glu Arg Ala Asn Leu Lys Ala Thr Ala Pro His ile His Arg ile
 265 270 275

ggc cag cac ttt acc gtg ttg aac atg gag cct ggc ccg gat cat gat 979
 Gly Gln His Phe Thr Val Leu Asn Met Glu Pro Gly Pro Asp His Asp
 280 285 290

aaa tac agt ggc gga att gtc gcc att gtt gca ggt agt ggc acc tat 1027
 Lys Tyr Ser Gly Gly ile Val Gly ile Val Ala Gly Ser Gly Thr Tyr
 295 300 305

cca ggt gct gct gtg ctg tcg gtg aag gcg gct gtc agg gcc aca agc 1075
 Pro Gly Ala Ala Val Leu Ser Val Lys Ala Ala Val Arg Ala Thr Ser
 310 315 320 325

gcc atg gtt cga tac gtt ggc cct gcg tta aat ttt gtc atc cag tcg 1123
 Ala Met Val Arg Tyr Val Gly Pro Ala Leu Asn Phe Val ile Gln Ser
 330 335 340

ctg ccg gag gtc gtc gca acg caa tca ctt gcc acc gcc ggc cgc gtg 1171
 Leu Pro Glu Val Val Ala Thr Gln Ser Leu Ala Thr Ala Gly Arg Val
 345 350 355

caa gcg tgg gtg cac ggc ccc gga cgc ggg ctg gag gct gag caa tca 1219
 Gln Ala Trp Val His Gly Pro Gly Arg Gly Leu Glu Ala Glu Gln Ser
 360 365 370

gcc gag ctt gcg gag ctt ttg agc cgg cct gag cct gtg ctt atc gac 1267
 Ala Glu Leu Ala Glu Leu Leu Ser Arg Pro Glu Pro Val Leu ile Asp
 375 380 385

gcc gac agc ctc tca tta ctc cag ctc tca gcg gag ctt cgg cag gcg 1315
Ala Asp Ser Leu Ser Leu Leu Gln Leu Ser Ala Glu Leu Arg Gln Ala
390 395 400 405

ttg cgc gag cga aaa gca cca acg gtg ctc act cgg cac aag ggc gaa 1363
Leu Arg Glu Arg Lys Ala Pro Thr Val Leu Thr Pro His Lys Gly Glu
410 415 420

ttt gaa cgc atc gca gca gaa tta cgc tct gaa ggc gtc gag att ccc 1411
Phe Glu Arg Ile Ala Ala Glu Leu Arg Ser Glu Gly Val Glu Ile Pro
425 430 435

caa gcg gac aaa gat ccc att ggt gct gcg caa gcg tta gct aaa gaa 1459
Gln Ala Asp Lys Asp Pro Ile Gly Ala Ala Gln Ala Leu Ala Lys Glu
440 445 450

ttt gat tgt tgc gta ctg ctc aag ggg aaa tac acc gtc att gca gct 1507
Phe Asp Cys Cys Val Leu Leu Lys Gly Lys Tyr Thr Val Ile Ala Ala
455 460 465

cac gac ttt gtg cat gcg atc aac gct ggg cat tcc tgg ttg gct aca 1555
His Asp Phe Val His Ala Ile Asn Ala Gly His Ser Trp Leu Ala Thr
470 475 480 485

cct ggc tct ggc gat gtg ttg tca ggt ctt gtc ggt gca cac ttg gct 1603
Pro Gly Ser Gly Asp Val Leu Ser Gly Leu Val Gly Ala His Leu Ala
490 495 500

caa agc tac gca gaa tta aac cgc ttg cgg gag ttt ttc ccc gat gtg 1651
Gln Ser Tyr Ala Glu Leu Asn Arg Leu Pro Glu Phe Phe Pro Asp Val
505 510 515

acc ttg tct gat tgc gcg att tac acc cag att gca cct gct gcg acc 1699
Thr Leu Ser Asp Ser Ala Ile Tyr Thr Gln Ile Ala Pro Ala Ala Thr
520 525 530

atc cac gcg gtt gct gct ggg ttg gcc gca cga acc gaa ttt ggg ttt 1747
Ile His Ala Val Ala Ala Gly Leu Ala Ala Arg Thr Glu Phe Gly Phe
535 540 545

gcg cgg acc tcc gca agt ttg atc gct gat gcc atc cct gca gcg acc 1795
Ala Pro Thr Ser Ala Ser Leu Ile Ala Asp Ala Ile Pro Ala Ala Thr
550 555 560 565

gcc aag gtg gat ttg aag cga att gtc tagctctgca tgaattccgt 1842
Ala Lys Val Asp Leu Lys Arg Ile Val
570

atg 1845

<210> 254
<211> 574
<212> PRT
<213> *Corynebacterium glutamicum*

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Met Lys Pro Val Phe Ser Val Asp Gln Ile Arg Arg Ala Glu Asn Thr
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Leu Phe Glu Leu Gln Ala Asp Pro Asp Glu Leu Met Ile Ser Ala Ala

20										25					30				
Ser	Ala	Val	Ala	Asp	Val	Ala	Leu	Ala	Met	Val	Asp	Gly	Pro	Ala	Pro				
35										40					45				
Ala	Val	Ser	Ser	Glu	Glu	Ser	Ile	Leu	Leu	Leu	Val	Gly	Pro	Gly	Gly				
50										55					60				
Asn	Gly	Gly	Asp	Ala	Leu	Tyr	Ala	Gly	Ala	Phe	Leu	Ala	Glu	Glu	Gly				
65										70					75				
His	His	Val	Asp	Ala	Leu	Leu	Leu	Gly	Asn	Gly	Lys	Val	His	Gln	Ser				
85										90					95				
Ala	Leu	Ala	Tyr	Tyr	Glu	Ser	Leu	Gly	Gly	Gln	Ile	Ile	Ser	Asp	Phe				
100										105					110				
Pro	Pro	His	Tyr	Leu	Tyr	Arg	Leu	Val	Ile	Asp	Gly	Leu	Phe	Gly	Ile				
115										120					125				
Gly	Gly	Arg	Gly	Gly	Leu	Thr	Pro	Glu	Leu	Ala	Ser	Leu	Val	Glu	Ser				
130										135					140				
Phe	Ser	Ala	Ser	Gly	Ile	Pro	Ile	Leu	Ala	Ile	Asp	Val	Pro	Ser	Gly				
145										150					155				
Val	His	Ala	Asp	Ser	Gly	Glu	Leu	Pro	Pro	Gly	Val	Met	Val	Thr	Val				
165										170					175				
Glu	Gly	Phe	Asp	Asn	Asp	Ala	Pro	Met	Ala	Arg	Gln	Lys	Ile	Pro	Ala				
180										185					190				
His	Ile	Asp	Ala	Asp	Val	Thr	Ile	Thr	Phe	Gly	Gly	Leu	Arg	Arg	Ala				
195										200					205				
His	Ala	Val	Ser	Pro	Ala	Cys	Gly	Glu	Val	Leu	Cys	Ala	Asp	Ile	Asn				
210										215					220				
Ile	Ala	Gly	Gly	Gly	Gly	Lys	Ser	Leu	Ser	Ala	Glu	Leu	Ser	Gln	Val				
225										230					235				
Gln	Ala	Glu	Asp	Ala	Thr	Pro	Gln	Met	Phe	Ala	Ser	Lys	Ala	Tyr	Gln				
245										250					255				
Arg	Lys	Asp	Ser	Leu	Phe	Glu	Arg	Ala	Asn	Leu	Lys	Ala	Thr	Ala	Pro				
260										265					270				
His	Ile	His	Arg	Ile	Gly	Gln	His	Phe	Thr	Val	Leu	Asn	Met	Glu	Pro				
275										280					285				
Gly	Pro	Asp	His	Asp	Lys	Tyr	Ser	Gly	Gly	Ile	Val	Gly	Ile	Val	Ala				
290										295					300				
Gly	Ser	Gly	Thr	Tyr	Pro	Gly	Ala	Ala	Val	Leu	Ser	Val	Lys	Ala	Ala				
305										310					315				
Val	Arg	Ala	Thr	Ser	Ala	Met	Val	Arg	Tyr	Val	Gly	Pro	Ala	Leu	Asn				
325										330					335				
Phe	Val	Ile	Gln	Ser	Leu	Pro	Glu	Val	Val	Ala	Thr	Gln	Ser	Leu	Ala				
340										345					350				


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Thr Ala Gly Arg Val Gln Ala Trp Val His Gly Pro Gly Arg Gly Leu
  355                      360                      365

Glu Ala Glu Gln Ser Ala Glu Leu Ala Glu Leu Leu Ser Arg Pro Glu
  370                      375                      380

Pro Val Leu Ile Asp Ala Asp Ser Leu Ser Leu Leu Gln Leu Ser Ala
  385                      390                      395                      400

Glu Leu Arg Gln Ala Leu Arg Glu Arg Lys Ala Pro Thr Val Leu Thr
  405                      410                      415

Pro His Lys Gly Glu Phe Glu Arg Ile Ala Ala Glu Leu Arg Ser Glu
  420                      425                      430

Gly Val Glu Ile Pro Gln Ala Asp Lys Asp Pro Ile Gly Ala Ala Gln
  435                      440                      445

Ala Leu Ala Lys Glu Phe Asp Cys Cys Val Leu Leu Lys Gly Lys Tyr
  450                      455                      460

Thr Val Ile Ala Ala His Asp Phe Val His Ala Ile Asn Ala Gly His
  465                      470                      475                      480

Ser Trp Leu Ala Thr Pro Gly Ser Gly Asp Val Leu Ser Gly Leu Val
  485                      490                      495

Gly Ala His Leu Ala Gln Ser Tyr Ala Glu Leu Asn Arg Leu Pro Glu
  500                      505                      510

Phe Phe Pro Asp Val Thr Leu Ser Asp Ser Ala Ile Tyr Thr Gln Ile
  515                      520                      525

Ala Pro Ala Ala Thr Ile His Ala Val Ala Ala Gly Leu Ala Ala Arg
  530                      535                      540

Thr Glu Phe Gly Phe Ala Pro Thr Ser Ala Ser Leu Ile Ala Asp Ala
  545                      550                      555                      560

Ile Pro Ala Ala Thr Ala Lys Val Asp Leu Lys Arg Ile Val
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<210> 255

<211> 543

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(520)

<223> RXN00504

<400> 255

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 Met Thr Tyr Gly Phe
 1 5

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ctt gtc aac aca gat ctc acc cac cgc gcg att gac ttt gat tta gaa 163
Leu Val Asn Thr Asp Leu Thr His Arg Ala Ile Asp Phe Asp Leu Glu
      10      15      20

aac gct gcg aag ttc ctc ggc ggt gcc gat gat ggc cgc gtc gct gtc 211
Asn Ala Ala Lys Phe Leu Gly Gly Ala Asp Asp Gly Arg Val Ala Val
      25      30      35

gct ttc caa gag gat ggc acc ttg tac gcc gct ctc tac agc gcc agc 259
Ala Phe Gln Glu Asp Gly Thr Leu Tyr Ala Ala Leu Tyr Ser Ala Ser
      40      45      50

gca aaa gat gag ggt gcc gca gca aac cca gta gca tcc ctt ggc cgc 307
Ala Lys Asp Glu Gly Ala Ala Asn Pro Val Ala Ser Leu Gly Arg
      55      60      65

aac gcc gct gct acc ggt gat ggc tcc ttc ttc tct gat ccg acc act 355
Asn Ala Ala Ala Thr Gly Asp Gly Ser Phe Phe Ser Asp Pro Thr Thr
      70      75      80      85

gca atc tgt ggc cct gtg atc ttc gtg ggg gcc gaa ggc gaa gac atc 403
Ala Ile Cys Gly Pro Val Ile Phe Val Gly Ala Glu Gly Glu Asp Ile
      90      95      100

acg ttg gat gaa att gag cga att aag gac ggc att cgc gcc gct cgt 451
Thr Leu Asp Glu Ile Glu Arg Ile Lys Asp Gly Ile Arg Ala Ala Arg
      105      110      115

aac tac cgc gat gat tat cca gag gaa ttc aac ctg tgg cgc aac gct 499
Asn Tyr Arg Asp Asp Tyr Pro Glu Glu Phe Asn Leu Trp Arg Asn Ala
      120      125      130

gta tat aac ctg cgt acg gct taaagtgttg ctgccatgtg aat 543
Val Tyr Asn Leu Arg Thr Ala
      135      140

<210> 256
<211> 140
<212> PRT
<213> Corynebacterium glutamicum

<400> 256
Met Thr Tyr Gly Phe Leu Val Asn Thr Asp Leu Thr His Arg Ala Ile
  1      5      10      15

Asp Phe Asp Leu Glu Asn Ala Ala Lys Phe Leu Gly Gly Ala Asp Asp
      20      25      30

Gly Arg Val Ala Val Ala Phe Gln Glu Asp Gly Thr Leu Tyr Ala Ala
      35      40      45

Leu Tyr Ser Ala Ser Ala Lys Asp Glu Gly Ala Ala Ala Asn Pro Val
      50      55      60

Ala Ser Leu Gly Arg Asn Ala Ala Ala Thr Gly Asp Gly Ser Phe Phe
      65      70      75      80

Ser Asp Pro Thr Thr Ala Ile Cys Gly Pro Val Ile Phe Val Gly Ala
      85      90      95

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Glu Gly Glu Asp Ile Thr Leu Asp Glu Ile Glu Arg Ile Lys Asp Gly
 100 105 110
 Ile Arg Ala Ala Arg Asn Tyr Arg Asp Asp Tyr Pro Glu Glu Phe Asn
 115 120 125
 Leu Trp Arg Asn Ala Val Tyr Asn Leu Arg Thr Ala
 130 135 140

<210> 257
 <211> 346
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(346)
 <223> FRXA00504

<400> 257
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 Met Thr Tyr Gly Phe
 1 5
 ctt gtc aac aca gat ctc acc cac cgc gcg att gac ttt gat tta gaa 163
 Leu Val Asn Thr Asp Leu Thr His Arg Ala Ile Asp Phe Asp Leu Glu
 10 15 20
 aac gct gcg aag ttc ctc ggc ggt gcc gat gat ggc cgc gtc gct gtc 211
 Asn Ala Ala Lys Phe Leu Gly Gly Ala Asp Asp Gly Arg Val Ala Val
 25 30 35
 gct ttc caa gag gat ggc acc ttg tac gcc gct ctc tac agc gcc agc 259
 Ala Phe Gln Glu Asp Gly Thr Leu Tyr Ala Ala Leu Tyr Ser Ala Ser
 40 45 50
 gca aaa gat gag ggt gcc gca gca aac cca gta gca tcc ctt ggc cgc 307
 Ala Lys Asp Glu Gly Ala Ala Ala Asn Pro Val Ala Ser Leu Gly Arg
 55 60 65
 aac gcc gct gct acc ggt gat ggc tcc ttc ttc tct gat 346
 Asn Ala Ala Ala Thr Gly Asp Gly Ser Phe Phe Ser Asp
 70 75 80

<210> 258
 <211> 82
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 258
 Met Thr Tyr Gly Phe Leu Val Asn Thr Asp Leu Thr His Arg Ala Ile
 1 5 10 15
 Asp Phe Asp Leu Glu Asn Ala Ala Lys Phe Leu Gly Gly Ala Asp Asp
 20 25 30
 Gly Arg Val Ala Val Ala Phe Gln Glu Asp Gly Thr Leu Tyr Ala Ala

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<210> 259
<211> 618
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(595)
<223> RXN00505
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4400> 259																			
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tccgcgcata tgtttaagtg aatacgttta aggagcagca						atg	aaa	tct	gag	ttt		115							
						Met	Lys	Ser	Glu	Phe									
						1				5									
cgc gta tcc ggc acg agg cgt ttt gag	cat	gcc	gca	gat	acc	caa	aat	163											
Pro Val Ser Gly Thr 10 Arg Arg Phe	Glu	His	Ala	Ala	Asp	Thr	Asn												
						15				20									
ttt ggg gaa gaa tta ggc agg cat cta gaa gct ggc gat	gtg	gtg	att	211															
Phe Gly Glu Glu Leu Leu Gly Arg His	Leu	Glu	Ala	Gly	Asp	Val	Val	Ile											
						25				35									
ttg gac ggc cgc ctg ggt gct gga aaa acc aca ttt act	caa	ggt	atc	259															
Leu Asp Gly Pro Leu Leu Gly Ala Gly Lys Thr Thr	Phe	Thr	Gln	Gly	Ile														
						40				50									
gct cgt gga ttg cag gtg aag ggg cgg gtg aca tgc cgc acg ttt	gtg	307																	
Ala Arg Gly Leu Gln Val Lys Gly Arg Val Thr	Ser	Pro	Thr	Phe	Val														
						55				60									
atc cgc agg gaa cac cgc tgc gaa atc ggt ggg cca gat	ctg	atc	cac	355															
Ile Ala Arg Glu His Arg Ser Glu Ile Gly	Gly	Pro	Asp	Leu	Ile	His													
						70				80									
atg gat gcc tac cga ttg ctg ggc gaa gac agc gag gat	gct	gat	cgc	403															
Met Asp Ala Tyr Arg Leu Leu Gly Glu Asp Ser	Glu	Asp	Ala	Gly	Pro														
						90				95									
atc ggt ggc ctg gac tct ttg gat ttg gat acc gat	ttg	gac	ttg	gct	451														
Ile Gly Ala Leu Asp Ser Leu Asp Leu Asp Thr	Asp	Leu	Asp	Leu	Ala														
						105				110									
gtg gtt gtt gcg gaa tgg ggc ggt ggc ttg gtg gag	cag	atc	gct	gac	499														
Val Val Val Ala Glu Trp Gly Gly Glu Leu Val Glu	Gln	Ile	Ala	Asp															
						120				125									

tgc tat ctt ttg att acc att gat cga gag acc gct gtg cag gaa gac 547
 Ser Tyr Leu Leu Ile Thr Ile Asp Arg Glu Thr Ala Val Gln Glu Asp
 135 140 145

cgc gaa tct gag gct cga att ttc cat tgg gaa tgg cgc gaa ggc cgc 595
 Pro Glu Ser Glu Ala Arg Ile Phe His Trp Glu Trp Arg Glu Gly Arg
 150 155 160 165

tgagaaagtt ttccacgcta aaa 618

<210> 260

<211> 165

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 260

Met Lys Ser Glu Phe Pro Val Ser Gly Thr Arg Arg Phe Glu His Ala
 1 5 10 15

Ala Asp Thr Gln Asn Phe Gly Glu Glu Leu Gly Arg His Leu Glu Ala
 20 25 30

Gly Asp Val Val Ile Leu Asp Gly Pro Leu Gly Ala Gly Lys Thr Thr
 35 40 45

Phe Thr Gln Gly Ile Ala Arg Gly Leu Gln Val Lys Gly Arg Val Thr
 50 55 60

Ser Pro Thr Phe Val Ile Ala Arg Glu His Arg Ser Glu Ile Gly Gly
 65 70 75 80

Pro Asp Leu Ile His Met Asp Ala Tyr Arg Leu Leu Gly Glu Asp Ser
 85 90 95

Glu Asp Ala Asp Pro Ile Gly Ala Leu Asp Ser Leu Asp Leu Asp Thr
 100 105 110

Asp Leu Asp Leu Ala Val Val Ala Glu Trp Gly Gly Glu Leu Val
 115 120 125

Glu Gln Ile Ala Asp Ser Tyr Leu Leu Ile Thr Ile Asp Arg Glu Thr
 130 135 140

Ala Val Gln Glu Asp Pro Glu Ser Glu Ala Arg Ile Phe His Trp Glu
 145 150 155 160

Trp Arg Glu Gly Arg
 165

<210> 261

<211> 275

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {1}..(252)

<223> FRXA00505

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<400> 261
gat ctg atc cac atg gat gcc tac cga ttg ctg ggc gaa gac agc gag      48
Asp Leu Ile His Met Asp Ala Tyr Arg Leu Leu Gly Glu Asp Ser Glu
   1             5             10             15

gat gct gat ccg atc ggt gcg ctg gac tct ttg gat ttg gat acc gat      96
Asp Ala Asp Pro Ile Gly Ala Leu Asp Ser Leu Asp Leu Asp Thr Asp
           20             25             30

ttg gac ttg gct gtg gtt gtt gcg gaa tgg ggc ggt ggc ttg gtg gag      144
Leu Asp Leu Ala Val Val Val Ala Glu Trp Gly Gly Glu Leu Val Glu
           35             40             45

cag atc gct gac tcg tat ctt ttg att acc att gat cga gag acc gct      192
Gln Ile Ala Asp Ser Tyr Leu Leu Ile Thr Ile Asp Arg Glu Thr Ala
           50             55             60

gtg cag gaa gac ccg gaa tct gag gct cga att ttc cat tgg gaa tgg      240
Val Gln Glu Asp Pro Glu Ser Glu Ala Arg Ile Phe His Trp Glu Trp
           65             70             75             80

cgc gaa ggc cgc tgagaaagtt ttccacgcta aaa      275
Arg Glu Gly Arg

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<210> 262
<211> 84
<212> PRT
<213> Corynebacterium glutamicum

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<400> 262
Asp Leu Ile His Met Asp Ala Tyr Arg Leu Leu Gly Glu Asp Ser Glu
   1             5             10             15

Asp Ala Asp Pro Ile Gly Ala Leu Asp Ser Leu Asp Leu Asp Thr Asp
           20             25             30

Leu Asp Leu Ala Val Val Val Ala Glu Trp Gly Gly Glu Leu Val Glu
           35             40             45

Gln Ile Ala Asp Ser Tyr Leu Leu Ile Thr Ile Asp Arg Glu Thr Ala
           50             55             60

Val Gln Glu Asp Pro Glu Ser Glu Ala Arg Ile Phe His Trp Glu Trp
           65             70             75             80

Arg Glu Gly Arg

```

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<210> 263
<211> 978
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> {101}..(955)
<223> RXN00507

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<400> 263
gttcattgtg aactattgtg ccaccaacgc cggacagaaa tacgattggt gccgggggta 60
gtgccagtat tgccccacgc ttccaactat ccttaaacac gtg gct gag aat ctg 115
Val Ala Glu Asn Leu
1 5
aac aaa cac ctg tcc aaa ctg tcc aag cgc gga cgc cac cgc gtg ctg 163
Asn Lys His Leu Ser Lys Leu Ser Lys Arg Gly Pro His Arg Val Leu
10 15 20
gta ggc gat atg aac tac gcc ggc atc ccg ggc aaa atc tac acc cca 211
Val Gly Asp Met Asn Tyr Ala Gly Ile Pro Gly Lys Ile Tyr Thr Pro
25 30 35
gca gaa ggc gac ggc atc cca ggt gta gct ttc ggc cac gac tgg atg 259
Ala Glu Gly Asp Gly Ile Pro Gly Val Ala Phe Gly His Asp Trp Met
40 45 50
aaa tcc atc aag tac tac cac caa act ttg cga cac ctc gcg tcc tgg 307
Lys Ser Ile Lys Tyr Tyr His Gln Thr Leu Arg His Leu Ala Ser Trp
55 60 65
ggc atc gct gtt gcc gcc cca gac acc gaa aat ggc ttc atg cca gac 355
Gly Ile Ala Val Ala Ala Pro Asp Thr Glu Asn Gly Phe Met Pro Asp
70 75 80 85
cac aaa ggt ttc gcc tct gac ctc gaa tcc tcc att cag att ctc ggc 403
His Lys Gly Phe Ala Ser Asp Leu Glu Ser Ser Ile Gln Ile Leu Gly
90 95 100
ggc gta aaa ctc ggc tcc gga aac gtc acc gtc aac cca gcc tgc ctc 451
Gly Val Lys Leu Gly Ser Gly Asn Val Thr Val Asn Pro Ala Cys Leu
105 110 115
ggt gta gta ggc cac ggc atg ggt gct ggg gct gca gta cta tcc gca 499
Gly Val Val Gly His Gly Met Gly Ala Gly Ala Val Leu Ser Ala
120 125 130
gca aac cgc gac ctc gtg cgc gca gtc gga gca atc tac cca gcg aaa 547
Ala Asn Arg Asp Leu Val Arg Ala Val Gly Ala Ile Tyr Pro Ala Lys
135 140 145
acc tcc ccc tca gca atc gac gcc gcc ttc gct gtc aaa gcc cca ggc 595
Thr Ser Pro Ser Ala Ile Asp Ala Ala Phe Ala Val Lys Ala Pro Gly
150 155 160 165
cta gtc atc gga tcc tcc agc ctc ggc ctc ttt gaa tcc ggc gag cca 643
Leu Val Ile Gly Ser Ser Ser Leu Gly Leu Phe Glu Ser Gly Glu Pro
170 175 180
gca aaa ctc gca gcc aac tgg gcc ggc gat gtc tgc tac cgc gaa tca 691
Ala Lys Leu Ala Ala Asn Trp Ala Gly Asp Val Cys Tyr Arg Glu Ser
185 190 195
gaa aaa ggc aac caa cag ggc ttc tct gaa gac acc atg ttc aaa ctt 739
Glu Lys Gly Asn Gln Gln Gly Phe Ser Glu Asp Thr Met Phe Lys Leu
200 205 210
gtc gca gga atc ggc agc cca caa acc gga gct caa gaa acc gtc cgc 787
Val Ala Gly Ile Gly Ser Pro Gln Thr Gly Ala Gln Glu Thr Val Arg

215

220

225

ggc ctc ctc acc gga ttc ctt ctc cac caa ctt gcc gga gaa aag aaa 835
 Gly Leu Leu Thr Gly Phe Leu Leu His Gln Leu Ala Gly Glu Lys Lys
 230 235 240 245

tac aaa gca ttc tcc gaa cca gac gct gaa gct aag aaa gtt gtc tcc 883
 Tyr Lys Ala Phe Ser Glu Pro Asp Ala Glu Ala Lys Lys Val Val Ser
 250 255 260

tac ttc ggc cag gag ctg cag gaa cat gcc ttc cct aag gac acg tcc 931
 Tyr Phe Gly Gln Glu Leu Gln Glu His Ala Phe Pro Lys Asp Thr Ser
 265 270 275

cca ttc gcg ttc ctt aac gag aag tagttcgctt ttcttagtgg gtg 978
 Pro Phe Ala Phe Leu Asn Glu Lys
 280 285

<210> 264

<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 264

Val Ala Glu Asn Leu Asn Lys His Leu Ser Lys Leu Ser Lys Arg Gly
 1 5 10 15

Pro His Arg Val Leu Val Gly Asp Met Asn Tyr Ala Gly Ile Pro Gly
 20 25 30

Lys Ile Tyr Thr Pro Ala Glu Gly Asp Gly Ile Pro Gly Val Ala Phe
 35 40 45

Gly His Asp Trp Met Lys Ser Ile Lys Tyr Tyr His Gln Thr Leu Arg
 50 55 60

His Leu Ala Ser Trp Gly Ile Ala Val Ala Ala Pro Asp Thr Glu Asn
 65 70 75 80

Gly Phe Met Pro Asp His Lys Gly Phe Ala Ser Asp Leu Glu Ser Ser
 85 90 95

Ile Gln Ile Leu Gly Gly Val Lys Leu Gly Ser Gly Asn Val Thr Val
 100 105 110

Asn Pro Ala Cys Leu Gly Val Val Gly His Gly Met Gly Ala Gly Ala
 115 120 125

Ala Val Leu Ser Ala Ala Asn Arg Asp Leu Val Arg Ala Val Gly Ala
 130 135 140

Ile Tyr Pro Ala Lys Thr Ser Pro Ser Ala Ile Asp Ala Ala Phe Ala
 145 150 155 160

Val Lys Ala Pro Gly Leu Val Ile Gly Ser Ser Ser Leu Gly Leu Phe
 165 170 175

Glu Ser Gly Glu Pro Ala Lys Leu Ala Ala Asn Trp Ala Gly Asp Val
 180 185 190

Cys Tyr Arg Glu Ser Glu Lys Gly Asn Gln Gln Gly Phe Ser Glu Asp
 195 200 205
 Thr Met Phe Lys Leu Val Ala Gly Ile Gly Ser Pro Gln Thr Gly Ala
 210 215 220
 Gln Glu Thr Val Arg Gly Leu Leu Thr Gly Phe Leu Leu His Gln Leu
 225 230 235 240
 Ala Gly Glu Lys Lys Tyr Lys Ala Phe Ser Glu Pro Asp Ala Glu Ala
 245 250 255
 Lys Lys Val Val Ser Tyr Phe Gly Gln Glu Leu Gln Glu His Ala Phe
 260 265 270
 Pro Lys Asp Thr Ser Pro Phe Ala Phe Leu Asn Glu Lys
 275 280 285

<210> 265
 <211> 978
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(955)
 <223> FRXA00507

<400> 265
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 gtgccagtat tgccccacgc ttccaactat ccttaaacac gtg gct gag aat ctg 115
 Val Ala Glu Asn Leu
 1 5
 aac aaa cac ctg tcc aaa ctg tcc aag cgc gga ccg cac cgc gtg ctg 163
 Asn Lys His Leu Ser Lys Leu Ser Lys Arg Gly Pro His Arg Val Leu
 10 15 20
 gta ggc gat atg aac tac gcc ggc atc ccg ggc aaa atc tac acc cca 211
 Val Gly Asp Met Asn Tyr Ala Gly Ile Pro Gly Lys Ile Tyr Thr Pro
 25 30 35
 gca gaa ggc gac ggc atc cca ggt gta gct ttc ggc cac gac tgg atg 259
 Ala Glu Gly Asp Gly Ile Pro Gly Val Ala Phe Gly His Asp Trp Met
 40 45 50
 aaa tcc atc aag tac tac cac caa act ttg cga cac ctc gcg tcc tgg 307
 Lys Ser Ile Lys Tyr Tyr His Gln Thr Leu Arg His Leu Ala Ser Trp
 55 60 65
 ggc atc gct gtt gcc gcc cca gac acc gaa aat ggc ttc atg cca gac 355
 Gly Ile Ala Val Ala Ala Pro Asp Thr Glu Asn Gly Phe Met Pro Asp
 70 75 80 85
 cac aaa ggt ttc gcc tct gac ctc gaa tcc tcc att cag att ctc ggc 403
 His Lys Gly Phe Ala Ser Asp Leu Glu Ser Ser Ile Gln Ile Leu Gly
 90 95 100
 ggc gta aaa ctc ggc tcc gga aac gtc acc gtc aac cca gcc tgc ctc 451

Gly Val Lys Leu Gly Ser Gly Asn Val Thr Val Asn Pro Ala Cys Leu
105 110 115

ggt gta gta ggc cac ggc atg ggt gct ggg gct gca gta cta tcc gca 499
Gly Val Val Gly His Gly Met Gly Ala Gly Ala Val Leu Ser Ala
120 125 130

gca aac cgc gac ctc gtg cgc gca gtc gga gca atc tac cca gcg aaa 547
Ala Asn Arg Asp Leu Val Arg Ala Val Gly Ala Ile Tyr Pro Ala Lys
135 140 145

acc tcc ccc tca gca atc gac gcc gcc ttc gct gtc aaa gcc cca ggc 595
Thr Ser Pro Ser Ala Ile Asp Ala Ala Phe Ala Val Lys Ala Pro Gly
150 155 160 165

cta gtc atc gga tcc tcc agc ctc gcc ctc ttt gaa tcc ggc gag cca 643
Leu Val Ile Gly Ser Ser Ser Leu Gly Leu Phe Glu Ser Gly Glu Pro
170 175 180

gca aaa ctc gca gcc aac tgg gcc gcc gat gtc tgc tac cgc gaa tca 691
Ala Lys Leu Ala Ala Asn Trp Ala Gly Asp Val Cys Tyr Arg Glu Ser
185 190 195

gaa aaa ggc aac caa cag gcc ttc tct gaa gac acc atg ttc aaa ctt 739
Glu Lys Gly Asn Gln Gln Gly Phe Ser Glu Asp Thr Met Phe Lys Leu
200 205 210

gtc gca gga atc ggc agc cca caa acc gga gct caa gaa acc gtc cgc 787
Val Ala Gly Ile Gly Ser Pro Gln Thr Gly Ala Gln Glu Thr Val Arg
215 220 225

ggc ctc ctc acc gga ttc ctt ctc cac caa ctt gcc gga gaa aag aaa 835
Gly Leu Leu Thr Gly Phe Leu Leu His Gln Leu Ala Gly Glu Lys Lys
230 235 240 245

tac aaa gca ttc tcc gaa cca gac gct gaa gct aag aaa gtt gtc tcc 883
Tyr Lys Ala Phe Ser Glu Pro Asp Ala Glu Ala Lys Lys Val Val Ser
250 255 260

tac ttc ggc cag gag ctg cag gaa cat gcc ttc cct aag gac acg tcc 931
Tyr Phe Gly Gln Glu Leu Gln Glu His Ala Phe Pro Lys Asp Thr Ser
265 270 275

cca ttc gcg ttc ctt aac gag aag tagttcgctt ttcttagtgg gtg 978
Pro Phe Ala Phe Leu Asn Glu Lys
280 285

<210> 266

<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 266

Val Ala Glu Asn Leu Asn Lys His Leu Ser Lys Leu Ser Lys Arg Gly
1 5 10 15

Pro His Arg Val Leu Val Gly Asp Met Asn Tyr Ala Gly Ile Pro Gly
20 25 30

Lys Ile Tyr Thr Pro Ala Glu Gly Asp Gly Ile Pro Gly Val Ala Phe

35	40	45
Gly His Asp Trp Met Lys Ser Ile Lys Tyr Tyr His Gln Thr Leu Arg		
50	55	60
His Leu Ala Ser Trp Gly Ile Ala Val Ala Ala Pro Asp Thr Glu Asn		
65	70	75
Gly Phe Met Pro Asp His Lys Gly Phe Ala Ser Asp Leu Glu Ser Ser		
85	90	95
Ile Gln Ile Leu Gly Gly Val Lys Leu Gly Ser Gly Asn Val Thr Val		
100	105	110
Asn Pro Ala Cys Leu Gly Val Val Gly His Gly Met Gly Ala Gly Ala		
115	120	125
Ala Val Leu Ser Ala Ala Asn Arg Asp Leu Val Arg Ala Val Gly Ala		
130	135	140
Ile Tyr Pro Ala Lys Thr Ser Pro Ser Ala Ile Asp Ala Ala Phe Ala		
145	150	155
Val Lys Ala Pro Gly Leu Val Ile Gly Ser Ser Ser Leu Gly Leu Phe		
165	170	175
Glu Ser Gly Glu Pro Ala Lys Leu Ala Ala Asn Trp Ala Gly Asp Val		
180	185	190
Cys Tyr Arg Glu Ser Glu Lys Gly Asn Gln Gln Gly Phe Ser Glu Asp		
195	200	205
Thr Met Phe Lys Leu Val Ala Gly Ile Gly Ser Pro Gln Thr Gly Ala		
210	215	220
Gln Glu Thr Val Arg Gly Leu Leu Thr Gly Phe Leu Leu His Gln Leu		
225	230	235
Ala Gly Glu Lys Lys Tyr Lys Ala Phe Ser Glu Pro Asp Ala Glu Ala		
245	250	255
Lys Lys Val Val Ser Tyr Phe Gly Gln Glu Leu Gln Glu His Ala Phe		
260	265	270
Pro Lys Asp Thr Ser Pro Phe Ala Phe Leu Asn Glu Lys		
275	280	285

<210> 267

<211> 1632

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1609)

<223> RXN00510

<400> 267

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acaaagtgttt	tggtgccgga	tttgatggga	tgatccgaa	gtg	aat	gat	cct	tta	115
				Val	Asn	Asp	Pro	Leu	
				1				5	
gcc ggc tac gga gca gtg atc tcc gca cta caa ggc gcc agt ggt ggg	163								
Ala Gly Tyr Gly Ala Val Ile Ser Ala Leu Gln Gly Ala Ser Gly Gly									
		10						20	
atg tat cgc gga ccg gcg aaa tcc gaa ggc cag ttg cgc gag atg tac	211								
Met Tyr Arg Gly Pro Ala Lys Ser Glu Gly Gln Leu Arg Glu Met Tyr									
		25				30		35	
caa acc atc gaa ggg cta gac acc agc tcg ttg cgc gaa gct gcc gaa	259								
Gln Thr Ile Glu Gly Leu Asp Thr Ser Ser Leu Arg Gln Ala Ala Glu									
		40			45			50	
gca gca gtg ggc gga acg aac gaa gcc aga ata caa ggg tgg gtc gcc	307								
Ala Ala Val Gly Gly Thr Asn Glu Ala Arg Ile Gln Gly Trp Val Gly									
		55			60			65	
ccg ctc ttg aaa ttc ttc ggg acg gtt ggc ggg gga atg atc gcc acg	355								
Pro Leu Leu Lys Phe Phe Gly Thr Val Gly Gly Gly Met Ile Ala Thr									
		70			75			80	
gag ata gct gaa cgg gca gtc gat tgg ttc aaa aac cgt aat gat gtg	403								
Glu Ile Ala Glu Arg Ala Val Asp Trp Phe Lys Asn Arg Asn Asp Val									
				90				100	
gaa gaa gtc agc gaa gcc gct gat aaa gcc gcc gat gcg atc gac tcc	451								
Glu Glu Val Ser Glu Ala Ala Asp Lys Ala Ala Asp Ala Ile Asp Ser									
				105				115	
act gtc aca gag tcc gac cag ggc atg atg cac att atc cag cag ctc	499								
Thr Val Thr Glu Ser Asp Gln Gly Met Met His Ile Ile Gln Gln Leu									
				120		125		130	
ttg gac att gtg tct acg ttg acg cag att ctt ggc agc atg gat cgg	547								
Leu Asp Ile Val Ser Thr Leu Thr Gln Ile Leu Gly Ser Met Asp Arg									
				135		140		145	
ggg aaa ttt cct caa gaa ttc cgg gac tgt gtc caa act gga gct gat	595								
Gly Lys Phe Pro Gln Glu Phe Arg Asp Cys Val Gln Thr Gly Ala Asp									
				150		155		160	
ctt att gac cag gca ggg gac atg ctt gaa gga ttg tgc gct gat cga	643								
Leu Ile Asp Gln Ala Gly Asp Met Leu Glu Gly Leu Cys Ala Asp Arg									
				170				175	
gat gat gcg att tca cag tgt ttc tcc gcg ttg acc gat cat gga aaa	691								
Asp Asp Ala Ile Ser Gln Cys Phe Thr Ser Ala Leu Thr Asp His Gly Lys									
				185				190	
caa gtt tgt gaa act gag cca aag ccg ttg tgt agt gca gct tct ggg	739								
Gln Val Cys Glu Thr Glu Pro Lys Pro Leu Cys Ser Ala Ala Ser Gly									
				200		205		210	
ggt tca tct ggt gga gcg act tct tcg gct gcg gcc tct tca ggt ggt	787								
Gly Ser Ser Gly Gly Ala Thr Ser Ser Ala Ala Ala Ser Ser Gly Gly									
				215		220		225	
tca agc tcg agc act gct agc tct ggg agt tct gcc gga tcg agc agt	833								

Ser 230	Ser	Ser	Ser	Thr	Ala 235	Ser	Ser	Gly	Ser	Ser	Gly 240	Gly	Ser	Ser	Ser	245	
gct	gcg	gat	agt	tcg	acg	tcg	acc	aat	gct	gaa	tcc	agt	gtt	gaa	aag		883
Ala	Ala	Asp	Ser	Ser	Thr	Ser	Thr	Asn	Ala	Glu	Ser	Ser	Val	Glu	Lys		
				250					255					260			
gaa	aag	acc	aca	cct	gct	gcc	gtt	gag	aaa	cct	gac	gag	aaa	cca	gtg		931
Glu	Lys	Thr	Thr	Pro	Ala	Ala	Val	Glu	Lys	Pro	Asp	Glu	Lys	Pro	Val		
			265					270					275				
gag	aag	ccg	gtt	gaa	aag	acg	cca	gaa	aag	ccg	gta	gaa	aaa	cct	gtc		979
Glu	Lys	Pro	Val	Glu	Lys	Thr	Pro	Glu	Lys	Pro	Val	Glu	Lys	Pro	Val		
		280					285					290					
gag	aag	caa	gag	tgt	gaa	gaa	aag	cct	gac	cct	gac	ccg	gaa	aaa	tgc		1027
Glu	Lys	Gln	Glu	Cys	Glu	Glu	Lys	Pro	Asp	Pro	Asp	Pro	Glu	Lys	Cys		
		295				300					305						
aaa	aca	gag	ccg	gtc	gag	tgt	gag	cca	aca	ccg	aaa	cct	gaa	aca	gag		1075
Lys	Thr	Glu	Pro	Val	Glu	Cys	Glu	Pro	Thr	Pro	Lys	Pro	Glu	Thr	Glu		
		310				315				320					325		
cct	gaa	cca	aaa	ccg	aca	ccc	acg	ccc	aca	ccc	gga	aca	cca	aca	cca		1123
Pro	Glu	Pro	Lys	Pro	Thr	Pro	Thr	Pro	Thr	Pro	Gly	Thr	Pro	Thr	Pro		
				330					335					340			
ata	cct	gag	cta	gag	act	gag	gat	tgt	gaa	cct	ggc	aag	gag	acg	ggc		1171
Ile	Pro	Glu	Leu	Glu	Thr	Glu	Asp	Cys	Glu	Pro	Gly	Lys	Glu	Thr	Gly		
			345					350					355				
aca	gac	tca	gaa	tct	gaa	tcg	gaa	gag	tgc	gcc	ccc	gag	ctc	aat	gac		1219
Thr	Asp	Ser	Glu	Ser	Glu	Ser	Glu	Glu	Cys	Ala	Pro	Glu	Leu	Asn	Asp		
		360					365					370					
gtt	cca	gaa	gag	tcg	gat	ctg	att	ggg	caa	ctc	atc	aag	gga	gca	atc		1267
Val	Pro	Glu	Glu	Ser	Asp	Leu	Ile	Gly	Gln	Leu	Ile	Lys	Gly	Ala	Ile		
		375				380					385						
ggt	att	ggg	att	gtt	gtt	gta	ggc	gtt	ggg	ctg	ttg	gtg	aat	ttc	ctg		1315
Gly	Ile	Gly	Ile	Val	Val	Val	Gly	Val	Gly	Leu	Leu	Val	Asn	Phe	Leu		
		390			395				400					405			
gag	cag	tgc	gtc	cct	gtg	att	gaa	gaa	gta	cct	gtg	ccg	gag	ccc	gag		1363
Glu	Gln	Cys	Val	Pro	Val	Ile	Glu	Glu	Val	Pro	Val	Pro	Glu	Pro	Glu		
			410					415						420			
cct	ata	cct	gaa	ccc	gct	ccg	cag	cct	gag	cca	act	tca	gtg	aaa	cca		1411
Pro	Ile	Pro	Glu	Pro	Ala	Pro	Gln	Pro	Glu	Pro	Thr	Ser	Val	Lys	Pro		
			425				430						435				
cca	gag	tct	gaa	cta	gat	aag	gtg	gct	gag	cct	gcg	ccg	aag	cca	att		1459
Pro	Glu	Ser	Glu	Leu	Asp	Lys	Val	Ala	Glu	Pro	Ala	Pro	Lys	Pro	Ile		
		440					445				450						
cca	caa	gct	aat	tac	act	gct	gct	gca	gca	act	aac	tat	tcc	gct	ccc		1507
Pro	Gln	Ala	Asn	Tyr	Thr	Ala	Ala	Ala	Ala	Thr	Asn	Tyr	Ser	Ala	Pro		
		455				460				465							
gcg	cac	gct	ccc	gtt	gtc	cca	att	acg	ccg	gca	gca	cct	gaa	gtt	ccg		1555
Ala	His	Ala	Pro	Val	Val	Pro	Ile	Thr	Pro	Ala	Ala	Pro	Glu	Val	Pro		

ggg tgg tagcgggtgga gtatgcggaa ttt 1632
Gly Trp

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<210> 268
<211> 503
<212> PRT
<213> Corynebacterium glutamicum
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<400> 268
Val Asn Asp Pro Leu Ala Gly Tyr Gly Ala Val Ile Ser Ala Leu Gln
1 5 10 15

Gly Ala Ser Gly Gly Met Tyr Arg Gly Pro Ala Lys Ser Glu Gly Gln
20 25 30

Leu Arg Glu Met Tyr Gln Thr Ile Glu Gly Leu Asp Thr Ser Ser Leu
35 40 45

Arg Glu Ala Ala Glu Ala Ala Val Gly Gly Thr Asn Glu Ala Arg Ile
50 55 60

Gln Gly Trp Val Gly Pro Leu Leu Lys Phe Phe Gly Thr Val Gly Gly
65 70 75 80

Gly Met Ile Ala Thr Glu Ile Ala Glu Arg Ala Val Asp Trp Phe Lys
85 90 95

Asn Arg Asn Asp Val Glu Glu Val Ser Glu Ala Ala Asp Lys Ala Ala
100 105 110

Asp Ala Ile Asp Ser Thr Val Thr Glu Ser Asp Gln Gly Met Met His
115 120 125

Ile Ile Gln Gln Leu Leu Asp Ile Val Ser Thr Leu Thr Gln Ile Leu
130 135 140

Gly Ser Met Asp Arg Gly Lys Phe Pro Gln Glu Phe Arg Asp Cys Val
145 150 155 160

Gln Thr Gly Ala Asp Leu Ile Asp Gln Ala Gly Asp Met Leu Glu Gly
165 170 175

Leu Cys Ala Asp Arg Asp Asp Ala Ile Ser Gln Cys Phe Ser Ala Leu
180 185 190

Thr Asp His Gly Lys Gln Val Cys Glu Thr Glu Pro Lys Pro Leu Cys
195 200 205

Ser Ala Ala Ser Gly Gly Ser Ser Gly Gly Ala Thr Ser Ser Ala Ala
210 215 220

Ala Ser Ser Gly Gly Ser Ser Ser Ser Thr Ala Ser Ser Gly Ser Ser
225 230 235 240

[illegible]

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<210> 269
<211> 300
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> {101}..(277)
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<400> 269

Leu Val Asp Val Glu
1 5

Leu Ser Ala Ala Leu Leu Asp Pro Pro Glu Leu Pro Glu Leu Ala Val
10 15 20

Leu Glu Leu Glu Pro Pro Glu Glu Ala Ala Ala Glu Glu Val Ala Pro
25 30 35

Pro Asp Glu Pro Pro Glu Ala Ala Leu His Asn Gly Phe Gly Ser Val
40 45 50

Ser Gln Thr Cys Phe Pro
55

<211> 59

<212> PRT

<213> Cor

.....

Leu Val A

1	5	10	15
---	---	----	----

Pro Glu Leu Ala Val Leu Glu Leu Glu Pro Pro Glu Glu Ala Ala Ala

$\mathbb{Z}_2 \oplus \mathbb{Z}_2$
 $\mathbb{Z}_2 \oplus \mathbb{Z}_2$
 $\mathbb{Z}_2 \oplus \mathbb{Z}_2$

Glu Glu Val Ala Pro Pro Asp Glu Pro Pro Glu Ala Ala Leu His Asn
35 40 45

Gly Phe Gly Ser Val Ser Gln Thr Cys Phe Pro

50 55

<210> 271

<211> 631

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

 $\langle 222 \rangle \quad (101) \dots (631)$

<223> FRXA00510

<400> 271

gagcagtgct gcggatagtt cgacgtcgac caatgctgaa tccagtgttg aaaaggaaaa 60

gaccacacct gctaccgttg agaaacctga cgagaaacca gtg gag aag ccg gtt 115

Val	Glu	Lys	Pro	Val
1				5

gaa aag acg cca gaa aag ccg gta gaa aaa cct gtc gag aag caa gag 163
 Glu Lys Thr Pro Glu Lys Pro Val Glu Lys Pro Val Glu Lys Gln Glu
 10 15 20

tgt gaa gaa aag cct gac cct gac ccg gaa ana atg caa aan can gag 211
 Cys Glu Glu Lys Pro Asp Pro Asp Pro Glu Xaa Met Gln Xaa Xaa Glu
 25 30 35

ccg gtc gag tgt gag cca aca ccg aaa cct gaa aca gag cct gaa cca 259
 Pro Val Glu Cys Glu Pro Thr Pro Lys Pro Glu Thr Glu Pro Glu Pro
 40 45 50

aaa ccn gac acc cac gcc can cna ccc gga aca cca aca cca ata cct 307
 Lys Pro Asp Thr His Ala Xaa Xaa Pro Gly Thr Thr Pro Ile Pro
 55 60 65

gna gct aga gna ctg agg att gnt gna nac nct gng caa gga gan cgn 355
 Xaa Ala Arg Xaa Leu Arg Ile Xaa Xaa Xaa Xaa Xaa Gln Gly Xaa Arg
 70 75 80 85

ggc aca gac tca gnn ana tnc tnn nnn nnn gaa tcg gaa gag tgc gcc 403
 Gly Thr Asp Ser Xaa Xaa Xaa Xaa Xaa Glu Ser Glu Glu Cys Ala
 90 95 100

ccc gag ctg aat gac gtt cca gaa gag tcg gat ctg att ggg caa ctg 451
 Pro Glu Leu Asn Asp Val Pro Glu Glu Ser Asp Leu Ile Gly Gln Leu
 105 110 115

atc aag gga gca atc ggt att ggg att gtt gtt gta ggc gtt ggg ctg 499
 Ile Lys Gly Ala Ile Gly Ile Gly Ile Val Val Val Gly Val Gly Leu
 120 125 130

ttg gtg aat ttc ctg gag cag tgc gtc cct gtg att gaa gaa gta cct 547
 Leu Val Asn Phe Leu Glu Gln Cys Val Pro Val Ile Glu Glu Val Pro
 135 140 145

gtg ccg gag ccc gag cct ata cct gaa ccc gct ccg cag cct gag cca 595
 Val Pro Glu Pro Glu Pro Ile Pro Glu Pro Ala Pro Gln Pro Glu Pro
 150 155 160 165

act tca gtg aaa cca cca gag tct gaa cta gat aag 631
 Thr Ser Val Lys Pro Pro Glu Ser Glu Leu Asp Lys
 170 175

<210> 272

<211> 177

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

Val Glu Lys Pro Val Glu Lys Thr Pro Glu Lys Pro Val Glu Lys Pro
 1 5 10 15

Val Glu Lys Gln Glu Cys Glu Glu Lys Pro Asp Pro Asp Pro Glu Xaa
 20 25 30

Met Gln Xaa Xaa Glu Pro Val Glu Cys Glu Pro Thr Pro Lys Pro Glu
 35 40 45

```

Thr Glu Pro Glu Pro Lys Pro Asp Thr His Ala Xaa Xaa Pro Gly Thr
  50                      55                      60

Pro Thr Pro Ile Pro Xaa Ala Arg Xaa Leu Arg Ile Xaa Xaa Xaa Xaa
  65                      70                      75                      80

Xaa Gln Gly Xaa Arg Gly Thr Asp Ser Xaa Xaa Xaa Xaa Xaa Xaa Glu
  85                      90                      95

Ser Glu Glu Cys Ala Pro Glu Leu Asn Asp Val Pro Glu Glu Ser Asp
 100                      105                      110

Leu Ile Gly Gln Leu Ile Lys Gly Ala Ile Gly Ile Gly Ile Val Val
 115                      120                      125

Val Gly Val Gly Leu Leu Val Asn Phe Leu Glu Gln Cys Val Pro Val
 130                      135                      140

Ile Glu Glu Val Pro Val Pro Glu Pro Glu Pro Ile Pro Glu Pro Ala
 145                      150                      155                      160

Pro Gln Pro Glu Pro Thr Ser Val Lys Pro Pro Glu Ser Glu Leu Asp
 165                      170                      175

```

Lys

<210> 273
 <211> 825
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> {101}..{802}
 <223> RXN00515

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<400> 273
gttgacgcac tgaagaagta aagtctcttc acaaaaagcg ctgtgcttcc tcacatggaa 60

gcacagcgct ttttcatatt tttattgccaa taatgggcac atg cgt ttt tct cga 115
Met Arg Phe Ser Arg
1 5

gtt ctt ccc gca ctt ctt atc acc acc gcc gtg agc atc cca aca gca 163
Val Leu Pro Ala Leu Leu Ile Thr Thr Ala Val Ser Ile Pro Thr Ala
10 15 20

tot gct gcc aca ctc acc gcc gac acc gac aag gaa ttg tgc atc gcc 211
Ser Ala Ala Thr Leu Thr Ala Asp Thr Asp Lys Glu Leu Cys Ile Ala
25 30 35

agc aac acc gac gat tcc gcg gtg gtt acc ttc tgg aac tcc att gaa 259
Ser Asn Thr Asp Asp Ser Ala Val Val Thr Phe Trp Asn Ser Ile Glu
40 45 50

gac tcc gtg cgc gaa caa cgc ctc gac gaa cta gac gcc caa gat cca 307
Asp Ser Val Arg Glu Gln Arg Leu Asp Glu Leu Asp Ala Gln Asp Pro
55 60 65

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gga atc aaa gcg gcg att gaa agc tac atc gcc caa gat gac aac gcc 355
 Gly Ile Lys Ala Ala Ile Glu Ser Tyr Ile Ala Gln Asp Asp Asn Ala
 70 75 80 85
 cca act gct gct gaa ctg caa gta cgc ctc gat gcc atc gaa tcc gcc 403
 Pro Thr Ala Ala Glu Leu Gln Val Arg Leu Asp Ala Ile Glu Ser Gly
 90 95 100
 gaa ggc cta gcc atg ctc ctc cca gac gat ccc acg ctg gca gac ccc 451
 Glu Gly Leu Ala Met Leu Leu Pro Asp Asp Pro Thr Leu Ala Asp Pro
 105 110 115
 aac gcc gag gaa agt ttc aaa acg gag tac aca tac gac gaa gcc aaa 499
 Asn Ala Glu Glu Ser Phe Lys Thr Glu Tyr Thr Tyr Asp Glu Ala Lys
 120 125 130
 gac atc atc agc gga ttc tcc agc gat cca gcc agc gat gta ctc agc 547
 Asp Ile Ile Ser Gly Phe Ser Ser Asp Pro Ala Ser Asp Val Leu Ser
 135 140 145
 caa ctt caa caa gcc gcc acc acc gcc acc cgc acc gca gaa atc cgc 595
 Gln Leu Gln Gln Ala Ala Thr Thr Gly Thr Arg Thr Ala Glu Ile Arg
 150 155 160 165
 gcc gaa gta ttc gcc gac cgc acc gat gat tac aac gaa tcc caa acc 643
 Ala Glu Val Phe Ala Asp Arg Thr Asp Tyr Asn Glu Ser Gln Thr
 170 175 180
 gct ctt aaa gag gat ttc caa aac tgc atc gat gcc atc gat gac gcc 691
 Ala Leu Lys Glu Asp Phe Gln Asn Cys Ile Asp Ala Ile Asp Asp Ala
 185 190 195
 cgc cca atc cca ctg cag tac atc ctg att gga ggc gcc atc gct ttg 739
 Arg Pro Ile Pro Leu Gln Tyr Ile Leu Ile Gly Gly Ala Ile Ala Leu
 200 205 210
 gcg gtc atc gtc ctc ggg atc agg gcg tgg act aac tca agg aag cag 787
 Ala Val Ile Val Leu Gly Ile Arg Ala Trp Thr Asn Ser Arg Lys Gln
 215 220 225
 tcc aag cac agc cag taatacgcca agcaaaaaat tgc 825
 Ser Lys His Ser Gln
 230

<210> 274

<211> 234

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 274

Met Arg Phe Ser Arg Val Leu Pro Ala Leu Leu Ile Thr Thr Ala Val
 1 5 10 15
 Ser Ile Pro Thr Ala Ser Ala Ala Thr Leu Thr Ala Asp Thr Asp Lys
 20 25 30
 Glu Leu Cys Ile Ala Ser Asn Thr Asp Asp Ser Ala Val Val Thr Phe
 35 40 45
 Trp Asn Ser Ile Glu Asp Ser Val Arg Glu Gln Arg Leu Asp Glu Leu

50 55 60
 Asp Ala Gln Asp Pro Gly Ile Lys Ala Ala Ile Glu Ser Tyr Ile Ala
 65 70 75 80
 Gln Asp Asp Asn Ala Pro Thr Ala Ala Glu Leu Gln Val Arg Leu Asp
 85 90 95
 Ala Ile Glu Ser Gly Glu Gly Leu Ala Met Leu Leu Pro Asp Asp Pro
 100 105 110
 Thr Leu Ala Asp Pro Asn Ala Glu Glu Ser Phe Lys Thr Glu Tyr Thr
 115 120 125
 Tyr Asp Glu Ala Lys Asp Ile Ile Ser Gly Phe Ser Ser Asp Pro Ala
 130 135 140
 Ser Asp Val Leu Ser Gln Leu Gln Gln Ala Ala Thr Thr Gly Thr Arg
 145 150 155 160
 Thr Ala Glu Ile Arg Ala Glu Val Phe Ala Asp Arg Thr Asp Asp Tyr
 165 170 175
 Asn Glu Ser Gln Thr Ala Leu Lys Glu Asp Phe Gln Asn Cys Ile Asp
 180 185 190
 Ala Ile Asp Asp Ala Arg Pro Ile Pro Leu Gln Tyr Ile Leu Ile Gly
 195 200 205
 Gly Ala Ile Ala Leu Ala Val Ile Val Leu Gly Ile Arg Ala Trp Thr
 210 215 220
 Asn Ser Arg Lys Gln Ser Lys His Ser Gln
 225 230

<210> 275

<211> 503

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(480)

<223> FRXA00515

<400> 275

att gaa agc tac atc gcc caa gat gac aac gcc cca act gct gct gaa 48
 ile Glu Ser Tyr Ile Ala Gln Asp Asp Asn Ala Pro Thr Ala Ala Glu
 1 5 10 15

ctg caa gta cgc ctc gat gcc atc gaa tcc gcc gaa gcc cta gcc atg 96
 Leu Gln Val Arg Leu Asp Ala Ile Glu Ser Gly Glu Gly Leu Ala Met
 20 25 30

ctc ctc cca gac gat ccc acg ctg gca gac ccc aac gcc gag gaa agt 144
 Leu Leu Pro Asp Asp Pro Thr Leu Ala Asp Pro Asn Ala Glu Glu Ser
 35 40 45

ttc aaa acg gag tac aca tac gac gaa gcc aaa gac atc atc agc gga 192
 Phe Lys Thr Glu Tyr Thr Tyr Asp Glu Ala Lys Asp Ile Ile Ser Gly

50	55	60	
ttc tcc agc gat cca gcc agc gat gta ctc agc caa ctt caa caa gcc			240
Phe Ser Ser Asp Pro Ala Ser Asp Val Leu Ser Gln Leu Gln Gln Ala			
65	70	75	80
gcc acc acc ggc acc cgc acc gca gaa atc cgc gcc gaa gta ttc gcc			288
Ala Thr Thr Gly Thr Arg Thr Ala Glu Ile Arg Ala Glu Val Phe Ala			
	85	90	95
gac cgc acc gat gat tac aac gaa tcc caa acc gct ctt aaa gag gat			336
Asp Arg Thr Asp Asp Tyr Asn Glu Ser Gln Thr Ala Leu Lys Glu Asp			
	100	105	110
ttc caa aac tgc atc gat gcc atc gat gac gcc cgc cca atc cca ctg			384
Phe Gln Asn Cys Ile Asp Ala Ile Asp Asp Ala Arg Pro Ile Pro Leu			
	115	120	125
cag tac atc ctg att gga ggc gcc atc gct ttg ggc gtc atc gtc ctc			432
Gln Tyr Ile Leu Ile Gly Gly Ala Ile Ala Leu Ala Val Ile Val Leu			
	130	135	140
ggg atc agg gcg tgg act aac tca agg aag cag tcc aag cac agc cag			480
Gly Ile Arg Ala Trp Thr Asn Ser Arg Lys Gln Ser Lys His Ser Gln			
145	150	155	160
taatacgcaca agcaaaaaat tgc			503
<210> 276			
<211> 160			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 276			
Ile Glu Ser Tyr Ile Ala Gln Asp Asp Asn Ala Pro Thr Ala Ala Glu			
1	5	10	15
Leu Gln Val Arg Leu Asp Ala Ile Glu Ser Gly Glu Gly Leu Ala Met			
	20	25	30
Leu Leu Pro Asp Asp Pro Thr Leu Ala Asp Pro Asn Ala Glu Glu Ser			
	35	40	45
Phe Lys Thr Glu Tyr Thr Tyr Asp Glu Ala Lys Asp Ile Ile Ser Gly			
	50	55	60
Phe Ser Ser Asp Pro Ala Ser Asp Val Leu Ser Gln Leu Gln Gln Ala			
65	70	75	80
Ala Thr Thr Gly Thr Arg Thr Ala Glu Ile Arg Ala Glu Val Phe Ala			
	85	90	95
Asp Arg Thr Asp Asp Tyr Asn Glu Ser Gln Thr Ala Leu Lys Glu Asp			
	100	105	110
Phe Gln Asn Cys Ile Asp Ala Ile Asp Asp Ala Arg Pro Ile Pro Leu			
	115	120	125
Gln Tyr Ile Leu Ile Gly Gly Ala Ile Ala Leu Ala Val Ile Val Leu			
	130	135	140

Gly Ile Arg Ala Trp Thr Asn Ser Arg Lys Gln Ser Lys His Ser Gln
 145 150 155 160

<210> 277

<211> 298

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(298)

<223> FRXA00520

<400> 277

gttgacgcac tgaagaagta aagtctcttc acaaaaagcg ctgtgcttcc tcacatggaa 60

gcacagcgct ttttcatatt tttattgccaa taatggggcac atg cgt ttt tct cga 115
 Met Arg Phe Ser Arg
 1 5

gtt ctt ccc gca ctt ctt atc acc acc gcc gtg agc atc cca aca gca 163
 Val Leu Pro Ala Leu Leu Ile Thr Thr Ala Val Ser Ile Pro Thr Ala
 10 15 20

tct gct gcc aca ctc acc ggc gac acc gac aag gaa ttg tgc atc gcc 211
 Ser Ala Ala Thr Leu Thr Gly Asp Thr Asp Lys Glu Leu Cys Ile Ala
 25 30 35

agc aac acc gac gat tcc gcg gtg gtt acc ttc tgg aac tcc att gaa 259
 Ser Asn Thr Asp Asp Ser Ala Val Val Thr Phe Trp Asn Ser Ile Glu
 40 45 50

gac tcc gtg cgc gaa caa cgc ctc gac gaa cta gac gcc 298
 Asp Ser Val Arg Glu Gln Arg Leu Asp Glu Leu Asp Ala
 55 60 65

<210> 278

<211> 66

<212> PRT

<213> Corynebacterium glutamicum

<400> 278

Met Arg Phe Ser Arg Val Leu Pro Ala Leu Leu Ile Thr Thr Ala Val
 1 5 10 15

Ser Ile Pro Thr Ala Ser Ala Ala Thr Leu Thr Gly Asp Thr Asp Lys
 20 25 30

Glu Leu Cys Ile Ala Ser Asn Thr Asp Asp Ser Ala Val Val Thr Phe
 35 40 45

Trp Asn Ser Ile Glu Asp Ser Val Arg Glu Gln Arg Leu Asp Glu Leu
 50 55 60

Asp Ala

65

<210> 279
 <211> 1887
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1864)
 <223> RXN00527

<400> 279
 ttccttgccc ccgaagaaat taatcattgt gcccggtggtc ctgattttga tcaattgcgc 60
 tgccctggtt tattttctgc gtccatcatc gaatgaccag gtg att gcc act tct 115
 Val Ile Ala Thr Ser
 1 5
 gat gtt cgg gag att tcc tcc gag gga atc gtg gcg cgt gtg tct gtc 163
 Asp Val Arg Glu Ile Ser Ser Glu Gly Ile Val Ala Arg Val Ser Val
 10 15 20
 aac gga aat att gaa gct gcg cga acc acc acc att tac acc agt ctg 211
 Asn Gly Asn Ile Glu Ala Ala Arg Thr Thr Ile Tyr Thr Ser Leu
 25 30 35
 act gtg ccg gtc gcg aac ttg ccg gtt gcg gtt ggt gac cgt gtg gca 259
 Thr Val Pro Val Ala Asn Leu Pro Val Ala Val Gly Asp Arg Val Ala
 40 45 50
 gct gat cag gtg ttg gct gag ttg gat gcc tct gcc ctg caa cga cag 307
 Ala Asp Gln Val Leu Ala Glu Leu Asp Ala Ser Ala Leu Gln Arg Gln
 55 60 65
 ttg gat gaa act gat gcc aac aat gcg cgt gca gcc atg gcg aac cgc 355
 Leu Asp Glu Thr Asp Ala Asn Asn Ala Arg Ala Ala Met Ala Asn Arg
 70 75 80 85
 aat tcc atc gcg cag tgc cag caa gca tat gag cag tcc agg gaa ctt 403
 Asn Ser Ile Ala Gln Ser Gln Gln Ala Tyr Glu Gln Ser Arg Glu Leu
 90 95 100
 ctt gat agt ggt ttg agc ccg gag atc aac tgc gcg cgg tcc tgc ttg 451
 Leu Asp Ser Gly Leu Ser Pro Glu Ile Asn Ser Ala Arg Ser Ser Leu
 105 110 115
 cgg gcg tcc tca cag gca tat cag gat gcg atc cgc agt ttt gaa gcg 499
 Arg Ala Ser Ser Gln Ala Tyr Gln Asp Ala Ile Arg Ser Phe Glu Ala
 120 125 130
 aag cag cga gat gtg gat gcc gga ttg gat tcc acc atg gtc gct caa 547
 Lys Gln Arg Asp Val Asp Gly Gly Leu Asp Ser Thr Met Val Ala Gln
 135 140 145
 tcg gat gct ctc aag gca gct cgt gag caa gca gat gct gct gaa att 595
 Ser Asp Ala Leu Lys Ala Ala Arg Glu Gln Ala Asp Ala Ala Glu Ile
 150 155 160 165
 gaa cga ctg cgc gcg gac ttc gga ctg ctc aac aac gat cgc agc aac 643

Glu Arg Leu Arg Ala Asp Phe Gly Leu Leu Asn Asn Asp Arg Ser Asn	
170 175 180	
ctc aac gat gtc att ggt ctg ctc gat gag aga gaa tct ttg gct tct	691
Leu Asn Asp Val Ile Gly Leu Leu Asp Glu Arg Glu Ser Leu Ala Ser	
185 190 195	
gcg gaa tcc gaa cta gct caa gcc cgc gct gca ggt gac cta gag gca	739
Ala Glu Ser Glu Leu Ala Gln Ala Arg Ala Ala Gly Asp Leu Glu Ala	
200 205 210	
gtc gct gca gct gaa gca aag gtt gca ggc ctg gaa caa tca att gct	787
Val Ala Ala Ala Glu Ala Lys Val Ala Gly Leu Glu Gln Ser Ile Ala	
215 220 225	
tcc aaa acc tcc acg tgg cct agc caa gat cag act tac ttg cag tcc	835
Ser Lys Thr Ser Thr Trp Pro Ser Gln Asp Gln Thr Tyr Leu Gln Ser	
230 235 240 245	
tac acc gct ttg gag gaa gct gag cga cgc gtc gca tcc acc act gaa	883
Tyr Thr Ala Leu Glu Glu Ala Glu Arg Arg Val Ala Ser Thr Thr Glu	
250 255 260	
gct cta gaa ata gcc gag cgg atc tac att gat tca ctc gga aaa gtt	931
Ala Leu Glu Ile Ala Glu Arg Ile Tyr Ile Asp Ser Leu Gly Lys Val	
265 270 275	
gac tca gaa cta gcc gcc gca cag cgc gcc gtt gcc gaa gcc cac tca	979
Asp Ser Glu Leu Ala Ala Ala Gln Arg Ala Val Ala Glu Ala His Ser	
280 285 290	
gca caa caa gac gca gca ctt ggc ctc gag acc gcg cag ctt tcc acc	1027
Ala Gln Gln Asp Ala Ala Leu Gly Leu Glu Thr Ala Gln Leu Ser Thr	
295 300 305	
caa cac caa ttg gaa gcc caa tca agc gcc atc gat gca gct tta ggt	1075
Gln His Gln Leu Glu Ala Gln Ser Ser Ala Ile Asp Ala Ala Leu Gly	
310 315 320 325	
ttg gca tca gta gat aat gaa gcc gcc acc aga tcc acg tcc cag ctg	1123
Leu Ala Ser Val Asp Asn Glu Ala Ala Thr Arg Ser Thr Ser Gln Leu	
330 335 340	
cgg atg gat atc aac aac acc acc gtt cgc tcc cca tac tca ggc att	1171
Arg Met Asp Ile Asn Asn Thr Thr Val Arg Ser Pro Tyr Ser Gly Ile	
345 350 355	
gtt tca tcc gtg cag gca gcc caa ggt caa cca gca gcc ggc gca ctg	1219
Val Ser Ser Val Gln Ala Ala Gln Gly Gln Pro Ala Ala Gly Ala Leu	
360 365 370	
ttg agt gtt gct gat gat tcc gaa ctg aag atc acc gcg aat gta aaa	1267
Leu Ser Val Ala Asp Asp Ser Glu Leu Lys Ile Thr Ala Asn Val Lys	
375 380 385	
gaa gcg gag atc agc aac gtc acc atc gga tcc cgc gtc acc ttc act	1315
Glu Ala Glu Ile Ser Asn Val Thr Ile Gly Ser Arg Val Thr Phe Thr	
390 395 400 405	
acc cca tcg acc gga acc aaa gaa ttc gcc ggc cga gta tcc aaa gtc	1363
Thr Pro Ser Thr Gly Thr Lys Glu Phe Ala Gly Arg Val Ser Lys Val	

	410	415	420	
tcc ccc att gca gct gcc gcc agt gcc cca gct aca ggt gaa gga gct				1411
Ser Pro Ile Ala Ala Ala Ser Ala Pro Ala Thr Gly Gly Ala	425	430	435	
gcc gca ggc gcc aca acc acc aac act gac gtc acc ttc ccc atc gaa				1459
Ala Ala Gly Ala Thr Thr Thr Arg Thr Asp Val Thr Phe Pro Ile Glu	440	445	450	
att tcc gtc acc ggc gac cgc gaa ggc ctc aac ctc ggc gga tcc gct				1507
Ile Ser Val Thr Gly Asp Arg Glu Gly Leu Asn Leu Gly Gly Ser Ala	455	460	465	
cga gta cgc atc gtc cat gaa atc gca cca cac gta ctg acc gtt cct				1555
Arg Val Arg Ile Val His Glu Ile Ala Pro His Val Leu Thr Val Pro	470	475	480	485
ttg gaa gct gtg tac aaa aat gat gac ggc aaa gac gct gtt ttg atc				1603
Leu Glu Ala Val Tyr Lys Asn Asp Asp Gly Lys Asp Ala Val Leu Ile	490	495	500	
atc agc gac gac aac aaa gta gaa gaa gta gaa gta aaa aca gct gaa				1651
Ile Ser Asp Asp Asn Lys Val Glu Glu Val Glu Val Lys Thr Ala Glu	505	510	515	
tcc gat gac ttt gat atc gca gtc agc ggt gct gga att tca gaa gac				1699
Ser Asp Asp Phe Asp Ile Ala Val Ser Gly Ala Gly Ile Ser Glu Asp	520	525	530	
gct cga gtg ctc acc cag cct gga aac tac cgg ggc ctc atc gga gaa				1747
Ala Arg Val Leu Thr Gln Pro Gly Asn Tyr Arg Gly Leu Ile Gly Glu	535	540	545	
act gtg aaa ctt cac gca gat acg gtg gag cag gcg gcg gct cct ttt				1795
Thr Val Lys Leu His Ala Asp Thr Val Glu Gln Ala Ala Ala Pro Phe	550	555	560	565
agt cct gcg gcc cct ttt gac cct gca gcc cct gcc gtt tct gcc aag				1843
Ser Pro Ala Ala Pro Phe Asp Pro Ala Ala Pro Ala Val Ser Ala Lys	570	575	580	
caa acc gtg ggc cag gtg att tagcctatga gacctcatga aat				1887
Gln Thr Val Gly Gln Val Ile	585			

<210> 280

<211> 588

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 280

Val	Ile	Ala	Thr	Ser	Asp	Val	Arg	Glu	Ile	Ser	Ser	Glu	Gly	Ile	Val
1				5					10					15	

Ala	Arg	Val	Ser	Val	Asn	Gly	Asn	Ile	Glu	Ala	Ala	Arg	Thr	Thr	Thr
		20						25					30		

Ile	Tyr	Thr	Ser	Leu	Thr	Val	Pro	Val	Ala	Asn	Leu	Pro	Val	Ala	Val
	35						40					45			

Gly Asp Arg Val Ala Ala Asp Gln Val Leu Ala Glu Leu Asp Ala Ser
 50 55 60
 Ala Leu Gln Arg Gln Leu Asp Glu Thr Asp Ala Asn Asn Ala Arg Ala
 65 70 75 80
 Ala Met Ala Asn Arg Asn Ser Ile Ala Gln Ser Gln Gln Ala Tyr Glu
 85 90 95
 Gln Ser Arg Glu Leu Leu Asp Ser Gly Leu Ser Pro Glu Ile Asn Ser
 100 105 110
 Ala Arg Ser Ser Leu Arg Ala Ser Ser Gln Ala Tyr Gln Asp Ala Ile
 115 120 125
 Arg Ser Phe Glu Ala Lys Gln Arg Asp Val Asp Gly Gly Leu Asp Ser
 130 135 140
 Thr Met Val Ala Gln Ser Asp Ala Leu Lys Ala Ala Arg Glu Gln Ala
 145 150 155 160
 Asp Ala Ala Glu Ile Glu Arg Leu Arg Ala Asp Phe Gly Leu Leu Asn
 165 170 175
 Asn Asp Arg Ser Asn Leu Asn Asp Val Ile Gly Leu Leu Asp Glu Arg
 180 185 190
 Glu Ser Leu Ala Ser Ala Glu Ser Glu Leu Ala Gln Ala Arg Ala Ala
 195 200 205
 Gly Asp Leu Glu Ala Val Ala Ala Glu Ala Lys Val Ala Gly Leu
 210 215 220
 Glu Gln Ser Ile Ala Ser Lys Thr Ser Thr Trp Pro Ser Gln Asp Gln
 225 230 235 240
 Thr Tyr Leu Gln Ser Tyr Thr Ala Leu Glu Glu Ala Glu Arg Arg Val
 245 250 255
 Ala Ser Thr Thr Glu Ala Leu Glu Ile Ala Glu Arg Ile Tyr Ile Asp
 260 265 270
 Ser Leu Gly Lys Val Asp Ser Glu Leu Ala Ala Ala Gln Arg Ala Val
 275 280 285
 Ala Glu Ala His Ser Ala Gln Gln Asp Ala Ala Leu Gly Leu Glu Thr
 290 295 300
 Ala Gln Leu Ser Thr Gln His Gln Leu Glu Ala Gln Ser Ser Ala Ile
 305 310 315 320
 Asp Ala Ala Leu Gly Leu Ala Ser Val Asp Asn Glu Ala Ala Thr Arg
 325 330 335
 Ser Thr Ser Gln Leu Arg Met Asp Ile Asn Asn Thr Thr Val Arg Ser
 340 345 350
 Pro Tyr Ser Gly Ile Val Ser Ser Val Gln Ala Ala Gln Gly Gln Pro
 355 360 365

Ala Ala Gly Ala Leu Leu Ser Val Ala Asp Asp Ser Glu Leu Lys Ile
370 375 380

Thr Ala Asn Val Lys Glu Ala Glu Ile Ser Asn Val Thr Ile Gly Ser
385 390 395 400

Arg Val Thr Phe Thr Thr Pro Ser Thr Gly Thr Lys Glu Phe Ala Gly
405 410 415

Arg Val Ser Lys Val Ser Pro Ile Ala Ala Ala Ser Ala Pro Ala
420 425 430

Thr Gly Glu Gly Ala Ala Ala Gly Ala Thr Thr Thr Asn Thr Asp Val
435 440 445

Thr Phe Pro Ile Glu Ile Ser Val Thr Gly Asp Arg Glu Gly Leu Asn
450 455 460

Leu Gly Gly Ser Ala Arg Val Arg Ile Val His Glu Ile Ala Pro His
465 470 475 480

Val Leu Thr Val Pro Leu Glu Ala Val Tyr Lys Asn Asp Asp Gly Lys
485 490 495

Asp Ala Val Leu Ile Ile Ser Asp Asp Asn Lys Val Glu Glu Val Glu
500 505 510

Val Lys Thr Ala Glu Ser Asp Asp Phe Asp Ile Ala Val Ser Gly Ala
515 520 525

Gly Ile Ser Glu Asp Ala Arg Val Leu Thr Gln Pro Gly Asn Tyr Arg
530 535 540

Gly Leu Ile Gly Glu Thr Val Lys Leu His Ala Asp Thr Val Glu Gln
545 550 555 560

Ala Ala Ala Pro Phe Ser Pro Ala Ala Pro Phe Asp Pro Ala Ala Pro
565 570 575

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<210> 281

<211> 1887

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1864)

<223> FRXA00527

<400> 281

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Val Ile Ala Thr Ser
1 5

gat gtt cgg gag att tcc tcc gag gga atc gtg gcg cgt gtg tct gtc 163

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Asp Val Arg Glu Ile Ser Ser Glu Gly Ile Val Ala Arg Val Ser Val
                10                      15                20

aac gga aat att gaa gct gcg cga acc acc acc att tac acc agt ctg   211
Asn Gly Asn Ile Glu Ala Ala Arg Thr Thr Thr Ile Tyr Ser Ser Leu
                25                      30                35

act gtg cgg gtc gcg aac ttg ccg gtt gcg gtt ggt gac cgt gtg gca   259
Thr Val Pro Val Ala Asn Leu Pro Val Ala Val Gly Asp Arg Val Ala
                40                      45                50

gct gat cag gtg ttg gct gag ttg gat gcc tct gcc ctg caa cga cag   307
Ala Asp Gln Val Leu Ala Glu Leu Asp Ala Ser Ala Leu Gln Arg Gln
                55                      60                65

ttg gat gaa act gat gcc aac aat gcg cgt gca gcc atg gcg aac cgc   355
Leu Asp Glu Thr Asp Asn Asn Ala Arg Ala Ala Met Ala Asn Arg
                70                      75                80                85

aat tcc atc gcg cag tcg cag caa gca tat gag cag tcc agg gaa ctt   403
Asn Ser Ile Ala Gln Ser Gln Gln Ala Tyr Glu Gln Ser Arg Glu Leu
                90                      95                100

ctt gat agt ggt ttg agc ccg gag atc aac tcg gcg cgg tcc tcg ttg   451
Leu Asp Ser Gly Leu Ser Pro Glu Ile Asn Ser Ala Arg Ser Ser Leu
                105                     110                115

cgg gcg tcc tca cag gca tat cag gat gcg atc cgc agt ttt gaa gcg   499
Arg Ala Ser Ser Gln Ala Tyr Gln Asp Ala Ile Arg Ser Phe Glu Ala
                120                     125                130

aag cag cga gat gtg gat ggc gga ttg gat tcc acc atg gtc gct caa   547
Lys Gln Arg Asp Val Asp Gly Gly Leu Asp Ser Thr Met Val Ala Gln
                135                     140                145

tcg gat gct ctc aag gca gct cgt gag caa gca gat gct gct gaa att   595
Ser Asp Ala Leu Lys Ala Ala Arg Glu Gln Ala Asp Ala Ala Glu Ile
                150                     155                160                165

gaa cga ctg cgc gcg gac ttc gga ctg ctc aac aac gat cgc agc aac   643
Glu Arg Leu Arg Ala Asp Phe Gly Leu Leu Asn Asn Asp Arg Ser Asn
                170                     175                180

ctc aac gat gtc att ggt ctg ctc gat gag aga gaa tct ttg gct tct   691
Leu Asn Asp Val Ile Gly Leu Leu Asp Glu Arg Glu Ser Leu Ala Ser
                185                     190                195

gcg gaa tcc gaa cta gct caa gcc cgc gct gca ggt gac cta gag gca   739
Ala Glu Ser Glu Leu Ala Gln Ala Arg Ala Ala Gly Asp Leu Glu Ala
                200                     205                210

gtc gct gca gct gaa gca aag gtt gca ggc ctg gaa caa tca att gct   787
Val Ala Ala Ala Glu Ala Lys Val Ala Gly Leu Glu Gln Ser Ile Ala
                215                     220                225

tcc aaa acc tcc acg tgg cct agc caa gat cag act tac ttg cag tcc   835
Ser Lys Thr Ser Thr Trp Pro Ser Gln Asp Gln Thr Tyr Leu Gln Ser
                230                     235                240                245

tac acc gct ttg gag gaa gct gag cga cgc gtc gca tcc acc act gaa   883
Tyr Thr Ala Leu Glu Glu Ala Glu Arg Arg Val Ala Ser Thr Thr Glu

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250	255	260	
gct cta gaa ata gcc gag cgg atc tac att gat tca ctc gga aaa gtt Ala Leu Glu Ile Ala Glu Arg Ile Tyr Ile Asp Ser Leu Gly Lys Val 265 270 275			931
gac tca gaa cta gcc gcc gca cag cgc gcc gtt gcc gaa gcc cac tca Asp Ser Glu Leu Ala Ala Ala Gln Arg Ala Val Ala Glu Ala His Ser 280 285 290			979
gca caa caa gac gca gca ctt ggc ctc gag acc gcg cag ctt tcc acc Ala Gln Gln Asp Ala Ala Leu Gly Leu Glu Thr Ala Gln Leu Ser Thr 295 300 305			1027
caa cac caa ttg gaa gcc caa tca agc gcc atc gat gca gct tta ggt Gln His Gln Leu Glu Ala Gln Ser Ser Ala Ile Asp Ala Ala Leu Gly 310 315 320 325			1075
ttg gca tca gta gat aat gaa gcc gcc acc aga tcc acg tcc cag ctg Leu Ala Ser Val Asp Asn Glu Ala Ala Thr Arg Ser Thr Ser Gln Leu 330 335 340			1123
cgg atg gat atc aac aac acc acc gtt cgc tcc cca tac tca ggc att Arg Met Asp Ile Asn Asn Thr Thr Val Arg Ser Pro Tyr Ser Gly Ile 345 350 355			1171
gtt tca tcc gtg cag gca gcc caa ggt caa cca gca gcc gcc gca ctg Val Ser Ser Val Gln Ala Ala Gln Gly Gln Pro Ala Ala Gly Ala Leu 360 365 370			1219
ttg agt gtt gct gat gat tcc gaa ctg aag atc acc gcg aat gta aaa Leu Ser Val Ala Asp Asp Ser Glu Leu Lys Ile Thr Ala Asn Val Lys 375 380 385			1267
gaa gcg gag atc agc aac gtc acc atc gga tcc cgc gtc acc ttc act Glu Ala Glu Ile Ser Asn Val Thr Ile Gly Ser Arg Val Thr Phe Thr 390 395 400 405			1315
acc cca tgc acc gga acc aaa gaa ttc gcc gcc cga gta tcc aaa gtc Thr Pro Ser Thr Gly Thr Lys Glu Phe Ala Gly Arg Val Ser Lys Val 410 415 420			1363
tcc ccc att gca gct gcc gcc agt gcc cca gct aca ggt gaa gga gct Ser Pro Ile Ala Ala Ala Ala Ser Ala Pro Ala Thr Gly Glu Gly Ala 425 430 435			1411
gcc gca ggc gcc aca acc acc aac act gac gtc acc ttc ccc atc gaa Ala Ala Gly Ala Thr Thr Thr Asn Thr Asp Val Thr Phe Pro Ile Glu 440 445 450			1459
att tcc gtc acc ggc gac cgc gaa ggc ctc aac ctc ggc gga tcc gct Ile Ser Val Thr Gly Asp Arg Glu Gly Leu Asn Leu Gly Gly Ser Ala 455 460 465			1507
cga gta cgc atc gtc cat gaa atc gca cca cac gta ctg acc gtt cct Arg Val Arg Ile Val His Glu Ile Ala Pro His Val Leu Thr Val Pro 470 475 480 485			1555
ttg gaa gct gtg tac aaa aat gat gac gcc aaa gac gct gtt ttg atc Leu Glu Ala Val Tyr Lys Asn Asp Asp Gly Lys Asp Ala Val Leu Ile 490 495 500			1603

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atc agc gac gac aac aaa gta gaa gaa gta gaa gta aaa aca gct gaa 1651
Ile Ser Asp Asp Asn Lys Val Glu Glu Val Glu Val Lys Thr Ala Glu
505 510 515

tcc gat gac ttt gat atc gca gtc agc ggt gct gga att tca gaa gac 1699
Ser Asp Asp Phe Asp Ile Ala Val Ser Gly Ala Gly Ile Ser Glu Asp
520 525 530

gct cga gtg ctc acc cag cct gga aac tac cgg ggc ctc atc gga gaa 1747
Ala Arg Val Leu Thr Gln Pro Gly Asn Tyr Arg Gly Leu Ile Gly Glu
535 540 545

act gtg aaa ctt cac gca gat acg gtg gag cag gcg gcg gct cct ttt 1795
Thr Val Lys Leu His Ala Asp Thr Val Glu Gln Ala Ala Ala Pro Phe
550 555 560

agt cct gcg gcc cct ttt gac cct gca gcc cct gcc gtt tct gcc aag 1843
Ser Pro Ala Ala Pro Phe Asp Pro Ala Ala Pro Ala Val Ser Ala Lys
570 575 580

caa acc gtg ggc cag gtg att tagcctatga gcctcatcga aat 1887
Gln Thr Val Gly Gln Val Ile
585

<210> 282
<211> 588
<212> PRT
<213> Corynebacterium glutamicum

<400> 282
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20 25 30
Ile Tyr Thr Ser Leu Thr Val Pro Val Ala Asn Leu Pro Val Ala Val
35 40 45
Gly Asp Arg Val Ala Ala Asp Gln Val Leu Ala Glu Leu Asp Ala Ser
50 55 60
Ala Leu Gln Arg Gln Leu Asp Glu Thr Asp Ala Asn Asn Ala Arg Ala
65 70 75 80
Ala Met Ala Asn Arg Asn Ser Ile Ala Gln Ser Gln Gln Ala Tyr Glu
85 90 95
Gln Ser Arg Glu Leu Leu Asp Ser Gly Leu Ser Pro Glu Ile Asn Ser
100 105 110
Ala Arg Ser Ser Leu Arg Ala Ser Ser Gln Ala Tyr Gln Asp Ala Ile
115 120
Arg Ser Phe Glu Ala Lys Gln Arg Asp Val Asp Gly Gly Leu Asp Ser
130 135 140
Thr Met Val Ala Gln Ser Asp Ala Leu Lys Ala Ala Arg Glu Gln Ala
145 150 155 160

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Asp Ala Ala Glu Ile Glu Arg Leu Arg Ala Asp Phe Gly Leu Leu Asn
 165 170 175
 Asn Asp Arg Ser Asn Leu Asn Asp Val Ile Gly Leu Leu Asp Glu Arg
 180 185 190
 Glu Ser Leu Ala Ser Ala Glu Ser Glu Leu Ala Gln Ala Arg Ala Ala
 195 200 205
 Gly Asp Leu Glu Ala Val Ala Ala Ala Glu Ala Lys Val Ala Gly Leu
 210 215 220
 Glu Gln Ser Ile Ala Ser Lys Thr Ser Thr Trp Pro Ser Gln Asp Gln
 225 230 235 240
 Thr Tyr Leu Gln Ser Tyr Thr Ala Leu Glu Glu Ala Glu Arg Arg Val
 245 250 255
 Ala Ser Thr Thr Glu Ala Leu Glu Ile Ala Glu Arg Ile Tyr Ile Asp
 260 265 270
 Ser Leu Gly Lys Val Asp Ser Glu Leu Ala Ala Ala Gln Arg Ala Val
 275 280 285
 Ala Glu Ala His Ser Ala Gln Gln Asp Ala Ala Leu Gly Leu Glu Thr
 290 295 300
 Ala Gln Leu Ser Thr Gln His Gln Leu Glu Ala Gln Ser Ser Ala Ile
 305 310 315 320
 Asp Ala Ala Leu Gly Leu Ala Ser Val Asp Asn Glu Ala Ala Thr Arg
 325 330 335
 Ser Thr Ser Gln Leu Arg Met Asp Ile Asn Asn Thr Thr Val Arg Ser
 340 345 350
 Pro Tyr Ser Gly Ile Val Ser Ser Val Gln Ala Ala Gln Gly Gln Pro
 355 360 365
 Ala Ala Gly Ala Leu Leu Ser Val Ala Asp Asp Ser Glu Leu Lys Ile
 370 375 380
 Thr Ala Asn Val Lys Glu Ala Glu Ile Ser Asn Val Thr Ile Gly Ser
 385 390 395 400
 Arg Val Thr Phe Thr Thr Pro Ser Thr Gly Thr Lys Glu Phe Ala Gly
 405 410 415
 Arg Val Ser Lys Val Ser Pro Ile Ala Ala Ala Ser Ala Pro Ala
 420 425 430
 Thr Gly Glu Gly Ala Ala Ala Gly Ala Thr Thr Thr Asn Thr Asp Val
 435 440 445
 Thr Phe Pro Ile Glu Ile Ser Val Thr Gly Asp Arg Glu Gly Leu Asn
 450 455 460
 Leu Gly Gly Ser Ala Arg Val Arg Ile Val His Glu Ile Ala Pro His
 465 470 475 480

Val Leu Thr Val Pro Leu Glu Ala Val Tyr Lys Asn Asp Asp Gly Lys
485 490 495

Asp Ala Val Leu Ile Ile Ser Asp Asp Asn Lys Val Glu Glu Val Glu
500 505 510

Val Lys Thr Ala Glu Ser Asp Asp Phe Asp Ile Ala Val Ser Gly Ala
515 520 525

Gly Ile Ser Glu Asp Ala Arg Val Leu Thr Gln Pro Gly Asn Tyr Arg
530 535 540

Gly Leu Ile Gly Glu Thr Val Lys Leu His Ala Asp Thr Val Glu Gln
545 550 555 560

Ala Ala Ala Pro Phe Ser Pro Ala Ala Pro Phe Asp Pro Ala Ala Pro
565 570 575

Ala Val Ser Ala Lys Gln Thr Val Gly Gln Val Ile
580 585

<210> 283

<211> 1521

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1498)

<223> RXN00547

<400> 283

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Val Ala Arg Asp Phe
1 5

atc aat gca atc gcc ggt cgg ttt ggt cgt ttt gcg cag gtg gcc act 163
Ile Asn Ala Ile Gly Gly Arg Phe Gly Arg Phe Ala Gln Val Gly Thr
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cag cgg ttc tgg act ccc ctg cgt gtt ttg atc acc act tcc ctg gtg 211
Gln Arg Phe Trp Thr Pro Leu Arg Val Leu Ile Thr Thr Ser Leu Val
25 30 35

ttt ttg gcc atg ggg ttt tta aca aaa gcc aat tgc atc cag ggt tct 259
Phe Leu Ala Met Gly Phe Leu Thr Lys Ala Asn Cys Ile Gln Gly Ser
40 45 50

aga ggt act gat ggt gtg gtt tct ttg aac tgg tgc gga agt cgc cag 307
Arg Gly Thr Asp Gly Val Val Ser Leu Asn Trp Ser Gly Ser Arg Gln
55 60 65

tac acc tca gcc tgt tac aac gac atc gtt cgg ctc tat ggg ggg cgc 355
Tyr Thr Ser Ala Cys Tyr Asn Asp Ile Val Pro Leu Tyr Gly Gly Arg
70 75 80 85

gga att gat gcg cca ggt ttc cct tat gcc ttt tgg tgg cag gaa ggt 403
Gly Ile Asp Ala Pro Gly Phe Pro Tyr Ala Phe Ser Trp Gln Glu Gly

	90	95	100	
	gat ctc acc agg tac atg gag tac ccg gtg ttg ggc gga att ttc cag	451		
	Asp Leu Thr Arg Tyr Met Glu Tyr Pro Val Leu Gly Gly Ile Phe Gln			
	105	110	115	
	tgg att tgt ggc att atc acg cgg ttt ttg tac ccg gtt gtt gat gtc	499		
	Trp Ile Cys Gly Ile Ile Thr Arg Phe Leu Tyr Pro Val Val Asp Val			
	120	125	130	
	att ccg ttt cat acg ctg cct gaa tct ggt ctt tat ttc atc gtc acc	547		
	Ile Pro Phe His Thr Leu Pro Glu Ser Gly Leu Tyr Phe Ile Val Thr			
	135	140	145	
	gcg ctt gcg ttg gcg ttc ttt tgg gtg ttg gtc atc cgc atg atg gtg	595		
	Ala Leu Ala Leu Ala Phe Phe Trp Val Leu Val Ile Arg Met Met Val			
	150	155	160	165
	gag ctc act ggc aat cga gtg tgg gat acc gtc ctt gtt gcg gcg tct	643		
	Glu Leu Thr Gly Asn Arg Val Trp Asp Thr Val Leu Val Ala Ala Ser			
	170	175	180	
	ccc ctg gtt gct gtg cat gcg ttt acc aac tgg gat act cca gcc att	691		
	Pro Leu Val Ala Val His Ala Phe Thr Asn Trp Asp Thr Pro Ala Ile			
	185	190	195	
	gcg gcg gtg att ggt gcg atg ctt gcg gtg aaa cgc gga aac ccc ttg	739		
	Ala Ala Val Ile Gly Ala Met Leu Ala Val Lys Arg Gly Asn Pro Leu			
	200	205	210	
	gtt gcg ggt gtg ctg atc gcc gcg ggt acg gcg ttc aaa ttg tgg ccg	787		
	Val Ala Gly Val Leu Ile Gly Ala Gly Thr Ala Phe Lys Leu Trp Pro			
	215	220	225	
	ctt tat ctt ctt ggt gcg tat ttg gtg ctg gcg gtc aag aat aag aat	835		
	Leu Tyr Leu Leu Gly Ala Tyr Leu Val Leu Ala Val Lys Asn Lys Asn			
	230	235	240	245
	ctc aag ccg ttt atc acc atg gct gca gcg gct gcg gtg aca tgg ctc	883		
	Leu Lys Pro Phe Ile Thr Met Ala Ala Ala Ala Val Thr Trp Leu			
	250	255	260	
	gtg gtg aat gtg cca gtg atg atc gcg tac ccc aag gcg tgg aat gaa	931		
	Val Val Asn Val Pro Val Met Ile Ala Tyr Pro Lys Ala Trp Asn Glu			
	265	270	275	
	ttc ttg cgc ctg aac cgg gag cgt ggt gcg gag tgg acc acg att tac	979		
	Phe Leu Arg Leu Asn Arg Glu Arg Gly Ala Glu Trp Thr Thr Ile Tyr			
	280	285	290	
	cag gtc atc gac cgt aat ttg ccg atc aat ttg aat gat cca gtg ctg	1027		
	Gln Val Ile Asp Arg Asn Leu Pro Ile Asn Leu Asn Asp Pro Val Leu			
	295	300	305	
	ctt aat gtg ctg agc ttc gcc ttg ttt ggt gca tcg tgt gtg gcc att	1075		
	Leu Asn Val Leu Ser Phe Gly Leu Phe Gly Ala Ser Cys Val Ala Ile			
	310	315	320	325
	ttg atc ctt ggg ctc aag gtg cag cgc act ccc cga gtc gct gag ctg	1123		
	Leu Ile Leu Gly Leu Lys Val Gln Arg Thr Pro Arg Val Ala Glu Leu			
	330	335	340	

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gcc ttt ttg att gtc gcg gcg ttt ttg ctg ttt aac aag gtg tgg agt 1171
Ala Phe Leu Ile Val Ala Ala Phe Leu Leu Phe Asn Lys Val Trp Ser
      345                        350      355

cct cag tat tca ctg tgg ctg gtc ccg ttg gct gtt ctg gca ttt cct 1219
Pro Gln Tyr Ser Leu Trp Leu Val Pro Leu Ala Val Leu Ala Phe Pro
      360      365      370

cag tgg aaa gtg ctg ttc ccg tgg atg gtt aca gac gcc atg gtg tgg 1267
Gln Trp Trp Lys Val Leu Phe Pro Trp Met Val Thr Asp Ala Met Val Trp
      375      380      385

cca att ttg atg tgg cac atg ctc ggc acg gac aac aag gga ctc ccc 1315
Pro Ile Leu Met Trp His Met Leu Gly Thr Asp Asn Lys Gly Leu Pro
      390      395      400      405

cat gaa atg ttg gat ctc atc gtg att tcc cga gat gcc ttc att gtg 1363
His Glu Met Leu Asp Leu Ile Val Ile Ser Arg Asp Ala Phe Ile Val
      410      415      420

gtc atg ata gta ggt gta atc ccg cag atg ctc gga cga cgt gca gat 1411
Val Met Ile Val Gly Val Ile Arg Gln Met Leu Gly Arg Arg Ala Asp
      425      430      435

ccg gtg atg gat gcg cac gcc ggg cgc gat ttg ttg gcc ggg ccc ttc 1459
Pro Val Met Asp Ala His Ala Gly Arg Asp Leu Leu Ala Gly Pro Phe
      440      445      450

ggc gca gcc gag cgt cga aaa gca ttg aag gaa gta agt tgagcacaac 1508
Gly Ala Gly Glu Arg Arg Lys Ala Leu Lys Glu Val Ser
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agttttgctg gtc 1521

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<211> 466
<212> PRT
<213> Corynebacterium glutamicum

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Ala Gln Val Gly Thr Gln Arg Phe Trp Thr Pro Leu Arg Val Leu Ile
      20          25          30

Thr Thr Ser Leu Val Phe Leu Ala Met Gly Phe Leu Thr Lys Ala Asn
      35          40          45

Cys Ile Gln Gly Ser Arg Gly Thr Asp Gly Val Val Ser Leu Asn Trp
      50          55          60

Ser Gly Ser Arg Gln Tyr Thr Ser Ala Cys Tyr Asn Asp Ile Val Pro
      65          70          75          80

Leu Tyr Gly Gly Arg Gly Ile Asp Ala Pro Gly Phe Pro Tyr Ala Phe
      85          90          95

Ser Trp Gln Glu Gly Asp Leu Thr Arg Tyr Met Glu Tyr Pro Val Leu

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100										105										110									
Gly	Gly	Ile	Phe	Gln	Trp	Ile	Cys	Gly	Ile	Ile	Thr	Arg	Phe	Leu	Tyr														
		115					120					125																	
Pro	Val	Val	Asp	Val	Ile	Pro	Phe	His	Thr	Leu	Pro	Glu	Ser	Gly	Leu														
		130				135					140																		
Tyr	Phe	Ile	Val	Thr	Ala	Leu	Ala	Leu	Ala	Phe	Phe	Trp	Val	Leu	Val														
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Ile	Arg	Met	Met	Val	Glu	Leu	Thr	Gly	Asn	Arg	Val	Trp	Asp	Thr	Val														
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Leu	Val	Ala	Ala	Ser	Pro	Leu	Val	Ala	Val	His	Ala	Phe	Thr	Asn	Trp														
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Asp	Thr	Pro	Ala	Ile	Ala	Ala	Val	Ile	Gly	Ala	Met	Leu	Ala	Val	Lys														
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Arg	Gly	Asn	Pro	Leu	Val	Ala	Gly	Val	Leu	Ile	Gly	Ala	Gly	Thr	Ala														
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Phe	Lys	Leu	Trp	Pro	Leu	Tyr	Leu	Leu	Gly	Ala	Tyr	Leu	Val	Leu	Ala														
					230					235					240														
Val	Lys	Asn	Lys	Asn	Leu	Lys	Pro	Phe	Ile	Thr	Met	Ala	Ala	Ala	Ala														
					245				250					255															
Ala	Val	Thr	Trp	Leu	Val	Val	Asn	Val	Pro	Val	Met	Ile	Ala	Tyr	Pro														
					260			265					270																
Lys	Ala	Trp	Asn	Glu	Phe	Leu	Arg	Leu	Asn	Arg	Glu	Arg	Gly	Ala	Glu														
		275					280					285																	
Trp	Thr	Thr	Ile	Tyr	Gln	Val	Ile	Asp	Arg	Asn	Leu	Pro	Ile	Asn	Leu														
		290				295					300																		
Asn	Asp	Pro	Val	Leu	Leu	Asn	Val	Leu	Ser	Phe	Gly	Leu	Phe	Gly	Ala														
					310					315					320														
Ser	Cys	Val	Ala	Ile	Leu	Ile	Leu	Gly	Leu	Lys	Val	Gln	Arg	Thr	Pro														
					325				330					335															
Arg	Val	Ala	Glu	Leu	Ala	Phe	Leu	Ile	Val	Ala	Ala	Phe	Leu	Leu	Phe														
			340					345					350																
Asn	Lys	Val	Trp	Ser	Pro	Gln	Tyr	Ser	Leu	Trp	Leu	Val	Pro	Leu	Ala														
		355					360					365																	
Val	Leu	Ala	Phe	Pro	Gln	Trp	Lys	Val	Leu	Phe	Pro	Trp	Met	Val	Thr														
						375					380																		
Asp	Ala	Met	Val	Trp	Pro	Ile	Leu	Met	Trp	His	Met	Leu	Gly	Thr	Asp														
					390					395					400														
Asn	Lys	Gly	Leu	Pro	His	Glu	Met	Leu	Asp	Leu	Ile	Val	Ile	Ser	Arg														

Gly Arg Arg Ala Asp Pro Val Met Asp Ala His Ala Gly Arg Asp Leu
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Leu Ala Gly Pro Phe Gly Ala Gly Glu Arg Arg Lys Ala Leu Lys Glu
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Val Ser
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<210> 285

<211> 514

<212> DNA

<213> *Corynebacterium glutamicum*

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<221> CDS

<222> (101)..(514)

<223> FRXA00547

<400> 285

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 Val Ala Ile Leu Ile
 1 5

ctt ggg ctc aag gtg cag cgc act ccc cga gtc gct gag ctg gcc ttt 163
 Leu Gly Leu Lys Val Gln Arg Thr Pro Arg Val Ala Glu Leu Ala Phe
 10 15 20

ttg att gtc gcg gcg ttt ttg ctg ttt aac aag gtg tgg agt cct cag 211
 Leu Ile Val Ala Ala Phe Leu Leu Phe Asn Lys Val Trp Ser Pro Gln
 25 30 35

tat tca ctg tgg ctg gtc cgc ttg gct gtt ctg gca ttt cct cag tgg 259
 Tyr Ser Leu Trp Leu Val Pro Leu Ala Val Leu Ala Phe Pro Gln Trp
 40 45 50

aaa gtg ctg ttc cgc tgg atg gtt aca gac gcc atg gtg tgg cca att 307
 Lys Val Leu Phe Pro Trp Met Val Thr Asp Ala Met Val Trp Pro Ile
 55 60 65

ttg atg tgg cac atg ctc ggc acg gac aac aag gga ctc ccc cat gaa 355
 Leu Met Trp His Met Leu Gly Thr Asp Asn Lys Gly Leu Pro His Glu
 70 75 80 85

atg ttg gat ctc atc gtg att tcc cga gat gcc ttc att gtg gtc atg 403
 Met Leu Asp Leu Ile Val Ile Ser Arg Asp Ala Phe Ile Val Val Met
 90 95 100

ata agt agg tgt aat cgc gca gat gct cgg acg acg tgc aaa tcc ggt 451
 Ile Ser Arg Cys Asn Pro Ala Asp Ala Arg Thr Thr Cys Lys Ser Gly
 105 110 115

gat gga tgc gca cgc cgg gcg cga att gtt ggc cgg gcc ctt cgg cgc 499
 Asp Gly Cys Ala Arg Arg Ala Arg Ile Val Gly Arg Ala Leu Arg Arg
 120 125 130

aag cga agc gtc gaa

514

Lys Arg Ser Val Glu
135

<210> 286

<211> 138

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 286

Val Ala Ile Leu Ile Leu Gly Leu Lys Val Gln Arg Thr Pro Arg Val
1 5 10 15

Ala Glu Leu Ala Phe Leu Ile Val Ala Ala Phe Leu Leu Phe Asn Lys
20 25 30

Val Trp Ser Pro Gln Tyr Ser Leu Trp Leu Val Pro Leu Ala Val Leu
35 40 45

Ala Phe Pro Gln Trp Lys Val Leu Phe Pro Trp Met Val Thr Asp Ala
50 55 60

Met Val Trp Pro Ile Leu Met Trp His Met Leu Gly Thr Asp Asn Lys
65 70 75 80

Gly Leu Pro His Glu Met Leu Asp Leu Ile Val Ile Ser Arg Asp Ala
85 90 95

Phe Ile Val Val Met Ile Ser Arg Cys Asn Pro Ala Asp Ala Arg Thr
100 105 110

Thr Cys Lys Ser Gly Asp Gly Cys Ala Arg Arg Ala Arg Ile Val Gly
115 120 125

Arg Ala Leu Arg Arg Lys Arg Ser Val Glu
130 135

<210> 287

<211> 713

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(690)

<223> FRXA00546

<400> 287

ccg gtg ttg ggc gga att ttc cag tgg att tgt ggc att atc acg cgg 48
Pro Val Leu Gly Gly Ile Phe Gln Trp Ile Cys Gly Ile Ile Thr Arg
1 5 10 15

ttt ttg tac ccg gtt gtt gat gtc att ccg ttt cat acg ctg cct gaa 96
Phe Leu Tyr Pro Val Val Asp Val Ile Pro Phe His Thr Leu Pro Glu
20 25 30

tct ggt ctt tat ttc atc gtc acc gcg ctt gcg ttg gcg ttc ttt tgg 144
Ser Gly Leu Tyr Phe Ile Val Thr Ala Leu Ala Leu Ala Phe Phe Thr
35 40 45

gtg ttg gtc atc cgc atg atg gtg gag ctc act ggc aat cga gtg tgg 192
Val Leu Val Ile Arg Met Met Val Glu Leu Thr Gly Asn Arg Val Trp
50 55 60

gat acc gtc ctt gtt gcg gcg tct ccc ctg gtt gct gtg cat gcg ttt 240
Asp Thr Val Leu Val Ala Ala Ser Pro Leu Val Ala Val His Ala Phe
65 70 75 80

acc aac tgg gat act cca gcc att gcg gcg gtg att ggt gcg atg ctt 288
Thr Asn Trp Asp Thr Pro Ala Ile Ala Ala Val Ile Gly Ala Met Leu
85 90 95

gcg gtg aaa cgc gga aac ccc ttg gtt gcg ggt gtg ctg atc ggc gcg 336
Ala Val Lys Arg Gly Asn Pro Leu Val Ala Gly Val Leu Ile Gly Ala
100 105 110

ggt acg gcg ttc aaa ttg tgg ccg ctt tat ctt ctt ggt gcg tat ttg 384
Gly Thr Ala Phe Lys Leu Trp Pro Leu Tyr Leu Leu Gly Ala Tyr Leu
115 120 125

gtg ctg gcg gtc aag aat aag aat ctc aag ccg ttt atc acc atg gct 432
Val Leu Ala Val Lys Asn Lys Asn Leu Lys Pro Phe Ile Thr Met Ala
130 135 140

gca gcg gct gcg gtg aca tgg ctc gtg gtg aat gtg cca gtg atg atc 480
Ala Ala Ala Ala Val Thr Trp Leu Val Val Asn Val Pro Val Met Ile
145 150 155 160

gcg tac ccc aag gcg tgg aat gaa ttc ttg cgc ctg aac cgg gag cgt 528
Ala Tyr Pro Lys Ala Trp Asn Glu Phe Leu Arg Leu Asn Arg Glu Arg
165 170 175

ggt gcg gag tgg acc acg att tac cag gtc atc gac cgt aat ttg ccg 576
Gly Ala Glu Trp Thr Thr Ile Tyr Gln Val Ile Asp Arg Asn Leu Pro
180 185 190

atc aat ttg aat gat cca gtg ctg ctt aat gtg ctg agc ttc ggc ttg 624
Ile Asn Leu Asn Asp Pro Val Leu Leu Asn Val Leu Ser Phe Gly Leu
195 200 205

ttt ggt gca tca gtg tgt gcc cat ttt gat cct tgg gct caa ggt gca 672
Phe Gly Ala Ser Val Cys Gly His Phe Asp Pro Trp Ala Gln Gly Ala
210 215 220

gcg cac tcc ccg agt cgc tgagctggcc tttttgattg tcg 713
Ala His Ser Pro Ser Arg
225 230

<210> 288

<211> 230

<212> PRT

<213> Corynebacterium glutamicum

<400> 288

Pro Val Leu Gly Gly Ile Phe Gln Trp Ile Cys Gly Ile Ile Thr Arg
1 5 10 15

Phe Leu Tyr Pro Val Val Asp Val Ile Pro Phe His Thr Leu Pro Glu
20 25 30

[illegible]

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<220>  
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<222> (101)..(1036)  
<223> RXN00552
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gtttttaagg tagccacaca tcgcactaga ctgaagaact gtg gct acc tca aaa 115
Val Ala Thr Ser Lys
1 5

att ctt ctt tat tac gca ttc acc cgg ctc tct gac cct aaa gcg gtt 163
Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser Asp Pro Lys Ala Val
10 15 20

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cag ctg tgg	cag cgt	gag ctc	tgc	gag tca	ctg	aat	ctt	cgt	ggc	cgc	211
Gln Leu Trp	Gln Arg	Glu Leu	Cys	Glu Ser	Leu	Asn	Leu	Arg	Gly	Arg	
	25			30				35			
atc ctg atc	tcc act	cac ggc	atc	aat gga	acc	gtg	ggc	gga	gat	att	259
Ile Leu Ile	Ser Thr	His Gly	Ile	Asn Gly	Thr	Val	Gly	Gly	Asp	Ile	
	40		45				50				
gat gat tgc	aag cgc	tac att	aaa	aag acc	cgc	gag	tac	cca	ggt	ttc	307
Asp Asp	Cys Lys	Ala Tyr	Ile	Lys Lys	Thr	Arg	Glu	Tyr	Pro	Gly	
	55		60				65				
aac cgc atg	cag ttt	aag tgg	tcc	gag ggt	ggc	gct	gag	gat	ttc	cca	355
Asn Arg	Met Gln	Phe Lys	Trp	Ser Glu	Gly	Ala	Glu	Asp	Phe	Pro	
	70		75		80				85		
aag ctc agt	gtc aaa	gtc cgc	gat	gag atc	gtt	gcc	ttc	ggc	gct	cca	403
Lys Leu	Ser Val	Lys Val	Arg	Asp Glu	Ile	Val	Ala	Phe	Gly	Ala	
		90			95				100		
gat gag ctc	aaa gtg	gat gaa	aac	ggc gtc	gtc	ggt	ggc	ggc	gtt	cac	451
Asp Glu	Leu Val	Asp Glu	Asn	Gly Val	Val	Gly	Gly	Gly	Val	His	
	105			110			115				
ctg aaa cca	cag cag	gtc aat	gag	ctt gtg	gaa	gcc	cgt	ggc	gat	gaa	499
Leu Lys	Pro Gln	Gln Val	Asn	Glu Leu	Val	Glu	Ala	Arg	Gly	Asp	
	120			125			130				
gtt gtg ttc	ttt gac	ggc cgc	aac	gca atg	gaa	gcc	cag	atc	ggc	aag	547
Val Val	Phe Phe	Asp Gly	Arg	Asn Ala	Met	Glu	Ala	Gln	Ile	Gly	
	135			140			145				
ttc aag gac	gct gtt	gtc cct	gac	gta gaa	acc	act	cat	gat	ttc	atc	595
Phe Lys	Asp Ala	Val Val	Pro	Asp Val	Glu	Thr	His	Asp	Phe	Ile	
	150		155		160				165		
gca gaa att	gag tct	gga aaa	tac	gac gat	ctc	aaa	gac	aag	cct	gtg	643
Ala Glu	Ile Glu	Ser Gly	Lys Tyr	Asp Asp	Leu	Lys	Asp	Lys	Pro	Val	
		170			175				180		
gtc acc tac	tgc acc	ggc gga	att	cgt tgt	gag	atc	ctg	agt	tca	ctc	691
Val Thr	Tyr Cys	Thr Gly	Gly Ile	Arg Cys	Glu	Ile	Leu	Ser	Ser	Leu	
	185			190			195				
atg atc aac	cgt ggt	ttc aaa	gag	gtc tac	caa	atc	gat	ggc	ggc	atc	739
Met Ile	Asn Arg	Gly Phe	Lys Glu	Val Tyr	Gln	Ile	Asp	Gly	Gly	Ile	
	200		205				210				
gtt cgc tac	ggc gag	cag ttt	ggc	aac aag	ggc	ctg	tgg	gaa	ggc	tcc	787
Val Arg	Tyr Gly	Glu Gln	Phe	Gly Asn	Lys	Gly	Leu	Trp	Glu	Gly	
	215		220				225				
ctc tac gtt	ttc gat	aag cgc	atg	cat atg	gaa	ttc	ggc	gag	gat	tac	835
Leu Tyr	Val Phe	Asp Lys	Arg Met	His Met	Glu	Phe	Gly	Glu	Asp	Tyr	
	230		235		240				245		
aaa gag gtc	gga cac	gtc atc	cat	tgc gat	act	ccc	acc	aac	aaa	ttt	883
Lys Glu	Val Gly	His Cys	Ile His	Cys Asp	Thr	Pro	Thr	Asn	Lys	Phe	
		250			255				260		
gag cac tgc	ctc aac	gaa gat	gat	tgc cgc	gag	ctc	gtg	ttg	atg	tgc	931

Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys
 265 270 275

cct gat tgc ttc gcc aat gtt gag acc cgt cat tgc aag cgc gaa cgc 979
 Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg
 280 285 290

tgt gca gca att gct gcg gat ttc gct gag caa gga att gat ccg ctc 1027
 Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln Gly Ile Asp Pro Leu
 295 300 305

ggt act tct taaaaagggt atgggtggctg ggt 1059
 Val Thr Ser
 310

<210> 290

<211> 312

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 290

Val Ala Thr Ser Lys Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser
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Asp Pro Lys Ala Val Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu
 20 25 30

Asn Leu Arg Gly Arg Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr
 35 40 45

Val Gly Gly Asp Ile Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg
 50 55 60

Glu Tyr Pro Gly Phe Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly
 65 70 75 80

Ala Glu Asp Phe Pro Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val
 85 90 95

Ala Phe Gly Ala Pro Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val
 100 105 110

Gly Gly Gly Val His Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu
 115 120 125

Ala Arg Gly Asp Glu Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu
 130 135 140

Ala Gln Ile Gly Lys Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr
 145 150 155 160

Thr His Asp Phe Ile Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu
 165 170 175

Lys Asp Lys Pro Val Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu
 180 185 190

Ile Leu Ser Ser Leu Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln
 195 200 205

Ile Asp Gly Gly Ile Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly
 210 215 220
 Leu Trp Glu Gly Ser Leu Tyr Val Phe Asp Lys Arg Met His Met Glu
 225 230 235 240
 Phe Gly Glu Asp Tyr Lys Glu Val Gly His Cys Ile His Cys Asp Thr
 245 250 255
 Pro Thr Asn Lys Phe Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu
 260 265 270
 Leu Val Leu Met Cys Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His
 275 280 285
 Cys Lys Arg Glu Arg Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln
 290 295 300
 Gly Ile Asp Pro Leu Val Thr Ser
 305 310

<210> 291
 <211> 740
 <212> DNA
 <213> *Corynebacterium glutamicum*
 <220>
 <221> CDS
 <222> {1}..(717)
 <223> PRXA00552

<400> 291
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 Phe Lys Trp Ser Glu Gly Gly Ala Glu Asp Phe Pro Lys Leu Ser Val
 1 5 10 15
 aaa gtc cgc gat gag atc gtt gcc ttc ggc gct cca gat gag ctc aaa 96
 Lys Val Arg Asp Glu Ile Val Ala Phe Gly Ala Pro Asp Glu Leu Lys
 20 25 30
 gtg gat gaa aac ggc gtc gtc ggt ggc ggc gtt cac ctg aaa cca cag 144
 Val Asp Glu Asn Gly Val Val Gly Gly Gly Val His Leu Lys Pro Gln
 35 40 45
 cag gtc aat gag ctt gtg gaa gcc cgt ggc gat gaa gtt gtg ttc ttt 192
 Gln Val Asn Glu Leu Val Glu Ala Arg Gly Asp Glu Val Val Phe Phe
 50 55 60
 gac ggc cgc aac gca atg gaa gcc cag atc ggc aag ttc aag gac gct 240
 Asp Gly Arg Asn Ala Met Glu Ala Gln Ile Gly Lys Phe Lys Asp Ala
 65 70 75 80
 gtt gtc cct gac gta gaa acc act cat gat ttc atc gca gaa att gag 288
 Val Val Pro Asp Val Glu Thr Thr His Asp Phe Ile Ala Glu Ile Glu
 85 90 95
 tct gga aaa tac gac gat ctc aaa gac aag cct gtg gtc acc tac tgc 336
 Ser Gly Lys Tyr Asp Asp Leu Lys Asp Lys Pro Val Val Thr Tyr Cys
 100 105 110

acc ggc gga att cgt tgt gag atc ctg agt tca ctc atg atc aac cgt 384
 Thr Gly Gly Ile Arg Cys Glu Ile Leu Ser Ser Leu Met Ile Asn Arg
 115 120 125

ggc ttc aaa gag gtc tac caa atc gat ggc ggc atc gtt cgc tac ggc 432
 Gly Phe Lys Glu Val Tyr Gln Ile Asp Gly Gly Ile Val Arg Tyr Gly
 130 135 140

gag cag ttt ggc aac aag ggc ctg tgg gaa ggc tcc ctc tac gtt ttc 480
 Glu Gln Phe Gly Asn Lys Gly Leu Trp Glu Gly Ser Leu Tyr Val Phe
 145 150 155 160

gat aag cgc atg cat atg gaa ttc ggc gag gat tac aaa gag gtc gga 528
 Asp Lys Arg Met His Met Glu Phe Gly Glu Asp Tyr Lys Glu Val Gly
 165 170 175

cac tgc atc cat tgc gat act ccc acc aac aaa ttt gag cac tgc ctc 576
 His Cys Ile His Cys Asp Thr Pro Thr Asn Lys Phe Glu His Cys Leu
 180 185 190

aac gaa gat gat tgc cgc gag ctc gtg ttg atg tgc cct gat tgc ttc 624
 Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys Pro Asp Cys Phe
 195 200 205

gcc aat gtt gag acc cgt cat tgc aag cgc gaa cgc tgt gca gca att 672
 Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg Cys Ala Ala Ile
 210 215 220

gct gcg gat ttc gct gag caa gga att gat ccg ctc gtt act tct 717
 Ala Ala Asp Phe Ala Glu Gln Gly Ile Asp Pro Leu Val Thr Ser
 225 230 235

taaaaagggt atgggtggctg ggt 740

<210> 292
 <211> 239
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 292
 Phe Lys Trp Ser Glu Gly Gly Ala Glu Asp Phe Pro Lys Leu Ser Val
 1 5 10 15
 Lys Val Arg Asp Glu Ile Val Ala Phe Gly Ala Pro Asp Glu Leu Lys
 20 25 30
 Val Asp Glu Asn Gly Val Val Gly Gly Gly Val His Leu Lys Pro Gln
 35 40 45
 Gln Val Asn Glu Leu Val Glu Ala Arg Gly Asp Glu Val Val Phe Phe
 50 55 60
 Asp Gly Arg Asn Ala Met Glu Ala Gln Ile Gly Lys Phe Lys Asp Ala
 65 70 75 80
 Val Val Pro Asp Val Glu Thr Thr His Asp Phe Ile Ala Glu Ile Glu
 85 90 95
 Ser Gly Lys Tyr Asp Asp Leu Lys Asp Lys Pro Val Val Thr Tyr Cys
 100 105 110

Thr Gly Gly Ile Arg Cys Glu Ile Leu Ser Ser Leu Met Ile Asn Arg
 115 120 125
 Gly Phe Lys Glu Val Tyr Gln Ile Asp Gly Gly Ile Val Arg Tyr Gly
 130 135 140
 Glu Gln Phe Gly Asn Lys Gly Leu Trp Glu Gly Ser Leu Tyr Val Phe
 145 150 155 160
 Asp Lys Arg Met His Met Glu Phe Gly Glu Asp Tyr Lys Glu Val Gly
 165 170 175
 His Cys Ile His Cys Asp Thr Pro Thr Asn Lys Phe Glu His Cys Leu
 180 185 190
 Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys Pro Asp Cys Phe
 195 200 205
 Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg Cys Ala Ala Ile
 210 215 220

Ala Ala Asp Phe Ala Glu Gln Gly Ile Asp Pro Leu Val Thr Ser
 225 230 235

<210> 293
 <211> 1062
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1039)
 <223> RXN00555

<400> 293
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 cggttcttaa cagttttctc catctcaact ccggaatttg atg aaa caa ccc ctt 115
 Met Lys Gln Pro Leu
 1 5
 cgc gta ctt att tct tgt cga ccc gaa gaa aat tcg ggt ggc aaa cgt 163
 Arg Val Leu Ile Ser Cys Arg Pro Glu Glu Asn Ser Gly Gly Lys Arg
 10 15 20
 agt gaa caa aat gat gct gtt ttt gag ttc gcc gca tgg cta gct cgt 211
 Ser Glu Gln Asn Asp Ala Val Phe Glu Phe Ala Ala Trp Leu Ala Arg
 25 30 35
 act tca gac atc aat gtt cgt gga atc aca act ttc ata cgc cct tgg 259
 Thr Ser Asp Ile Asn Val Arg Gly Ile Thr Thr Phe Ile Arg Pro Trp
 40 45 50
 ccg tct tcc tcc atc agt aag ctc gga gga aaa tat cat aag tgg tat 307
 Pro Ser Ser Ser Ile Ser Lys Leu Gly Gly Lys Tyr His Lys Trp Tyr
 55 60 65
 aag aat tta gat tct tac tac cgc agt cgc acg atc aag gga ctc aaa 355
 Lys Asn Leu Asp Ser Tyr Tyr Arg Ser Arg Thr Ile Lys Gly Leu Lys

70	75	80	85	
gag gcc gga gtt gag aag tcc caa tgg gac gat gat gtt tca gtt ttt				403
Glu Ala Gly Val Glu Lys Ser Gln Trp Asp Asp Val Ser Val Phe	90	95	100	
gta gat ggt cct tct gaa tcc acg ctg ctc acc cat gct gct gaa gaa				451
Val Asp Gly Pro Ser Glu Ser Thr Leu Leu Thr His Ala Ala Glu Glu	105	110	115	
ttc gaa gcg gac ctc att ctg ctt ggc tct gat gcg acc gca cca aaa				499
Phe Glu Ala Asp Leu Ile Leu Leu Gly Ser Asp Ala Thr Ala Pro Lys	120	125	130	
ggc cgc ttt ctg gcc agc tcc acc gca gat gcc ctc ctt cac tcc tcg				547
Gly Arg Phe Leu Ala Ser Ser Thr Ala Asp Ala Leu Leu His Ser Ser	135	140	145	
ccc gtc cca cta gga ctt gtg ccg cga ggg gtg aag ctt tcc aaa aag				595
Pro Val Pro Leu Gly Leu Val Pro Arg Gly Val Lys Leu Ser Lys Lys	150	155	160	165
ggg gtc acc cgc gtc aac tac gct ttc acc aat gaa agc gat gac ttt				643
Gly Val Thr Arg Val Asn Tyr Ala Phe Thr Asn Glu Ser Asp Asp Phe	170	175	180	
gag caa ggt tta cgc tct tcc gcg gag ctc gcc acc aat tgg aac gtt				691
Glu Gln Gly Leu Arg Ser Ser Ala Glu Leu Ala Thr Asn Trp Asn Val	185	190	195	
cct ctt cgg atc ctt gct ttt tca ccc aca ggc att act tcc gca cca				739
Pro Leu Arg Ile Leu Ala Phe Ser Pro Thr Gly Ile Thr Ser Ala Pro	200	205	210	
acg tcg cgg agc ttg gat att tcc act gag ctt tcc tcc gag tgg cgt				787
Thr Ser Arg Ser Leu Asp Ile Ser Thr Glu Leu Ser Ser Glu Trp Arg	215	220	225	
gaa cta acg ctc gcc atg ctt gat cga gcc cgt gat ggc gtc ctc aca				835
Glu Leu Thr Leu Ala Met Leu Asp Arg Ala Arg Asp Gly Val Leu Thr	230	235	240	245
gac cac cca aac ttg agc gtg agc agt gaa acc ggt tct ggc tgg ggt				883
Asp His Pro Asn Leu Ser Val Ser Ser Glu Thr Gly Ser Gly Trp Gly	250	255	260	
tgg agc ggt gca att gat gct ttg cga tgg aag aaa ggt gac ctg ctg				931
Trp Ser Gly Ala Ile Asp Ala Leu Arg Trp Lys Lys Gly Asp Leu Leu	265	270	275	
tgc atg gga agc cat cgc aca gac acc ctt tca cgt gtc ttt gtc ggt				979
Cys Met Gly Ser His Arg Thr Asp Thr Leu Ser Arg Val Phe Val Gly	280	285	290	
tcg gaa aca atg gaa att atc cga aac tct cct gta ccg acc atc att				1027
Ser Glu Thr Met Glu Ile Ile Arg Asn Ser Pro Val Pro Thr Ile Ile	295	300	305	
tat ccc ggt ctt taggctctcc aacagcagag gac				1062
Tyr Pro Gly Leu				
310				

<210> 294

<211> 313

<212> FRT

<213> *Corynebacterium glutamicum*

<400> 294

Met Lys Gln Pro Leu Arg Val Leu Ile Ser Cys Arg Pro Glu Glu Asn

1

5

10

15

Ser Gly Gly Lys Arg Ser Glu Gln Asn Asp Ala Val Phe Glu Phe Ala

20

25

30

Ala Trp Leu Ala Arg Thr Ser Asp Ile Asn Val Arg Gly Ile Thr Thr

35

40

45

Phe Ile Arg Pro Trp Pro Ser Ser Ser Ile Ser Lys Leu Gly Gly Lys

50

55

60

Tyr His Lys Trp Tyr Lys Asn Leu Asp Ser Tyr Tyr Arg Ser Arg Thr

65

70

75

80

Ile Lys Gly Leu Lys Glu Ala Gly Val Glu Lys Ser Gln Trp Asp Asp

85

90

95

Asp Val Ser Val Phe Val Asp Gly Pro Ser Glu Ser Thr Leu Leu Thr

100

105

110

His Ala Ala Glu Glu Phe Glu Ala Asp Leu Ile Leu Leu Gly Ser Asp

115

120

125

Ala Thr Ala Pro Lys Gly Arg Phe Leu Ala Ser Ser Thr Ala Asp Ala

130

135

140

Leu Leu His Ser Ser Pro Val Pro Leu Gly Leu Val Pro Arg Gly Val

145

150

155

160

Lys Leu Ser Lys Lys Gly Val Thr Arg Val Asn Tyr Ala Phe Thr Asn

165

170

175

Glu Ser Asp Asp Phe Glu Gln Gly Leu Arg Ser Ser Ala Glu Leu Ala

180

185

190

Thr Asn Trp Asn Val Pro Leu Arg Ile Leu Ala Phe Ser Pro Thr Gly

195

200

205

Ile Thr Ser Ala Pro Thr Ser Arg Ser Leu Asp Ile Ser Thr Glu Leu

210

215

220

Ser Ser Glu Trp Arg Glu Leu Thr Leu Ala Met Leu Asp Arg Ala Arg

225

230

235

240

Asp Gly Val Leu Thr Asp His Pro Asn Leu Ser Val Ser Ser Glu Thr

245

250

255

Gly Ser Gly Trp Gly Trp Ser Gly Ala Ile Asp Ala Leu Arg Trp Lys

260

265

270

Lys Gly Asp Leu Leu Cys Met Gly Ser His Arg Thr Asp Thr Leu Ser

275

280

285

Arg Val Phe Val Gly Ser Glu Thr Met Glu Ile Ile Arg Asn Ser Pro
 290 295 300

Val Pro Thr Ile Ile Tyr Pro Gly Leu
 305 310

<210> 295

<211> 914

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(891)

<223> FRXA00555

<400> 295

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 1 5 10 15

gca tgg cta gct cgt act tca gac atc aat gtt cgt gga atc aca act 96
 Ala Trp Leu Ala Arg Thr Ser Asp Ile Asn Val Arg Gly Ile Thr Thr
 20 25 30

ttc ata cgc cct tgg cgc tct tcc tcc atc agt aag ctc gga gga aaa 144
 Phe Ile Arg Pro Trp Pro Ser Ser Ser Ile Ser Lys Leu Gly Gly Lys
 35 40 45

tat cat aag tgg tat aag aat tta gat tct tac tac cgc agt cgc acg 192
 Tyr His Lys Trp Tyr Lys Asn Leu Asp Ser Tyr Arg Ser Arg Thr
 50 55 60

atc aag gga ctc aaa gag gcc gga gtt gag aag tcc caa tgg gac gat 240
 Ile Lys Gly Leu Lys Glu Ala Gly Val Glu Lys Ser Gln Trp Asp Asp
 65 70 75 80

gat gtt tca gtt ttt gta gat ggt cct tct gaa tcc acg ctg etc acc 288
 Asp Val Ser Val Phe Val Asp Gly Pro Ser Glu Ser Thr Leu Leu Thr
 85 90 95

cat gct gct gaa gaa ttc gaa gcg gac ctc att ctg ctt ggc tct gat 336
 His Ala Ala Glu Glu Phe Glu Ala Asp Leu Ile Leu Leu Gly Ser Asp
 100 105 110

gcg acc gca cca aaa ggc cgc ttt ctg gcc agc tcc acc gca gat gcc 384
 Ala Thr Ala Pro Lys Gly Arg Phe Leu Ala Ser Ser Thr Ala Asp Ala
 115 120 125

ctc ctt cac tcc tcg ccc gtc cca cta gga ctt gtg cgc cga ggg gtg 432
 Leu Leu His Ser Ser Pro Val Pro Leu Gly Leu Val Pro Arg Gly Val
 130 135 140

aag ctt tcc aaa aag ggt gtc acc cgc gtc aac tac gct ttc acc aat 480
 Lys Leu Ser Lys Lys Gly Val Thr Arg Val Asn Tyr Ala Phe Thr Asn
 145 150 155 160

gaa agc gat gac ttt gag caa ggt tta cgc tct tcc gcg gag etc gcc 528
 Glu Ser Asp Asp Phe Glu Gln Gly Leu Arg Ser Ser Ala Glu Leu Ala

	165	170	175	
	acc aat tgg aac gtt cct ctt cgg atc ctt gct ttt tca ccc aca ggc			576
	Thr Asn Trp Asn Val Pro Leu Arg Ile Leu Ala Phe Ser Pro Thr Gly			
	180	185	190	
	att act tcc gca cca acg tcg cgg agc ttg gat att tcc act gag ctt			624
	Ile Thr Ser Ala Pro Thr Ser Arg Ser Leu Asp Ile Ser Thr Glu Leu			
	195	200	205	
	tcc tcc gag tgg cgt gaa cta acg ctc gcc atg ctt gat cga gcc cgt			672
	Ser Ser Glu Trp Arg Glu Leu Thr Leu Ala Met Leu Asp Arg Ala Arg			
	210	215	220	
	gat ggc gtc ctc aca gac cac cca aac ttg agc gtg agc agt gaa acc			720
	Asp Gly Val Leu Thr Asp His Pro Asn Leu Ser Val Ser Ser Glu Thr			
	225	230	235	240
	ggt tct ggc tgg ggt tgg agc ggt gca att gat gct ttg cga tgg aag			768
	Gly Ser Gly Trp Gly Trp Ser Gly Ala Ile Asp Ala Leu Arg Trp Lys			
	245	250	255	
	aaa ggt gac ctg ctg tgc atg gga agc cat cgc aca gac acc ctt tca			816
	Lys Gly Asp Leu Leu Cys Met Gly Ser His Arg Thr Thr Leu Ser			
	260	265	270	
	cgt gtc ttt gtc ggt tcg gaa aca atg gaa att atc cga aac tct cct			864
	Arg Val Phe Val Gly Ser Glu Thr Met Glu Ile Ile Arg Asn Ser Pro			
	275	280	285	
	gta cgg acc atc att tat ccc ggt ctt tagctctccc aacagcagag			911
	Val Pro Thr Ile Ile Tyr Pro Gly Leu			
	290	295		
	gac			914
	<210> 296			
	<211> 297			
	<212> PRT			
	<213> Corynebacterium glutamicum			
	<400> 296			
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	1 5 10 15			
	Ala Trp Leu Ala Arg Thr Ser Asp Ile Asn Val Arg Gly Ile Thr Thr			
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	Phe Ile Arg Pro Trp Pro Ser Ser Ile Ser Lys Leu Gly Gly Lys			
	35 40 45			
	Tyr His Lys Trp Tyr Lys Asn Leu Asp Ser Tyr Tyr Arg Ser Arg Thr			
	50 55 60			
	Ile Lys Gly Leu Lys Glu Ala Gly Val Glu Lys Ser Gln Trp Asp Asp			
	65 70 75 80			
	Asp Val Ser Val Phe Val Asp Gly Pro Ser Glu Ser Thr Leu Leu Thr			
	85 90 95			


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His Ala Ala Glu Glu Phe Glu Ala Asp Leu Ile Leu Leu Gly Ser Asp
      100                      105                      110

Ala Thr Ala Pro Lys Gly Arg Phe Leu Ala Ser Ser Thr Ala Asp Ala
      115                      120                      125

Leu Leu His Ser Ser Pro Val Pro Leu Gly Leu Val Pro Arg Gly Val
      130                      135                      140

Lys Leu Ser Lys Lys Gly Val Thr Arg Val Asn Tyr Ala Phe Thr Asn
      145                      150                      155                      160

Glu Ser Asp Asp Phe Glu Gln Gly Leu Arg Ser Ser Ala Glu Leu Ala
      165                      170                      175

Thr Asn Trp Asn Val Pro Leu Arg Ile Leu Ala Phe Ser Pro Thr Gly
      180                      185                      190

Ile Thr Ser Ala Pro Thr Ser Arg Ser Leu Asp Ile Ser Thr Glu Leu
      195                      200                      205

Ser Ser Glu Trp Arg Glu Leu Thr Leu Ala Met Leu Asp Arg Ala Arg
      210                      215                      220

Asp Gly Val Leu Thr Asp His Pro Asn Leu Ser Val Ser Ser Glu Thr
      225                      230                      235

Gly Ser Gly Trp Gly Trp Ser Gly Ala Ile Asp Ala Leu Arg Trp Lys
      245                      250                      255

Lys Gly Asp Leu Leu Cys Met Gly Ser His Arg Thr Asp Thr Leu Ser
      260                      265                      270

Arg Val Phe Val Gly Ser Glu Thr Met Glu Ile Ile Arg Asn Ser Pro
      275                      280                      285

Val Pro Thr Ile Ile Tyr Pro Gly Leu
      290                      295

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<210> 297

<211> 498

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(475)

<223> RXN00560

<400> 297

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catatggaca ctttaacggt tcgtactagg ctgatgcttc atg agg att gat ccg 115
              Met Arg Ile Asp Pro
              1                      5

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ctg gaa acc cgg caa gcc gta ttg gcc gtc aaa gac tgg att gaa ggg 163
Leu Glu Thr Arg Gln Ala Val Leu Ala Val Lys Asp Trp Ile Gly
      10                      15                      20

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gag gga gac gtc aaa aag cct ggt cgt gcg gca ctt gcc gcc gca act 211
 Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala Leu Ala Ala Thr
 25 30 35

cgc ctg agc gtc cga ctg ctc gcg caa cac gcg ccg gga aac agc gtg 259
 Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala Pro Gly Asn Ser Val
 40 45 50

gag gtg cgg gta ccc cca ttt gtt gcg gtg caa tgc ata gag ggg cca 307
 Glu Val Arg Val Pro Pro Phe Val Ala Val Gln Cys Ile Glu Gly Pro
 55 60 65

aaa cat aca cgc gcc aca cca ccc aac gtg gtg gag acc gac gcc aag 355
 Lys His Thr Arg Gly Thr Pro Pro Asn Val Val Glu Thr Asp Ala Lys
 70 75 80 85

acc tgg tta cgc tta gca cct ggg caa acc aca ttt gat gca gaa ttt 403
 Thr Trp Leu Arg Leu Ala Pro Gly Gln Thr Thr Phe Asp Ala Glu Phe
 90 95 100

gaa agc gga aaa att agc gca tca ggt acc cga gcc aaa gag att gcg 451
 Glu Ser Gly Lys Ile Ser Ala Ser Gly Thr Arg Ala Lys Glu Ile Ala
 105 110 115

gag tgg tta cca gtg gtc aaa ctt tagatttcct aatgctcatt agt 498
 Asp Trp Leu Pro Val Val Lys Leu
 120 125

<210> 298
 <211> 125
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 298
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Asp Trp Ile Glu Gly Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala
 20 25 30

Leu Ala Ala Ala Thr Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala
 35 40 45

Pro Gly Asn Ser Val Glu Val Arg Val Pro Pro Phe Val Ala Val Gln
 50 55 60

Cys Ile Glu Gly Pro Lys His Thr Arg Gly Thr Pro Pro Asn Val Val
 65 70 75 80

Glu Thr Asp Ala Lys Thr Trp Leu Arg Leu Ala Pro Gly Gln Thr Thr
 85 90 95

Phe Asp Ala Glu Phe Glu Ser Gly Lys Ile Ser Ala Ser Gly Thr Arg
 100 105 110

Ala Lys Glu Ile Ala Asp Trp Leu Pro Val Val Lys Leu
 115 120 125

<210> 299

<211> 337
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(337)
 <223> FRXA00560

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                                     Met Arg Ile Asp Pro
                                     1           5

ctg gaa acc cgg caa gcc gta ttg gcc gtc aaa gac tgg att gaa ggg 163
Leu Glu Thr Arg Gln Ala Val Leu Ala Val Lys Asp Trp Ile Glu Gly
                                     10           15           20

gag gga gac gtc aaa aag cct ggt cgt gcg gca ctt gcc gcc gca act 211
Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala Leu Ala Ala Thr
                                     25           30           35

cgc ctg agc gtc cga ctg ctc gcg caa cac gcg ccg gga aac agc gtg 259
Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala Pro Gly Asn Ser Val
                                     40           45           50

gag gtg cgg gta ccc cca ttt gtt gcg gtg caa tgc ata gag ggg cca 307
Glu Val Arg Val Pro Pro Phe Val Ala Val Gln Cys Ile Glu Gly Pro
                                     55           60           65

aaa cat aca cgc gcc aca cca ccc aac gtg 337
Lys His Thr Arg Gly Thr Pro Pro Asn Val
                                     70           75

<210> 300
<211> 79
<212> PRT
<213> Corynebacterium glutamicum

<400> 300
Met Arg Ile Asp Pro Leu Glu Thr Arg Gln Ala Val Leu Ala Val Lys
 1           5           10           15

Asp Trp Ile Glu Gly Glu Gly Asp Val Lys Lys Pro Gly Arg Ala Ala
 20           25           30

Leu Ala Ala Ala Thr Arg Leu Ser Val Arg Leu Leu Ala Gln His Ala
 35           40           45

Pro Gly Asn Ser Val Glu Val Arg Val Pro Pro Phe Val Ala Val Gln
 50           55           60

Cys Ile Glu Gly Pro Lys His Thr Arg Gly Thr Pro Pro Asn Val
 65           70           75

<210> 301
<211> 1002

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<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(979)

<223> RXN00574

<400> 301

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tcaagcccg tgattcagtt cgatttgtgc aggtgaagaa atg agc ttc aaa gta 115
                                     Met Ser Phe Lys Val
                                     1 5
att tcc act ggc ccc caa gcc atc ttc caa gac cga ggt cgc ttc ggt 163
Ile Ser Thr Gly Pro Gln Ala Ile Phe Gln Asp Arg Gly Arg Phe Gly
                                     10 15 20
ttt gcc agc gct ggt gtt gga acc tca gga tcc ttt gat cgt tta tcc 211
Phe Ala Ser Ala Gly Val Gly Thr Ser Gly Ser Phe Asp Arg Leu Ser
                                     25 30 35
gct gct cgc gcg aat cac gct tta ggt aat gat ccc aat gca acc gtg 259
Ala Ala Arg Ala Asn His Ala Leu Gly Asn Asp Pro Asn Ala Thr Val
                                     40 45 50
gta gag att ctg ctc ggt ggc ttt gag gtg gag gcg ttg cac acc acc 307
Val Glu Ile Leu Leu Gly Gly Phe Glu Val Glu Ala Leu His Thr Thr
                                     55 60 65
tcg atc gtg ttc acg gga act gaa gct gaa gtg atg gtt cga acg gct 355
Ser Ile Val Phe Thr Gly Thr Glu Ala Glu Val Met Val Arg Thr Ala
                                     70 75 80 85
ggg gga caa tcc aaa aat gcc acc acc aac acc atc atc gat gtt gca 403
Gly Gly Gln Ser Lys Asn Ala Thr Thr Asn Thr Ile Ile Asp Val Ala
                                     90 95 100
gct ggt gaa cgt atc cgc gtc gag ccc gca acc tat ggc atg cgt gcc 451
Ala Gly Glu Arg Ile Arg Val Glu Pro Ala Thr Tyr Gly Met Arg Ala
                                     105 110 115
tac ttt gct gct cgc ggt gga ttt gca gta aaa aaa act ttg gga tct 499
Tyr Phe Ala Ala Arg Gly Gly Phe Ala Val Lys Lys Thr Leu Gly Ser
                                     120 125 130
get tca acc gat ctg atc tcc cac atg ggc cct tgc ccg atc gag ccc 547
Ala Ser Thr Asp Leu Ile Ser His Met Gly Pro Cys Pro Ile Glu Pro
                                     135 140 145
ggg gat gtc att gac gta gca aca gac att gca gat tct cag tgg tgg 595
Gly Asp Val Ile Asp Val Ala Thr Asp Ile Ala Asp Ser Gln Trp Trp
                                     150 155 160 165
cca aaa ctt cgg caa ctg ccc acc tta tgg aaa cgc atg cca aca gaa 643
Pro Lys Leu Arg Gln Leu Pro Thr Leu Trp Lys Arg Met Pro Thr Glu
                                     170 175 180
acg ctt acc gtc atc cga ggt cca cgt gac aaa tgg ttc acg caa gaa 691
Thr Leu Thr Val Ile Arg Gly Pro Arg Asp Lys Trp Phe Thr Gln Glu

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	185	190	195	
tcc ctc aac aac ttt ttt act cag gtg ttt acg gtg agc aat gac tcc				739
Ser Leu Asn Asn Phe Phe Thr Gln Val Phe Thr Val Ser Asn Asp Ser				
200	205	210		
aac cgg att ggt ttg cgc atg cac tca agc gag ccg atc caa cat cgt				787
Asn Arg Ile Gly Leu Arg Met His Ser Ser Glu Pro Ile Gln His Arg				
215	220	225		
gtg gaa ggc gag ctg aaa agt gaa gga atg gtc cgg ggg tcc atc cag				835
Val Glu Gly Glu Leu Lys Ser Glu Gly Met Val Arg Gly Ser Ile Gln				
230	235	240	245	
att ccg cct ggt gga aac ccc gtg gtg ttt ggt ccc gat cat cct gtg				883
Ile Pro Pro Gly Gly Asn Pro Val Val Phe Gly Pro Asp His Pro Val				
250	255	260		
acc ggt ggc tat cca gta ata gca gta ctt aca tca agg tcg tgt gat				931
Thr Gly Gly Tyr Pro Val Ile Ala Val Leu Thr Ser Arg Ser Cys Asp				
265	270	275		
cgt tcg gcc cag ctg ttg ccg ggc gat aaa gtc aga ttt aaa ttg ctt				979
Arg Ser Ala Gln Leu Leu Pro Gly Asp Lys Val Arg Phe Lys Leu Leu				
280	285	290		
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<213> Corynebacterium glutamicum				
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1 5 10 15				
Arg Gly Arg Phe Gly Phe Ala Ser Ala Gly Val Gly Thr Ser Gly Ser				
20 25 30				
Phe Asp Arg Leu Ser Ala Ala Arg Ala Asn His Ala Leu Gly Asn Asp				
35 40 45				
Pro Asn Ala Thr Val Val Glu Ile Leu Leu Gly Gly Phe Glu Val Glu				
50 55 60				
Ala Leu His Thr Thr Ser Ile Val Phe Thr Gly Thr Glu Ala Glu Val				
65 70 75 80				
Met Val Arg Thr Ala Gly Gly Gln Ser Lys Asn Ala Thr Thr Asn Thr				
85 90 95				
Ile Ile Asp Val Ala Ala Gly Glu Arg Ile Arg Val Glu Pro Ala Thr				
100 105 110				
Tyr Gly Met Arg Ala Tyr Phe Ala Ala Arg Gly Gly Phe Ala Val Lys				
115 120 125				
Lys Thr Leu Gly Ser Ala Ser Thr Asp Leu Ile Ser His Met Gly Pro				
130 135 140				

Cys Pro Ile Glu Pro Gly Asp Val Ile Asp Val Ala Thr Asp Ile Ala
145 150 155 160

Asp Ser Gln Trp Trp Pro Lys Leu Arg Gln Leu Pro Thr Leu Trp Lys
165 170 175

Arg Met Pro Thr Glu Thr Leu Thr Val Ile Arg Gly Pro Arg Asp Lys
180 185 190

Trp Phe Thr Gln Glu Ser Leu Asn Asn Phe Phe Thr Gln Val Phe Thr
195 200 205

Val Ser Asn Asp Ser Asn Arg Ile Gly Leu Arg Met His Ser Ser Glu
210 215 220

Pro Ile Gln His Arg Val Glu Gly Glu Leu Lys Ser Glu Gly Met Val
225 230 235 240

Arg Gly Ser Ile Gln Ile Pro Pro Gly Gly Asn Pro Val Val Phe Gly
245 250 255

Pro Asp His Pro Val Thr Gly Gly Tyr Pro Val Ile Ala Val Leu Thr
260 265 270

Ser Arg Ser Cys Asp Arg Ser Ala Gln Leu Leu Pro Gly Asp Lys Val
275 280 285

Arg Phe Lys Leu Leu
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<210> 303

<211> 1002

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(979)

<223> FRXA00574

<400> 303

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tcaagcccg tgattcagtt cgatttgtgc aggtgaagaa atg agc ttc aaa gta 115
Met Ser Phe Lys Val
1 5

att tcc act ggc ccc caa gcc atc ttc caa gac cga ggt cgc ttc ggt 163
Ile Ser Thr Gly Pro Gln Ala Ile Phe Gln Asp Arg Gly Arg Phe Gly
10 15 20

ttt gcc agc gct ggt gtt gga acc tca gga tcc ttt gat cgt tta tcc 211
Phe Ala Ser Ala Gly Val Gly Thr Ser Gly Ser Phe Asp Arg Leu Ser
25 30 35

gct gct cgc gcg aat cac gct tta ggt aat gat ccc aat gca acc gtg 259
Ala Ala Arg Ala Asn His Ala Leu Gly Asn Asp Pro Asn Ala Thr Val
40 45 50

gta gag att ctg ctc ggt ggc ttt gag gtg gag gcg ttg cac acc acc	307
Val Glu Ile Leu Leu Gly Gly Phe Glu Val Glu Ala Leu His Thr Thr	
55 60 65	
tcg atc gtg ttc acg gga act gaa gct gaa gtg atg gtt cga acg gct	355
Ser Ile Val Phe Thr Gly Thr Glu Ala Glu Val Met Val Arg Thr Thr	
70 75 80 85	
ggt gga caa tcc aaa aat gcc acc acc aac acc atc atc gat gtt gca	403
Gly Gly Gln Ser Lys Asn Ala Thr Thr Asn Thr Ile Ile Asp Val Ala	
90 95 100	
gct ggt gaa cgt atc cgc gtc gag ccc gca acc tat ggc atg cgt gcc	451
Ala Gly Glu Arg Ile Arg Val Glu Pro Ala Thr Tyr Gly Met Arg Ala	
105 110 115	
tac ttt gct gct cgc ggt gga ttt gca gta aaa aaa act ttg gga tct	499
Tyr Phe Ala Ala Arg Gly Gly Phe Ala Val Lys Lys Thr Leu Gly Ser	
120 125 130	
gct tca acc gat ctg atc tcc cac atg ggc cct tgc ccg atc gag ccc	547
Ala Ser Thr Asp Leu Ile Ser His Met Gly Pro Cys Pro Ile Glu Pro	
135 140 145	
ggg gat gtc att gac gta gca aca gac att gca gat tct cag tgg tgg	595
Gly Asp Val Ile Asp Val Ala Thr Asp Ile Ala Asp Ser Gln Trp Trp	
150 155 160 165	
cca aaa ctt cgg caa ctg ccc acc tta tgg aaa cgc atg cca aca gaa	643
Pro Lys Leu Arg Gln Leu Pro Thr Leu Trp Lys Arg Met Pro Thr Glu	
170 175 180	
acg ctt acc gtc atc cga ggt cca cgt gac aaa tgg ttc acg caa gaa	691
Thr Leu Thr Val Ile Arg Gly Pro Arg Asp Lys Trp Phe Thr Gln Glu	
185 190 195	
tcc ctc aac aac ttt ttt act cag gtg ttt acg gtg agc aat gac tcc	739
Ser Leu Asn Asn Phe Phe Thr Gln Val Phe Thr Val Ser Asn Asp Ser	
200 205 210	
aac cgg att ggt ttg cgc atg cac tca agc gag ccg atc caa cat cgt	787
Asn Arg Ile Gly Leu Arg Met His Ser Ser Glu Pro Ile Gln His Arg	
215 220 225	
gtg gaa ggc gag ctg aaa agt gaa gga atg gtc cgg ggg tcc atc cag	835
Val Glu Gly Glu Leu Lys Ser Glu Gly Met Val Arg Gly Ser Ile Gln	
230 235 240 245	
att ccg cct ggt gga aac ccc gtg gtg ttt ggt ccc gat cat cct gtg	883
Ile Pro Pro Gly Gly Asn Pro Val Val Phe Gly Pro Asp His Pro Val	
250 255 260	
acc ggt ggc tat cca gta ata gca gta ctt aca tca agg tcg tgt gat	931
Thr Gly Gly Tyr Pro Val Ile Ala Val Leu Thr Ser Arg Ser Cys Asp	
265 270 275	
cgt tcg gcc cag ctg ttg cgg ggc gat aaa gtc aga ttt aaa ttg ctt	979
Arg Ser Ala Gln Leu Leu Pro Gly Asp Lys Val Arg Phe Lys Leu Leu	
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<210> 304

<211> 293

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 304

Met Ser Phe Lys Val Ile Ser Thr Gly Pro Gln Ala Ile Phe Gln Asp
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 20 25 30

Phe Asp Arg Leu Ser Ala Ala Arg Ala Asn His Ala Leu Gly Asn Asp
 35 40 45

Pro Asn Ala Thr Val Val Glu Ile Leu Leu Gly Gly Phe Glu Val Glu
 50 55 60

Ala Leu His Thr Thr Ser Ile Val Phe Thr Gly Thr Glu Ala Glu Val
 65 70 75 80

Met Val Arg Thr Ala Gly Gly Gln Ser Lys Asn Ala Thr Thr Asn Thr
 85 90 95

Ile Ile Asp Val Ala Ala Gly Glu Arg Ile Arg Val Glu Pro Ala Thr
 100 105 110

Tyr Gly Met Arg Ala Tyr Phe Ala Ala Arg Gly Gly Phe Ala Val Lys
 115 120 125

Lys Thr Leu Gly Ser Ala Ser Thr Asp Leu Ile Ser His Met Gly Pro
 130 135 140

Cys Pro Ile Glu Pro Gly Asp Val Ile Asp Val Ala Thr Asp Ile Ala
 145 150 155 160

Asp Ser Gln Trp Trp Pro Lys Leu Arg Gln Leu Pro Thr Leu Trp Lys
 165 170 175

Arg Met Pro Thr Glu Thr Leu Thr Val Ile Arg Gly Pro Arg Asp Lys
 180 185 190

Trp Phe Thr Gln Glu Ser Leu Asn Asn Phe Phe Thr Gln Val Phe Thr
 195 200 205

Val Ser Asn Asp Ser Asn Arg Ile Gly Leu Arg Met His Ser Ser Glu
 210 215 220

Pro Ile Gln His Arg Val Glu Gly Glu Leu Lys Ser Glu Gly Met Val
 225 230 235 240

Arg Gly Ser Ile Gln Ile Pro Pro Gly Gly Asn Pro Val Val Phe Gly
 245 250 255

Pro Asp His Pro Val Thr Gly Gly Tyr Pro Val Ile Ala Val Leu Thr
 260 265 270

Ser Arg Ser Cys Asp Arg Ser Ala Gln Leu Leu Pro Gly Asp Lys Val
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Arg Phe Lys Leu Leu
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<210> 305
<211> 573
<212> DNA
<213> *Corynebacterium glutamicum*

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<222> (101)..(550)
<223> RXN00589

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Met Thr Thr Leu Ser
1 5
cgt aag ttc ttc gtt tct gct acc aca gcc ctg gcg gca gtc gca ctg 163
Arg Lys Phe Phe Val Ser Ala Thr Thr Ala Leu Ala Val Ala Leu
10 15 20
gtt gcg tgt tcc cct aat gag att gat tct gaa ctg aag gtg cca acg 211
Val Ala Cys Ser Pro Asn Glu Ile Asp Ser Glu Leu Lys Val Pro Thr
25 30 35
gca act ggc gtt tct tta cct tcg aag aac gtt tcc gcg acc tca act 259
Ala Thr Gly Val Ser Leu Pro Ser Lys Asn Val Ser Ala Thr Ser Thr
40 45 50
gct act aca gat gag gat gcg cct ggc tac att gat tgc gta gcc gca 307
Ala Thr Thr Asp Glu Asp Ala Pro Gly Tyr Ile Asp Cys Val Ala Ala
55 60 65
cca act cag caa cct gct gaa atc tca cta aac tgt gca atg gat att 355
Pro Thr Gln Gln Pro Ala Glu Ile Ser Leu Asn Cys Ala Met Asp Ile
70 75 80 85
gat cgg ctc acg gat att tct tgg agc gaa tgg gat act gat tcc gca 403
Asp Arg Leu Thr Asp Ile Ser Trp Ser Glu Trp Asp Thr Asp Ser Ala
90 95 100
act gga acc ggt acc cgc atc gta acc gct gca aat ggt caa gag acc 451
Thr Gly Thr Gly Thr Arg Ile Val Thr Ala Ala Asn Gly Gln Glu Thr
105 110 115
gaa acc gaa gat att gag gtg aag ctt tcc ttc ccc acc gag tct tcc 499
Glu Thr Glu Asp Ile Glu Val Lys Leu Ser Phe Pro Thr Glu Ser Ser
120 125 130
caa ggc cta gtg ttc act cag gtc acc gtc gat gga cag gtt ctc ttc 547
Gln Gly Leu Val Phe Thr Gln Val Thr Val Asp Gly Gln Val Leu Phe
135 140 145
ctc taatcctcca taattagaga gcg 573
Leu
150

<210> 306

<211> 150

<212> PRT

<213> Corynebacterium glutamicum

<400> 306

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35 40 45Ser Ala Thr Ser Thr Ala Thr Thr Asp Glu Asp Ala Pro Gly Tyr Ile
50 55 60Asp Cys Val Ala Ala Pro Thr Gln Gln Pro Ala Glu Ile Ser Leu Asn
65 70 75 80Cys Ala Met Asp Ile Asp Arg Leu Thr Asp Ile Ser Trp Ser Glu Trp
85 90 95Asp Thr Asp Ser Ala Thr Gly Thr Gly Thr Arg Ile Val Thr Ala Ala
100 105 110Asn Gly Gln Glu Thr Glu Thr Glu Asp Ile Glu Val Lys Leu Ser Phe
115 120 125Pro Thr Glu Ser Ser Gln Gly Leu Val Phe Thr Gln Val Thr Val Asp
130 135 140Gly Gln Val Leu Phe Leu
145 150

<210> 307

<211> 463

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(463)

<223> FRXA00589

<400> 307

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tccgcggcaa aaactaacca aggatttaaa agtcttcaaa atg aca act ctt tca 115
Met Thr Thr Leu Ser
1 5cgt aag ttc ttc gtt tct gct acc aca gcc ctg gcg gca gtc gca ctg 163
Arg Lys Phe Phe Val Ser Ala Thr Thr Ala Leu Ala Ala Val Ala Leu
10 15 20

gtt gcg tgt tcc cct aat gag att gat tct gaa ctg aag gtg cca acg 211

Val Ala Cys Ser Pro Asn Glu Ile Asp Ser Glu Leu Lys Val Pro Thr
 25 30 35

gca act ggc gtt tct tta cct tcg aag aac gtt tcc gcg acc tca act 259
 Ala Thr Gly Val Ser Leu Pro Ser Lys Asn Val Ser Ala Thr Ser Thr
 40 45 50

gct act aca gat gag gat gcg cct ggc tac att gat tgc gta gcc gca 307
 Ala Thr Thr Asp Glu Asp Ala Pro Gly Tyr Ile Asp Cys Val Ala Ala
 55 60 65

cca act cag caa cct gct gaa atc tca cta aac tgt gca atg gat att 355
 Pro Thr Gln Gln Pro Ala Glu Ile Ser Leu Asn Cys Ala Met Asp Ile
 70 75 80 85

gat cgg ctc acg gat att tct tgg agc gaa tgg gat act gat tcc gca 403
 Asp Arg Leu Thr Asp Ile Ser Trp Ser Glu Trp Asp Thr Asp Ser Ala
 90 95 100

act gga acc ggt acc cgc atc gta acc gct gca aat ggt caa gag acc 451
 Thr Gly Thr Gly Thr Arg Ile Val Thr Ala Ala Asn Gly Gln Glu Thr
 105 110 115

gaa acc gaa gat 463
 Glu Thr Glu Asp
 120

<210> 308
 <211> 121
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 308
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 20 25 30

Leu Lys Val Pro Thr Ala Thr Gly Val Ser Leu Pro Ser Lys Asn Val
 35 40 45

Ser Ala Thr Ser Thr Ala Thr Thr Asp Glu Asp Ala Pro Gly Tyr Ile
 50 55 60

Asp Cys Val Ala Ala Pro Thr Gln Gln Pro Ala Glu Ile Ser Leu Asn
 65 70 75 80

Cys Ala Met Asp Ile Asp Arg Leu Thr Asp Ile Ser Trp Ser Glu Trp
 85 90 95

Asp Thr Asp Ser Ala Thr Gly Thr Gly Thr Arg Ile Val Thr Ala Ala
 100 105 110

Asn Gly Gln Glu Thr Glu Thr Glu Asp
 115 120

<210> 309
 <211> 468

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(445)

<223> RXN00616

<400> 309

aaccgcaacc tcggcgcaatt ggagtgaaaa ttctcatctt catttcatct tgggtgctaa 60

caatggaata	cagattgagt	tgatcaaagg	agaaccccca	atg	aaa	tca	ctc	ccc	115
				Met	Lys	Ser	Leu	Pro	
				1				5	

cgt	ttc	gcc	cca	ctg	att	acg	att	ctg	gct	ctg	ctc	gta	ctc	gtt	gcc	163
Arg	Phe	Ala	Pro	Leu	Ile	Thr	Ile	Leu	Ala	Leu	Leu	Val	Leu	Val	Ala	
				10				15						20		

atc	gga	gga	tct	gca	ctg	gca	aat	aat	cgt	gct	acc	cct	aat	gtg	gaa	211
Ile	Gly	Gly	Ser	Ala	Leu	Ala	Asn	Asn	Arg	Ala	Thr	Pro	Asn	Val	Glu	
			25					30					35			

agt	gaa	ccc	gcc	acg	gtc	aac	cag	cgt	tcc	act	ccc	aca	act	tcc	gcg	259
Ser	Glu	Pro	Ala	Thr	Val	Asn	Gln	Arg	Ser	Thr	Pro	Thr	Thr	Ser	Ala	
		40					45					50				

tat	gag	ccc	cct	gct	aca	gaa	tct	ccg	gaa	gaa	cca	acc	aca	caa	att	307
Tyr	Glu	Pro	Pro	Ala	Thr	Glu	Ser	Pro	Glu	Glu	Pro	Thr	Thr	Gln	Ile	
		55				60					65					

caa	gaa	tcc	cca	gta	caa	ccc	cca	gtt	cct	gcc	ccc	gct	caa	att	cct	355
Gln	Glu	Ser	Pro	Val	Gln	Pro	Pro	Val	Pro	Ala	Pro	Ala	Gln	Ile	Pro	
		70			75					80				85		

caa	gcc	cca	caa	gtt	cca	ctc	aat	tat	cag	tac	tat	gac	gat	gac	tg	403
Gln	Ala	Pro	Gln	Val	Pro	Leu	Asn	Tyr	Gln	Tyr	Tyr	Asp	Asp	Asp	Trp	
			90						95					100		

gac	gac	gac	gat	gat	gac	ttc	gac	gac	gac	tg	gac	gac	gac			445
Asp	Asp	Asp	Asp	Asp	Asp	Phe	Asp	Asp	Asp	Trp	Asp	Asp	Asp			
			105				110						115			

taactaacc	ctgaggca	ctt														468
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<210> 310

<211> 115

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 310

Met	Lys	Ser	Leu	Pro	Arg	Phe	Ala	Pro	Leu	Ile	Thr	Ile	Leu	Ala	Leu
1				5					10					15	

Leu	Val	Leu	Val	Ala	Ile	Gly	Gly	Ser	Ala	Leu	Ala	Asn	Asn	Arg	Ala
			20					25					30		

Thr	Pro	Asn	Val	Glu	Ser	Glu	Pro	Ala	Thr	Val	Asn	Gln	Arg	Ser	Thr
			35				40					45			

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Pro Thr Thr Ser Ala Tyr Glu Pro Pro Ala Thr Glu Ser Pro Glu Glu
 50                      55                      60

Pro Thr Thr Gln Ile Gln Glu Ser Pro Val Gln Pro Pro Val Pro Ala
 65                      70                      75                      80

Pro Ala Gln Ile Pro Gln Ala Pro Gln Val Pro Leu Asn Tyr Gln Tyr
 85                      90                      95

Tyr Asp Asp Asp Trp Asp Asp Asp Asp Asp Asp Phe Asp Asp Asp Trp
100                      105                      110

Asp Asp Asp
115

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<210> 311
 <211> 468
 <212> DNA
 <213> *Corynebacterium glutamicum*

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<220>
<221> CDS
<222> (101)..(445)
<223> FRXA00616

<400> 311
aacgcgaacc tcgcgcactt ggagtgaaaa ttctcatctt catttcatct tggtgccata 60

caatggaata cagattgagt tgatcaaagg agaaccacca atg aaa tca ctc ccc 115
                                     Met Lys Ser Leu Pro
                                     1                      5

cgt ttc gcc cca ctg att acg att ctg gct ctg ctc gta ctc gtt gcc 163
Arg Phe Ala Pro Leu Ile Thr Ile Leu Ala Leu Leu Val Leu Val Ala
                      10                      15                      20

atc gga gga tct gca ctg gca aat aat cgt gct acc cct aat gtg gaa 211
Ile Gly Gly Ser Ala Leu Ala Asn Asn Arg Ala Thr Pro Asn Val Glu
                      25                      30                      35

agt gaa ccc gcc acg gtc aac cag cgt tcc act ccc aca act tcc gcg 259
Ser Glu Pro Ala Thr Val Asn Gln Arg Ser Thr Pro Thr Thr Ser Ala
                      40                      45                      50

tat gag ccc cct gct aca gaa tct ccg gaa gaa cca acc aca caa att 307
Tyr Glu Pro Pro Ala Thr Glu Ser Pro Glu Glu Pro Thr Thr Gln Ile
 55                      60                      65

caa gaa tcc cca gta caa ccc cca gtt cct gcc ccc gct caa att cct 355
Gln Glu Ser Pro Val Gln Pro Pro Val Pro Ala Pro Ala Gln Ile Pro
 70                      75                      80                      85

caa gcc cca caa gtt cca ctc aat tat cag tac tat gac gat gac tgg 403
Gln Ala Pro Gln Val Pro Leu Asn Tyr Gln Tyr Tyr Asp Asp Asp Trp
 90                      95                      100

gac gac gac gat gat gac ttc gac gac gac tgg gac gac gac 445
Asp Asp Asp Asp Asp Asp Phe Asp Asp Asp Trp Asp Asp Asp
105                      110                      115

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taactaaccc ctgaggcact ttc

468

<210> 312

<211> 115

<212> PRT

<213> Corynebacterium glutamicum

<400> 312

Met Lys Ser Leu Pro Arg Phe Ala Pro Leu Ile Thr Ile Leu Ala Leu
 1 5 10 15

Leu Val Leu Val Ala Ile Gly Gly Ser Ala Leu Ala Asn Asn Arg Ala
 20 25 30

Thr Pro Asn Val Glu Ser Glu Pro Ala Thr Val Asn Gln Arg Ser Thr
 35 40 45

Pro Thr Thr Ser Ala Tyr Glu Pro Pro Ala Thr Glu Ser Pro Glu Glu
 50 55 60

Pro Thr Thr Gln Ile Gln Glu Ser Pro Val Gln Pro Pro Val Pro Ala
 65 70 75 80

Pro Ala Gln Ile Pro Gln Ala Pro Gln Val Pro Leu Asn Tyr Gln Tyr
 85 90 95

Tyr Asp Asp Asp Trp Asp Asp Asp Asp Asp Phe Asp Asp Asp Trp
 100 105 110

Asp Asp Asp
 115

<210> 313

<211> 756

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(733)

<223> RXN00647

<400> 313

tgcatcttc ccacaatgac atgagcttat tgcaacatcg tgggtaaagt tgaatcgaga 60

agtcgagaaa taaccgaccg atgaaagagt tgagacgata atg ggc atc ttc gaa 115
 Met Gly Ile Phe Glu
 1 5

gcc atc cga gcc gca cgc gcg aag acc aaa gct gag atc aaa gca gcc 163
 Ala Ile Arg Ala Ala Arg Ala Lys Thr Lys Ala Glu Ile Lys Ala Ala
 10 15 20

gag gca aaa gta aaa act gag gcg aaa aac aaa gca aag cta gat ctc 211
 Glu Ala Lys Val Lys Thr Glu Ala Lys Asn Lys Ala Lys Leu Asp Leu
 25 30 35

aag cgc gag aag ctt ctt gtc cag cag gaa aag aat ctg ctc aag gtt 259
 Lys Arg Glu Lys Leu Leu Val Gln Gln Glu Lys Asn Leu Leu Lys Val

40	45	50	
gaa gaa aag ggc ctg aag aag cgc aac aag cat gag ctg aag atg gcc			307
Glu Glu Lys Gly Leu Lys Lys Arg Asn Lys His Glu Leu Lys Met Ala			
55	60	65	
aaa aat atc ctt gag caa aag cgc caa gga cgc cta aac aaa gac aag			355
Lys Asn Ile Leu Glu Gln Lys Arg Gln Gly Arg Leu Asn Lys Asp Lys			
70	75	80	85
gtg aag cgc tgg gct ggc acc gca cgt gtg ctc act cca cta ctg ctg			403
Val Lys Arg Trp Ala Gly Thr Ala Arg Val Leu Thr Pro Leu Leu Leu			
90	95	100	
cct att att tat cga ctc tcc acc gaa gca cgc gat cag gtt gtt aag			451
Pro Ile Ile Tyr Arg Leu Ser Thr Glu Ala Arg Asp Gln Val Val Lys			
105	110	115	
gga cgt gcc cgt cgt gca ggt gtc acc gcg gag cag ctt agc caa ttc			499
Gly Arg Ala Arg Arg Ala Gly Val Thr Ala Glu Leu Ser Gln Phe			
120	125	130	
gca ggt cac gca gca gcg ctg aag gct cgt att caa ggt gtt cgc gaa			547
Ala Gly His Ala Ala Ala Leu Lys Ala Arg Ile Gln Gly Val Arg Glu			
135	140	145	
acc gca aag aac tcc agc ctc cct gct ggc ttt gta cgc gat gtt gaa			595
Thr Ala Lys Asn Ser Ser Leu Pro Ala Gly Phe Val Arg Asp Val Glu			
150	155	160	165
gag cgt ctc aat gag ctc gag gct gct gcg aat aac tct gag ttc atg			643
Glu Arg Leu Asn Glu Leu Glu Ala Ala Asn Asn Ser Glu Phe Met			
170	175	180	
tct cca cag cag agg aac cgt gcg cac cag tgc atc agt cgt gat ctg			691
Ser Pro Gln Gln Arg Asn Arg Ala His Gln Ser Ile Ser Arg Asp Leu			
185	190	195	
aac cag gtg tca gat cag att cag gat cga cta ctg gac aag			733
Asn Gln Val Ser Asp Gln Ile Gln Asp Arg Leu Leu Asp Lys			
200	205	210	
tagctgctgg tcgagtcgct gcc			756

<210> 314

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 314

Met Gly Ile Phe Glu Ala Ile Arg Ala Ala Arg Ala Lys Thr Lys Ala
1 5 10 15

Glu Ile Lys Ala Ala Glu Ala Lys Val Lys Thr Glu Ala Lys Asn Lys
20 25 30

Ala Lys Leu Asp Leu Lys Arg Glu Lys Leu Leu Val Gln Gln Glu Lys
35 40 45

Asn Leu Leu Lys Val Glu Glu Lys Gly Leu Lys Lys Arg Asn Lys His

50										55										60									
Glu 65	Leu	Lys	Met	Ala	Lys 70	Asn	Ile	Leu	Glu	Gln 75	Lys	Arg	Gln	Gly	Arg 80														
Leu	Asn	Lys	Asp	Lys 85	Val	Lys	Arg	Trp	Ala 90	Gly	Thr	Ala	Arg	Val 95	Leu														
Thr	Pro	Leu	Leu 100	Pro	Ile	Ile	Tyr 105	Arg	Leu	Ser	Thr	Glu 110	Ala	Arg															
Asp	Gln	Val	Val 115	Lys	Gly	Arg	Ala 120	Arg	Arg	Ala	Gly	Val 125	Thr	Ala	Glu														
Gln	Leu	Ser	Gln	Phe	Ala	Gly 135	His	Ala	Ala	Ala	Leu 140	Lys	Ala	Arg	Ile														
Gln	Gly	Val	Arg	Glu	Thr 150	Ala	Lys	Asn	Ser	Ser 155	Leu	Pro	Ala	Gly	Phe 160														
Val	Arg	Asp	Val	Glu	Glu 165	Arg	Leu	Asn	Glu 170	Leu	Glu	Ala	Ala	Ala	Asn 175														
Asn	Ser	Glu	Phe	Met	Ser	Pro	Gln	Gln 185	Arg	Asn	Arg	Ala	His	Gln	Ser 190														
Ile	Ser	Arg	Asp	Leu	Asn	Gln	Val 200	Ser	Asp	Gln	Ile	Gln 205	Asp	Arg	Leu														
Leu	Asp	Lys																											
210																													
<210> 315 <211> 756 <212> DNA <213> <i>Corynebacterium glutamicum</i> <220> <221> CDS <222> (101)..(733) <223> FRXA00647 <400> 315 tgcattcttc ccacaatgac atgagcttat tgcaacatcg tgggtaaagt tgaatcgaga 60 agtcgagaaa taaccgacgc atgaaagagt tgagacgata atg ggc atc ttc gaa 115 <div style="text-align: right;">Met Gly Ile Phe Glu 5</div> gcc atc cga gcc gca cgc gcg aag acc aaa gct gag atc aaa gca gcc 163 <div style="text-align: right;">Ala Ile Arg Ala Ala Arg Ala Lys Thr Lys Ala Glu Ile Lys Ala Ala 20</div> gag gca aaa gta aaa act gag gcg aaa aac aaa gca aag cta gat ctc 211 <div style="text-align: right;">Glu Ala Lys Val Lys Thr Glu Ala Lys Asn Lys Ala Lys Leu Asp Leu 35</div> aag cgc gag aag ctt ctt gtc cag cag gaa aag aat ctg ctc aag gtt 259 <div style="text-align: right;">Lys Arg Glu Lys Leu Leu Val Gln Gln Glu Lys Asn Leu Leu Lys Val 40 45 50</div>																													

gaa gaa aag ggc ctg aag aag cgc aac aag cat gag ctg aag atg gcc 307
 Glu Glu Lys Gly Leu Lys Lys Arg Asn Lys His Glu Leu Lys Met Ala
 55 60 65
 aaa aat atc ctt gag caa aag cgc caa gga cgc cta aac aaa gac aag 355
 Lys Asn Ile Leu Glu Gln Lys Arg Gln Gly Arg Leu Asn Lys Asp Lys
 70 75 80 85
 gtg aag cgc tgg gct ggc acc gca cgt gtg ctc act cca cta ctg ctg 403
 Val Lys Arg Trp Ala Gly Thr Ala Arg Val Leu Thr Pro Leu Leu Leu
 90 95 100
 cct att att tat cga ctc tcc acc gaa gca cgc gat cag gtt gtt aag 451
 Pro Ile Ile Tyr Arg Leu Ser Thr Glu Ala Arg Asp Gln Val Val Lys
 105 110 115
 gga cgt gcc cgt cgt gca ggt gtc acc gcg gag cag ctt agc caa ttc 499
 Gly Arg Ala Arg Arg Ala Gly Val Thr Ala Glu Gln Leu Ser Gln Phe
 120 125 130
 gca ggt cac gca gca gcg ctg aag gct cgt att caa ggt gtt cgc gaa 547
 Ala Gly His Ala Ala Ala Leu Lys Ala Arg Ile Gln Gly Val Arg Glu
 135 140 145
 acc gca aag aac tcc agc ctc cct gct ggc ttt gta cgc gat gtt gaa 595
 Thr Ala Lys Asn Ser Ser Leu Pro Ala Gly Phe Val Arg Asp Val Glu
 150 155 160 165
 gag cgt ctc aat gag ctc gag gct gct gcg aat aac tct gag ttc atg 643
 Glu Arg Leu Asn Glu Leu Glu Ala Ala Asn Asn Ser Glu Phe Met
 170 175 180
 tct cca cag cag agg aac cgt gcg cac cag tcg atc agt cgt gat ctg 691
 Ser Pro Gln Gln Arg Asn Arg Ala His Gln Ser Ile Ser Arg Asp Leu
 185 190 195
 aac cag gtg tca gat cag att cag gat cga cta ctg gac aag 733
 Asn Gln Val Ser Asp Gln Ile Gln Asp Arg Leu Leu Asp Lys
 200 205 210
 tagctgctgg tcgagtcgct gcc 756

<210> 316

<211> 211

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 316

Met Gly Ile Phe Glu Ala Ile Arg Ala Ala Arg Ala Lys Thr Lys Ala
 1 5 10 15

Glu Ile Lys Ala Ala Glu Ala Lys Val Lys Thr Glu Ala Lys Asn Lys
 20 25 30

Ala Lys Leu Asp Leu Lys Arg Glu Lys Leu Leu Val Gln Gln Lys
 35 40 45

Asn Leu Leu Lys Val Glu Glu Lys Gly Leu Lys Lys Arg Asn Lys His
 50 55 60

Glu Leu Lys Met Ala Lys Asn Ile Leu Glu Gln Lys Arg Gln Gly Arg
65 70 75 80

Leu Asn Lys Asp Lys Val Lys Arg Trp Ala Gly Thr Ala Arg Val Leu
85 90 95

Thr Pro Leu Leu Leu Pro Ile Ile Tyr Arg Leu Ser Thr Glu Ala Arg
100 105 110

Asp Gln Val Val Lys Gly Arg Ala Arg Arg Ala Gly Val Thr Ala Glu
115 120 125

Gln Leu Ser Gln Phe Ala Gly His Ala Ala Ala Leu Lys Ala Arg Ile
130 135 140

Gln Gly Val Arg Glu Thr Ala Lys Asn Ser Ser Leu Pro Ala Gly Phe
145 150 155 160

Val Arg Asp Val Glu Glu Arg Leu Asn Glu Leu Glu Ala Ala Ala Asn
165 170 175

Asn Ser Glu Phe Met Ser Pro Gln Gln Arg Asn Arg Ala His Gln Ser
180 185 190

Ile Ser Arg Asp Leu Asn Gln Val Ser Asp Gln Ile Gln Asp Arg Leu
195 200 205

Leu Asp Lys
210

<210> 317

<211> 888

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(865)

<223> RXN00653

<400> 317

gttgagattc gectaacaaa gattttggac gaaaacagta acgatgacag ccacgttaag 60

cgcggaatct tctcgcaatg gtaaaaaagcc gcggcctcga gtg agt gtt tcc cag 115
Val Ser Val Ser Gln
1 5

gtt gtt ggt gaa atc ttg ctc acc gta ggc att ttg gcc ttg tta ttc 163
Val Val Gly Glu Ile Leu Leu Thr Val Gly Ile Leu Ala Leu Leu Phe
10 15 20

gca tac tat gag gcc tat tgg acc aac gtg gaa tct ggg aaa tta caa 211
Ala Tyr Tyr Glu Ala Tyr Trp Thr Asn Val Glu Ser Gly Lys Leu Gln
25 30 35

gaa tcg gct ggt caa aag ctt gat gaa gac tgg aat gaa gct cgg gtg 259
Glu Ser Ala Gly Gln Lys Leu Asp Glu Asp Trp Asn Glu Ala Arg Val
40 45 50

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aat cct cga caa aag ctc acc ccg gaa ctt ggt gag gca ttt gcc cgg 307
Asn Pro Arg Gln Lys Leu Thr Pro Glu Leu Gly Glu Ala Phe Ala Arg
55 60 65

atg tat gtt cca gct ttc ggc tct gac ttc aac ttc gca gtg att gaa 355
Met Tyr Val Pro Ala Phe Gly Ser Asp Phe Asn Phe Ala Val Ile Glu
70 75 80 85

gga acc gat gag gaa gac ctt ctt gcc ggt cct ggc cgt tat gtg gat 403
Gly Thr Asp Glu Glu Asp Leu Leu Ala Gly Pro Gly Arg Tyr Val Asp
90 95 100

tcc caa atg cct ggt gaa gcc gga aac ttt gca gtg gca ggc cac cga 451
Ser Gln Met Pro Gly Glu Ala Gly Asn Phe Ala Val Ala Gly His Arg
105 110 115

gtg ggc aag ggt gcg cca ttc aat gat cta gga aac ctg gaa gtc tgc 499
Val Gly Lys Gly Ala Pro Phe Asn Asp Leu Gly Asn Leu Glu Val Cys
120 125 130

gat gcg atc gtg gtg gag act tac aat tcc tgg gat gtg tac cgc gtg 547
Asp Ala Ile Val Val Thr Tyr Asn Ser Trp Asp Val Tyr Arg Val
135 140 145

atg ccg atg tcc acc aac ggt gca gat cgt gca gca gaa gct gcg gat 595
Met Pro Met Ser Thr Asn Gly Ala Asp Arg Ala Ala Glu Ala Ala Asp
150 155 160 165

tgc ttc aac gaa aac cag gtc agc cgc atg gct gaa ggt gac tat gtg 643
Cys Phe Asn Glu Asn Gln Val Ser Arg Met Ala Glu Gly Asp Tyr Val
170 175 180

aat gtg tcc gga cga agc atc acc act ccg gat cgc atc gat gcc acc 691
Asn Val Ser Gly Arg Ser Ile Thr Thr Pro Asp Arg Ile Asp Ala Thr
185 190 195

tac ccc aca ccg ggc gtc ttc gac act gca gtg cgt gaa gga tca gaa 739
Tyr Pro Thr Pro Gly Val Phe Asp Thr Ala Val Arg Glu Gly Ser Glu
200 205 210

gct ctg ctt acc ttg acc acg tgt cac ccg cag ttc tcc aac gct gag 787
Ala Leu Leu Thr Leu Thr Thr Cys His Pro Gln Phe Ser Asn Ala Glu
215 220 225

cgc atg att gtg cac gca atg ttg gtg gaa gaa atc gat aaa tca agt 835
Arg Met Ile Val His Ala Met Leu Val Glu Glu Ile Asp Lys Ser Ser
230 235 240 245

ggc gaa cgc cct gca gct ttg gag gaa aac taaatgtatt cactttctgtg 885
Gly Glu Arg Pro Ala Ala Leu Glu Glu Asn
250 255

gca 888

<210> 318
<211> 255
<212> PRT
<213> Corynebacterium glutamicum

<400> 318

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Val Ser Val Ser Gln Val Val Gly Glu Ile Leu Leu Thr Val Gly Ile
  1          5          10          15

Leu Ala Leu Leu Phe Ala Tyr Tyr Glu Ala Tyr Trp Thr Asn Val Glu
      20          25          30

Ser Gly Lys Leu Gln Glu Ser Ala Gly Gln Lys Leu Asp Glu Asp Trp
      35          40          45

Asn Glu Ala Arg Val Asn Pro Arg Gln Lys Leu Thr Pro Glu Leu Gly
      50          55          60

Glu Ala Phe Ala Arg Met Tyr Val Pro Ala Phe Gly Ser Asp Phe Asn
      65          70          75          80

Phe Ala Val Ile Glu Gly Thr Asp Glu Glu Asp Leu Leu Ala Gly Pro
      85          90          95

Gly Arg Tyr Val Asp Ser Gln Met Pro Gly Glu Ala Gly Asn Phe Ala
      100          105          110

Val Ala Gly His Arg Val Gly Lys Gly Ala Pro Phe Asn Asp Leu Gly
      115          120          125

Asn Leu Glu Val Cys Asp Ala Ile Val Val Glu Thr Tyr Asn Ser Trp
      130          135          140

Asp Val Tyr Arg Val Met Pro Met Ser Thr Asn Gly Ala Asp Arg Ala
      145          150          155          160

Ala Glu Ala Ala Asp Cys Phe Asn Glu Asn Gln Val Ser Arg Met Ala
      165          170          175

Glu Gly Asp Tyr Val Asn Val Ser Gly Arg Ser Ile Thr Thr Pro Asp
      180          185          190

Arg Ile Asp Ala Thr Tyr Pro Thr Pro Gly Val Phe Asp Thr Ala Val
      195          200          205

Arg Glu Gly Ser Glu Ala Leu Leu Thr Leu Thr Thr Cys His Pro Gln
      210          215          220

Phe Ser Asn Ala Glu Arg Met Ile Val His Ala Met Leu Val Glu Glu
      225          230          235          240

Ile Asp Lys Ser Ser Gly Glu Arg Pro Ala Ala Leu Glu Glu Asn
      245          250          255

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<210> 319

<211> 888

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> {101}...(865)

<223> FRXA00653

<400> 319

gttgagattc gcctaacaaa gattttggac gaaaacagta acgatgacag coacgttaag 60

cgcggaatct tctcgcaatg gtaaaaagcc gcggcctcga gtg agt gtt tcc cag 115
 Val Ser Val Ser Gln
 1 5

gtt gtt ggt gaa atc ttg ctc acc gta ggc att ttg gcc ttg tta ttc 163
 Val Val Gly Glu Ile Leu Leu Thr Val Gly Ile Leu Ala Leu Leu Phe
 10 15 20

gca tac tat gag gcc tat tgg acc aac gtg gaa tct ggg aaa tta caa 211
 Ala Tyr Tyr Glu Ala Tyr Trp Thr Asn Val Glu Ser Gly Lys Leu Gln
 25 30 35

gaa tcg gct ggt caa aag ctt gat gaa gac tgg aat gaa gct cgg gtg 259
 Glu Ser Ala Gly Gln Lys Leu Asp Glu Asp Trp Asn Glu Ala Arg Val
 40 45 50

aat cct cga caa aag ctc acc ccg gaa ctt ggt gag gca ttt gcc cgg 307
 Asn Pro Arg Gln Lys Leu Thr Pro Glu Leu Gly Glu Ala Phe Ala Arg
 55 60 65

atg tat gtt cca gct ttc ggc tct gac ttc aac ttc gca gtg att gaa 355
 Met Tyr Val Pro Ala Phe Gly Ser Asp Phe Asn Phe Ala Val Ile Glu
 70 75 80 85

gga acc gat gag gaa gac ctt ctt gcc ggt cct ggc cgt tat gtg gat 403
 Gly Thr Asp Glu Glu Asp Leu Leu Ala Gly Pro Gly Arg Tyr Val Asp
 90 95 100

tcc caa atg cct ggt gaa gcc gga aac ttt gca gtg gca ggc cac cga 451
 Ser Gln Met Pro Gly Glu Ala Gly Asn Phe Ala Val Ala Gly His Arg
 105 110 115

gtg ggc aag ggt cgc cca ttc aat gat cta gga aac ctg gaa gtc tgc 499
 Val Gly Lys Gly Ala Pro Phe Asn Asp Leu Gly Asn Leu Glu Val Cys
 120 125 130

gat cgc atc gtg gtg gag act tac aat tcc tgg gat gtg tac cgc gtg 547
 Asp Ala Ile Val Val Glu Thr Tyr Asn Ser Trp Asp Val Tyr Arg Val
 135 140 145

atg ccg atg tcc acc aac ggt gca gat cgt gca gca gaa gct gcg gat 595
 Met Pro Met Ser Thr Asn Gly Ala Asp Arg Ala Ala Glu Ala Ala Asp
 150 155 160 165

tgc ttc aac gaa aac cag gtc agc cgc atg gct gaa ggt gac tat gtg 643
 Cys Phe Asn Glu Asn Gln Val Ser Arg Met Ala Glu Gly Asp Tyr Val
 170 175 180

aat gtg tcc gga cga agc atc acc act ccg gat cgc atc gat gcc acc 691
 Asn Val Ser Gly Arg Ser Ile Thr Thr Pro Asp Arg Ile Asp Ala Thr
 185 190 195

tac ccc aca ccg ggc gtc ttc gac act gca gtg cgt gaa gga tca gaa 739
 Tyr Pro Thr Pro Gly Val Phe Asp Thr Ala Val Arg Glu Gly Ser Glu
 200 205 210

gct ctg ctt acc ttg acc acg tgt cac ccg cag ttc tcc aac gct gag 787
 Ala Leu Leu Thr Leu Thr Thr Cys His Pro Gln Phe Ser Asn Ala Glu
 215 220 225

cgc atg att gtg cac gca atg ttg gtg gaa gaa atc gat aaa tca agt 835
 Arg Met Ile Val His Ala Met Leu Val Glu Glu Ile Asp Lys Ser Ser
 230 235 240 245

ggc gaa cgc cct gca gct ttg gag gaa aac taaatgtatt cactctgtg 885
 Gly Glu Arg Pro Ala Ala Leu Glu Glu Asn
 250 255

gca 888

<210> 320

<211> 255

<212> FRT

<213> *Corynebacterium glutamicum*

<400> 320

Val Ser Val Ser Gln Val Val Gly Glu Ile Leu Leu Thr Val Gly Ile
 1 5 10 15

Leu Ala Leu Leu Phe Ala Tyr Tyr Glu Ala Tyr Trp Thr Asn Val Glu
 20 25 30

Ser Gly Lys Leu Gln Glu Ser Ala Gly Gln Lys Leu Asp Glu Asp Trp
 35 40 45

Asn Glu Ala Arg Val Asn Pro Arg Gln Lys Leu Thr Pro Glu Leu Gly
 50 55 60

Glu Ala Phe Ala Arg Met Tyr Val Pro Ala Phe Gly Ser Asp Phe Asn
 65 70 75 80

Phe Ala Val Ile Glu Gly Thr Asp Glu Glu Asp Leu Leu Ala Gly Pro
 85 90 95

Gly Arg Tyr Val Asp Ser Gln Met Pro Gly Glu Ala Gly Asn Phe Ala
 100 105 110

Val Ala Gly His Arg Val Gly Lys Gly Ala Pro Phe Asn Asp Leu Gly
 115 120 125

Asn Leu Glu Val Cys Asp Ala Ile Val Val Glu Thr Tyr Asn Ser Trp
 130 135 140

Asp Val Tyr Arg Val Met Pro Met Ser Thr Asn Gly Ala Asp Arg Ala
 145 150 155 160

Ala Glu Ala Ala Asp Cys Phe Asn Glu Asn Gln Val Ser Arg Met Ala
 165 170 175

Glu Gly Asp Tyr Val Asn Val Ser Gly Arg Ser Ile Thr Thr Pro Asp
 180 185 190

Arg Ile Asp Ala Thr Tyr Pro Thr Pro Gly Val Phe Asp Thr Ala Val
 195 200 205

Arg Glu Gly Ser Glu Ala Leu Leu Thr Leu Thr Thr Cys His Pro Gln
 210 215 220

Phe Ser Asn Ala Glu Arg Met Ile Val His Ala Met Leu Val Glu Glu
 225 230 235 240

Ile Asp Lys Ser Ser Gly Glu Arg Pro Ala Ala Leu Glu Glu Asn
 245 250 255

<210> 321

<211> 1392

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1369)

<223> RXN00662

<400> 321

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tttactggct atagtggtgc gcgtgccaaa tcgagttcct gtg tca acc att cgg 115
 Val Ser Thr Ile Pro
 1 5

ctg aat cgt cta gcc gtt atc gct gcc atc att ggt gtc ggt acc ggg 163
 Leu Asn Arg Leu Ala Val Ile Ala Ala Ile Ile Gly Val Gly Thr Gly
 10 15 20

ctg ttt gtt gct gca ctg aac tgg tct gcc att ggc gtg gag cgt tta 211
 Leu Phe Val Ala Ala Leu Asn Trp Ser Ala Ile Gly Val Glu Arg Leu
 25 30 35

gtt tat ggc gct gac cat ttg cat aat tac aat ccg gtg gcc aat gtg 259
 Val Tyr Gly Ala Asp His Leu His Asn Tyr Asn Pro Val Ala Asn Val
 40 45 50

tgc cca ctt cgc ctg tcc atc acg gtg att gtg ctt agc gtg gtg gcc 307
 Ser Pro Leu Arg Leu Ser Ile Thr Val Ile Val Leu Ser Val Val Ala
 55 60 65

tcc tgg gcg tgg ttt ttt gtg cac cgc acg ggg ccg aaa gag gtt tcg 355
 Ser Trp Ala Trp Phe Phe Val His Arg Thr Gly Pro Lys Glu Val Ser
 70 75 80 85

att gtg ggt gcg atc cgg ggc gag aag atg ccg att ttg gag acc ata 403
 Ile Val Gly Ala Ile Arg Gly Glu Lys Met Pro Ile Leu Glu Thr Ile
 90 95 100

gcg tcc gca ttt ttg cag gtc acc acg gtt gct gcg ggt gcg ccg gtg 451
 Ala Ser Ala Phe Leu Gln Val Thr Val Ala Ala Gly Ala Pro Val
 105 110 115

ggt gca gag aac gct cca cgt att gct gga gcc ttg gtg gga gag cgg 499
 Gly Ala Glu Asn Ala Pro Arg Ile Ala Gly Ala Leu Val Gly Glu Arg
 120 125 130

ttt agt cgg tgg ttg cag ctc gat att gat gca aag cgc atc ttg gtg 547
 Phe Ser Arg Trp Leu Gln Leu Asp Ile Asp Ala Lys Arg Ile Leu Val
 135 140 145

gcc tct gcc gcg gga gct ggt ttg gga gca agc ttc cac ctt ccc cta 595
 Ala Ser Ala Ala Gly Ala Gly Leu Gly Ala Ser Phe His Leu Pro Leu
 150 155 160 165

gca ggc gtg ctg ttt gcc ctt gag gtc cta ctg gtt gag gcc tcc act 643
Ala Gly Val Leu Phe Ala Leu Glu Val Leu Leu Val Glu Ala Ser Thr
170 175 180

cgg acc gtg gtt atc gca att atc acc acg acc gcc gcc gtt gcc acc 691
Arg Thr Val Val Ile Ala Ile Ile Thr Thr Thr Ala Ala Val Ala Thr
185 190 195

act gga ttt ttc gtg caa acc cca gat gtg ttc agc act gtc ccg ctg 739
Thr Gly Phe Phe Val Gln Thr Pro Asp Val Phe Ser Thr Val Pro Leu
200 205 210

acg gaa agc cca tgg atg ctg ctt gcc gcg atg gtc acc gga gta gtc 787
Thr Glu Ser Pro Trp Met Leu Leu Ala Ala Met Val Thr Gly Val Val
215 220 225

gcc ggc atg tgc ggg cac tgg ttt tca gcg gcg gcg cac aaa atg gcg 835
Ala Gly Met Cys Gly His Trp Phe Ser Ala Ala Ala His Lys Met Ala
230 235 240 245

cag gcc tcg ccc aag ggt gtg aag att ttg tgg cag atg ccg ttg ggt 883
Gln Ala Ser Pro Lys Gly Val Lys Ile Leu Trp Gln Met Pro Leu Gly
250 255 260

ttc gtg gtg atc gct gcg gtg att tat ttc ttc ccc gaa acc ctg gcg 931
Phe Val Val Ile Ala Ala Val Ile Tyr Phe Phe Pro Glu Thr Leu Ala
265 270 275

aat ccc cgt tgg ctt gcc gat tcc atg ctc ggc gat ggc ctg atc ctc 979
Asn Pro Arg Trp Leu Ala Asp Ser Met Leu Gly Asp Gly Leu Ile Leu
280 285 290

agc acc att tta ttg gta ctt gtt ctg cgc acc gcc atg ttt ttg ctc 1027
Ser Thr Ile Leu Leu Val Leu Val Leu Arg Thr Ala Met Phe Leu Leu
295 300 305

gcc ttc cgc gtg gcc atg gtc gcc ggt aac ctg atc ccc gca ttc gca 1075
Ala Phe Arg Val Gly Met Val Gly Gly Asn Leu Ile Pro Ala Phe Ala
310 315 320 325

ctc gga tcc atg gtc ggt ggg gta gtg ggt gct gta ttg gaa ccc atc 1123
Leu Gly Ser Met Val Gly Gly Val Val Gly Ala Val Leu Glu Pro Ile
330 335 340

act aac gtc ccg atc gcc gct ttt gcg ctg ctt ggc gcc gcc gca ttt 1171
Thr Asn Val Pro Ile Ala Ala Phe Ala Leu Leu Gly Ala Ala Ala Phe
345 350 355

ttg tcc acc acc atg gca gcg cca ctg ttc ggg ctc atc gcc gca gtg 1219
Leu Ser Thr Thr Met Ala Ala Pro Leu Phe Gly Leu Ile Ala Ala Val
360 365 370

gaa ttc acc gac atg gaa gcc caa ggc tac ctt ccg att ttc ctc gca 1267
Glu Phe Thr Asp Met Glu Ala Gln Gly Tyr Leu Pro Ile Phe Leu Ala
375 380 385

gta gcc tcc gcg gtc ctc gcc gtg cgc gtg tgg tct gtc atc gcc aag 1315
Val Ala Ser Ala Val Leu Ala Val Arg Val Trp Ser Val Ile Ala Lys
390 395 400 405

cac gag ctc cgc gcc atc ccg atc acg tac gcg agc tgg acg ggc gag 1363
 His Glu Leu Arg Ala Ile Pro Ile Thr Tyr Ala Ser Trp Thr Gly Glu
 410 415 420

ctt aaa taagcttgtc gacgcctccc tcc 1392
 Leu Lys

<210> 322

<211> 423

<212> PRT

<213> Corynebacterium glutamicum

<400> 322

Val Ser Thr Ile Pro Leu Asn Arg Leu Ala Val Ile Ala Ala Ile Ile
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Gly Val Gly Thr Gly Leu Phe Val Ala Ala Leu Asn Trp Ser Ala Ile
 20 25 30

Gly Val Glu Arg Leu Val Tyr Gly Ala Asp His Leu His Asn Tyr Asn
 35 40 45

Pro Val Ala Asn Val Ser Pro Leu Arg Leu Ser Ile Thr Val Ile Val
 50 55 60

Leu Ser Val Val Ala Ser Trp Ala Trp Phe Phe Val His Arg Thr Gly
 65 70 75 80

Pro Lys Glu Val Ser Ile Val Gly Ala Ile Arg Gly Glu Lys Met Pro
 85 90 95

Ile Leu Glu Thr Ile Ala Ser Ala Phe Leu Gln Val Thr Thr Val Ala
 100 105 110

Ala Gly Ala Pro Val Gly Ala Glu Asn Ala Pro Arg Ile Ala Gly Ala
 115 120 125

Leu Val Gly Glu Arg Phe Ser Arg Trp Leu Gln Leu Asp Ile Asp Ala
 130 135 140

Lys Arg Ile Leu Val Ala Ser Ala Ala Gly Ala Gly Leu Gly Ala Ser
 145 150 155 160

Phe His Leu Pro Leu Ala Gly Val Leu Phe Ala Leu Glu Val Leu Leu
 165 170 175

Val Glu Ala Ser Thr Arg Thr Val Val Ile Ala Ile Ile Thr Thr Thr
 180 185 190

Ala Ala Val Ala Thr Thr Gly Phe Phe Val Gln Thr Pro Asp Val Phe
 195 200 205

Ser Thr Val Pro Leu Thr Glu Ser Pro Trp Met Leu Leu Ala Ala Met
 210 215 220

Val Thr Gly Val Val Ala Gly Met Cys Gly His Trp Phe Ser Ala Ala
 225 230 235 240

Ala His Lys Met Ala Gln Ala Ser Pro Lys Gly Val Lys Ile Leu Trp

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                245                250                255
Gln Met Pro Leu Gly Phe Val Val Ile Ala Ala Val Ile Tyr Phe Phe
      260                265                270
Pro Glu Thr Leu Ala Asn Pro Arg Trp Leu Ala Asp Ser Met Leu Gly
      275                280                285
Asp Gly Leu Ile Leu Ser Thr Ile Leu Leu Val Leu Val Leu Arg Thr
      290                295                300
Ala Met Phe Leu Leu Ala Phe Arg Val Gly Met Val Gly Gly Asn Leu
      305                310                315
Ile Pro Ala Phe Ala Leu Gly Ser Met Val Gly Gly Val Val Gly Ala
      325                330                335
Val Leu Glu Pro Ile Thr Asn Val Pro Ile Ala Ala Phe Ala Leu Leu
      340                345                350
Gly Ala Ala Ala Phe Leu Ser Thr Thr Met Ala Ala Pro Leu Phe Gly
      355                360                365
Leu Ile Ala Ala Val Glu Phe Thr Asp Met Glu Ala Gln Gly Tyr Leu
      370                375                380
Pro Ile Phe Leu Ala Val Ala Ser Ala Val Leu Ala Val Arg Val Trp
      385                390                395                400
Ser Val Ile Ala Lys His Glu Leu Arg Ala Ile Pro Ile Thr Tyr Ala
      405                410                415
Ser Trp Thr Gly Glu Leu Lys
      420

<210> 323
<211> 1392
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1369)
<223> FRXA00662

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tttactggct atagtgttgc cggtgccaaa togagttcct gtg tca acc att cgg 115
                               Val Ser Thr Ile Pro
                               1                               5

ctg aat cgt cta gcc gtt atc gct gcc atc att ggt gtc ggt acc ggg 163
Leu Asn Arg Leu Ala Val Ile Ala Ala Ile Ile Gly Val Gly Thr Gly
      10                15                20

ctg ttt gtt gct gca ctg aac tgg tct gcc att ggc gtg gag cgt tta 211
Leu Phe Val Ala Ala Leu Asn Trp Ser Ala Ile Gly Val Glu Arg Leu
      25                30                35

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gtt tat ggc gct gac cat ttg cat aat tac aat ccg gtg gcc aat gtg Val Tyr Gly Ala Asp His Leu His Asn Tyr Asn Pro Val Ala Asn Val 40 45 50	259
tcg cca ctt cgc ctg tcc atc acg gtg att gtg ctt agc gtg gtg gcc Ser Pro Leu Arg Leu Ser Ile Thr Val Ile Val Leu Ser Val Val Ala 55 60 65	307
tcc tgg gcg tgg ttt ttt gtg cac cgc acg ggg ccg aaa gag gtt tcg Ser Trp Ala Trp Phe Phe Val His Arg Thr Gly Pro Lys Glu Val Ser 70 75 80 85	355
att gtg ggt gcg atc cgg ggc gag aag atg ccg att ttg gag acc ata Ile Val Gly Ala Ile Arg Gly Glu Lys Met Pro Ile Leu Glu Thr Ile 90 95 100	403
gcg tcc gca ttt ttg cag gtc acc acg gtt gct gcg ggt gcg ccg gtg Ala Ser Ala Phe Leu Gln Val Thr Thr Val Ala Ala Gly Ala Pro Val 105 110 115	451
ggt gca gag aac gct cca cgt att gct gga gcc ttg gtg gga gag cgg Gly Ala Glu Asn Ala Pro Arg Ile Ala Gly Ala Leu Val Gly Glu Arg 120 125 130	499
ttt agt cgg tgg ttg cag ctc gat att gat gca aag cgc atc ttg gtg Phe Ser Arg Trp Leu Gln Leu Asp Ile Asp Ala Lys Arg Ile Leu Val 135 140 145	547
gcc tct gcc gcg gga gct ggt ttg gga gca agc ttc cac ctt ccc cta Ala Ser Ala Ala Gly Ala Gly Leu Gly Ala Ser Phe His Leu Pro Leu 150 155 160 165	595
gca ggc gtg ctg ttt gcc ctt gag gtc cta ctg gtt gag gcc tcc act Ala Gly Val Leu Phe Ala Leu Glu Val Leu Leu Val Glu Ala Ser Thr 170 175 180	643
cgg acc gtg gtt atc gca att atc acc acg acc gcc gcc gtt gcc acc Arg Thr Val Val Ile Ala Ile Ile Thr Thr Thr Ala Ala Val Ala Thr 185 190 195	691
act gga ttt ttc gtg caa acc cca gat gtg ttc agc act gtc ccg ctg Thr Gly Phe Phe Val Gln Thr Pro Asp Val Phe Ser Thr Val Pro Leu 200 205 210	739
acg gaa agc cca tgg atg ctg ctt gcc gcg atg gtc acc gga gta gtc Thr Glu Ser Pro Trp Met Leu Leu Ala Ala Met Val Thr Gly Val Val 215 220 225	787
gcc ggc atg tgc ggg cac tgg ttt tca gcg gcg gcg cac aaa atg gcg Ala Gly Met Cys Gly His Trp Phe Ser Ala Ala Ala His Lys Met Ala 230 235 240 245	835
cag gcc tcg ccc aag ggt gtg aag att ttg tgg cag atg ccg ttg ggt Gln Ala Ser Pro Lys Gly Val Lys Ile Leu Trp Gln Met Pro Leu Gly 250 255 260	883
ttc gtg gtg atc gct gcg gtg att tat ttc ttc ccc gaa acc ctg gcg Phe Val Val Ile Ala Ala Val Ile Tyr Phe Phe Pro Glu Thr Leu Ala 265 270 275	931
aat ccc cgt tgg ctt gcc gat tcc atg ctc ggc gat gcc ctg atc ctc	979

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Asn Pro Arg Trp Leu Ala Asp Ser Met Leu Gly Asp Gly Leu Ile Leu
280                               285                               290

agc acc att tta ttg gta ctt gtt ctg cgc acc gcc atg ttt ttg ctc 1027
Ser Thr Ile Leu Leu Val Leu Val Leu Arg Thr Ala Met Phe Leu Leu
295                               300                               305

gcc ttc cgc gtg ggc atg gtc ggc ggt aac ctg atc ccc gca ttc gca 1075
Ala Phe Arg Val Gly Met Val Gly Gly Asn Leu Ile Pro Ala Phe Ala
310                               315                               320                               325

ctc gga tcc atg gtc ggt ggg gta gtg ggt gct gta ttg gaa ccc atc 1123
Leu Gly Ser Met Val Gly Gly Val Val Gly Ala Val Leu Glu Pro Ile
330                               335                               340

act aac gtc ccg atc gcc gct ttt gcg ctg ctt ggc gcc gcc gca ttt 1171
Thr Asn Val Pro Ile Ala Ala Phe Ala Leu Leu Gly Ala Ala Ala Phe
345                               350                               355

ttg tcc acc acc atg gca gcg cca ctg ttc ggg ctc atc gcc gca gtg 1219
Leu Ser Thr Thr Met Ala Ala Pro Leu Phe Gly Leu Ile Ala Ala Val
360                               365                               370

gaa ttc acc gac atg gaa gcc caa ggc tac ctt ccg att ttc ctc gca 1267
Glu Phe Thr Asp Met Glu Ala Gln Gly Tyr Leu Pro Ile Phe Leu Ala
375                               380                               385

gta gcc tcc gcg gtc ctc gcc gtg cgc gtg tgg tct gtc atc gcc aag 1315
Val Ala Ser Ala Val Leu Ala Val Arg Val Trp Ser Val Ile Ala Lys
390                               395                               400                               405

cac gag ctc cgc gcc atc ccg atc acg tac gcg agc tgg acg ggc gag 1363
His Glu Leu Arg Ala Ile Pro Ile Thr Tyr Ala Ser Trp Thr Gly Glu
410                               415                               420

ctt aaa taagcttgtc gacgcctccc tcc 1392
Leu Lys

<210> 324
<211> 423
<212> PRT
<213> Corynebacterium glutamicum

<400> 324
Val Ser Thr Ile Pro Leu Asn Arg Leu Ala Val Ile Ala Ala Ile Ile
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Gly Val Gly Thr Gly Leu Phe Val Ala Leu Asn Trp Ser Ala Ile
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Gly Val Glu Arg Leu Val Tyr Gly Ala Asp His Leu His Asn Tyr Asn
35 40 45

Pro Val Ala Asn Val Ser Pro Leu Arg Leu Ser Ile Thr Val Ile Val
50 55 60

Leu Ser Val Val Ala Ser Trp Ala Trp Phe Phe Val His Arg Thr Gly
65 70 75 80

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Pro	Lys	Glu	Val	Ser	Ile	Val	Gly	Ala	Ile	Arg	Gly	Glu	Lys	Met	Pro
				85					90					95	
Ile	Leu	Glu	Thr	Ile	Ala	Ser	Ala	Phe	Leu	Gln	Val	Thr	Thr	Val	Ala
			100					105						110	
Ala	Gly	Ala	Pro	Val	Gly		Ala	Glu	Asn	Ala	Pro	Arg	Ile	Ala	Gly
								120						125	
Leu	Val	Gly	Glu	Arg	Phe	Ser	Arg	Trp	Leu	Gln	Leu	Asp	Ile	Asp	Ala
								135							
Lys	Arg	Ile	Leu	Val	Ala	Ser	Ala	Ala	Gly	Ala	Gly	Leu	Gly	Ala	Ser
															160
Phe	His	Leu	Pro	Leu	Ala	Gly	Val	Leu	Phe	Ala	Leu	Glu	Val	Leu	Leu
															175
Val	Glu	Ala	Ser	Thr	Arg	Thr	Val	Val	Ile	Ala	Ile	Ile	Thr	Thr	Thr
Ala	Ala	Val	Ala	Thr	Thr	Gly	Phe	Phe	Val	Gln	Thr	Pro	Asp	Val	Phe
Ser	Thr	Val	Pro	Leu	Thr	Glu	Ser	Pro	Trp	Met	Leu	Leu	Ala	Ala	Met
Val	Thr	Gly	Val	Val	Ala	Gly	Met	Cys	Gly	His	Trp	Phe	Ser	Ala	Ala
															240
Ala	His	Lys	Met	Ala	Gln	Ala	Ser	Pro	Lys	Gly	Val	Lys	Ile	Leu	Trp
															255
Gln	Met	Pro	Leu	Gly	Phe	Val	Val	Ile	Ala	Ala	Val	Ile	Tyr	Phe	Phe
Pro	Glu	Thr	Leu	Ala	Asn	Pro	Arg	Trp	Leu	Ala	Asp	Ser	Met	Leu	Gly
Asp	Gly	Leu	Ile	Leu	Ser	Thr	Ile	Leu	Leu	Val	Leu	Val	Leu	Arg	Thr
Ala	Met	Phe	Leu	Leu	Ala	Phe	Arg	Val	Gly	Met	Val	Gly	Gly	Asn	Leu
															320
Ile	Pro	Ala	Phe	Ala	Leu	Gly	Ser	Met	Val	Gly	Gly	Val	Val	Gly	Ala
															335
Val	Leu	Glu	Pro	Ile	Thr	Asn	Val	Pro	Ile	Ala	Ala	Phe	Ala	Leu	Leu
Gly	Ala	Ala	Ala	Phe	Leu	Ser	Thr	Thr	Met	Ala	Ala	Pro	Leu	Phe	Gly
Leu	Ile	Ala	Ala	Val	Glu	Phe	Thr	Asp	Met	Glu	Ala	Gln	Gly	Tyr	Leu
Pro	Ile	Phe	Leu	Ala	Val	Ala	Ser	Ala	Val	Leu	Ala	Val	Arg	Val	Trp
															400
Ser	Val	Ile	Ala	Lys	His	Glu	Leu	Arg	Ala	Ile	Pro	Ile	Thr	Tyr	Ala

405

410

415

Ser Trp Thr Gly Glu Leu Lys
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<210> 325

<211> 1038

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1015)

<223> RXN00666

<400> 325

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acgattgagc gtgcttgatc tcgtcgcgct gagtgaaggg atg acg gcc ggc gag 115
Met Thr Ala Gly Glu
1 5

gcc att gca cac agt gtt cgc gct gcg cag atc gcc gaa gag cac aat 163
Ala Ile Ala His Ser Val Arg Ala Ala Gln Ile Ala Glu Glu His Asn
10 15 20

tat gcg cgt ttc tgg gtg gcg gag cac cac aac tcg gaa ggc ttg gca 211
Tyr Ala Arg Phe Trp Val Ala Glu His His Asn Ser Glu Gly Leu Ala
25 30 35

tct tcc gcg acg acg ctg ctc atg ggt cat att gca ggc cac act tca 259
Ser Ser Ala Thr Thr Leu Leu Met Gly His Ile Ala Gly His Thr Ser
40 45 50

cgc att cgc gtt ggc tcc ggt ggc atc atg atg ccc aac cac tcc gcg 307
Arg Ile Arg Val Gly Ser Gly Gly Ile Met Met Pro Asn His Ser Ala
55 60 65

ctg cac gtc gcc gaa gaa ctc ggc acc ctt gag gcc att tac ccc ggc 355
Leu His Val Ala Glu Glu Leu Gly Thr Leu Glu Ala Ile Tyr Pro Gly
70 75 80 85

cgc atc gag gcc ggc cta ggg cgc gca cca gga acc gac ccc atg acg 403
Arg Ile Glu Ala Gly Leu Gly Arg Ala Pro Gly Thr Asp Pro Met Thr
90 95 100

gcg cgg gaa ttg ggt cgg gca agt tcg ctt gtc gac gac gtc ctc tcc 451
Ala Arg Glu Leu Gly Arg Ala Ser Ser Leu Val Asp Asp Val Leu Ser
105 110 115

aca atc gtc tcc ctc cag aat tat ttg gac acc ccc gaa gaa cgc ccg 499
Thr Ile Val Ser Leu Gln Asn Tyr Leu Asp Thr Pro Glu Glu Arg Pro
120 125 130

aac atc atc gcg cat cca gga ata aat tcc cgt gtg ccg cta ttc atg 547
Asn Ile Ile Ala His Pro Gly Ile Asn Ser Arg Val Pro Leu Phe Met
135 140 145

ctg gga tct tcc ctc aac ggc gct gcg atg gcc gct aaa tta gac ctt 595
Leu Gly Ser Ser Leu Asn Gly Ala Ala Met Ala Ala Lys Leu Asp Leu

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150                155                160                165
cca ttc gcc ttc gcc agc cac ttc gca ccc ttc caa atg ggg ccc gcc 643
Pro Phe Ala Phe Ala Ser His Phe Ala Pro Phe Gln Met Gly Pro Ala
                170                175                180

atc gcc tcc tat cgc gaa cta gca gcc aat cct tat gtc atg gcc gca 691
Ile Ala Ser Tyr Arg Glu Leu Ala Ala Asn Pro Tyr Val Met Ala Ala
                185                190                195

gcg aat gtc ctg gtg tgc gac acc gag gaa gaa gcc gaa ttc cag atc 739
Ala Asn Val Leu Val Cys Asp Thr Glu Glu Glu Ala Glu Phe Gln Ile
                200                205                210

tcc aca ctg cac caa atg ttc gcc gga atc gtg acg aac tcc cgc ggc 787
Ser Thr Leu His Gln Met Phe Ala Gly Ile Val Thr Asn Ser Arg Gly
                215                220                225

aaa ctt gcc cca cca gtg cgg aat ctg aaa gac aaa ctc gac cgg atg 835
Lys Leu Ala Pro Pro Val Arg Asn Leu Lys Asp Lys Leu Asp Pro Met
                230                235                240                245

atc tgg aaa cac atc gaa gat tca ttg gaa atg act ttc atc gga aca 883
Ile Trp Lys His Ile Glu Asp Ser Leu Glu Met Thr Phe Ile Gly Thr
                250                255                260

gcc gaa tca gtg gta tta caa ctg cag gaa ttc gct gat cgc tac aag 931
Ala Glu Ser Val Val Leu Gln Leu Gln Glu Phe Ala Asp Arg Tyr Lys
                265                270                275

tta gat gag atc att aca gtc acc tac tcc tac gac ccc gaa gtc agg 979
Leu Asp Glu Ile Ile Thr Val Thr Tyr Ser Tyr Asp Pro Glu Val Arg
                280                285                290

ttc cgc tcc ata gct gca ctt ggc acg gca tgg aat tagtgtaaaa 1025
Phe Arg Ser Ile Ala Ala Leu Gly Thr Ala Trp Asn
                295                300                305

agcctcaaaa ata 1038

<210> 326
<211> 305
<212> PRT
<213> Corynebacterium glutamicum

<400> 326
Met Thr Ala Gly Glu Ala Ile Ala His Ser Val Arg Ala Ala Gln Ile
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Ala Glu Glu His Asn Tyr Ala Arg Phe Trp Val Ala Glu His His Asn
  20                25                30

Ser Glu Gly Leu Ala Ser Ser Ala Thr Thr Leu Leu Met Gly His Ile
  35                40                45

Ala Gly His Thr Ser Arg Ile Arg Val Gly Ser Gly Gly Ile Met Met
  50                55                60

Pro Asn His Ser Ala Leu His Val Ala Glu Glu Leu Gly Thr Leu Glu
  65                70                75                80

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Ala Ile Tyr Pro Gly Arg Ile Glu Ala Gly Leu Gly Arg Ala Pro Gly
85 90 95

Thr Asp Pro Met Thr Ala Arg Glu Leu Gly Arg Ala Ser Ser Leu Val
100 105 110

Asp Asp Val Leu Ser Thr Ile Val Ser Leu Gln Asn Tyr Leu Asp Thr
115 120 125

Pro Glu Glu Arg Pro Asn Ile Ile Ala His Pro Gly Ile Asn Ser Arg
130 135 140

Val Pro Leu Phe Met Leu Gly Ser Ser Leu Asn Gly Ala Ala Met Ala
145 150 155 160

Ala Lys Leu Asp Leu Pro Phe Ala Phe Ala Ser His Phe Ala Pro Phe
165 170 175

Gln Met Gly Pro Ala Ile Ala Ser Tyr Arg Glu Leu Ala Ala Asn Pro
180 185 190

Tyr Val Met Ala Ala Ala Asn Val Leu Val Cys Asp Thr Glu Glu Glu
195 200 205

Ala Glu Phe Gln Ile Ser Thr Leu His Gln Met Phe Ala Gly Ile Val
210 215 220

Thr Asn Ser Arg Gly Lys Leu Ala Pro Pro Val Arg Asn Leu Lys Asp
225 230 235 240

Lys Leu Asp Pro Met Ile Trp Lys His Ile Glu Asp Ser Leu Glu Met
245 250 255

Thr Phe Ile Gly Thr Ala Glu Ser Val Val Leu Gln Leu Gln Glu Phe
260 265 270

Ala Asp Arg Tyr Lys Leu Asp Glu Ile Ile Thr Val Thr Tyr Ser Tyr
275 280 285

Asp Pro Glu Val Arg Phe Arg Ser Ile Ala Ala Leu Gly Thr Ala Trp
290 295 300

Asn
305

<210> 327

<211> 487

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(487)

<223> FRXA00666

<400> 327

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Met Thr Ala Gly Glu
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Ala Ile Ala His Ser Val Arg Ala Ala Gln Ile Ala Glu Glu His Asn
10      15      20

tat gcg cgt ttc tgg gtg gcg gag cac cac aac tcg gaa ggc ttg gca 211
Tyr Ala Arg Phe Trp Val Ala Glu His His Asn Ser Glu Gly Leu Ala
25      30      35

tct tcc gcg acg acg ctg ctc atg ggt cat att gca ggc cac act tca 259
Ser Ser Ala Thr Thr Leu Leu Met Gly His Ile Ala Gly His Thr Ser
40      45      50

cgc att cgc gtt ggc tcc ggt ggc atc atg atg ccc aac cac tcc gcg 307
Arg Ile Arg Val Gly Ser Gly Gly Ile Met Met Pro Asn His Ser Ala
55      60      65

ctg cac gtc gcc gaa gaa ctc ggc acc ctt gag gcc att tac ccc ggc 355
Leu His Val Ala Glu Glu Leu Gly Thr Leu Glu Ala Ile Tyr Pro Gly
70      75      80      85

cgc atc gag gcc ggc cta ggg cgc gca cca gga acc gac ccc atg acg 403
Arg Ile Glu Ala Gly Leu Gly Arg Ala Pro Gly Thr Asp Pro Met Thr
90      95      100

gcg cgg gaa ttg ggt cgg gca agt tcg ctt gtc gac gac gtc ctc tcc 451
Ala Arg Glu Leu Glu Gly Arg Ala Ser Ser Leu Val Asp Asp Val Leu Ser
105      110      115

aca atc gtc tcc ctc cag aat tat ttg gac acc ccc 487
Thr Ile Val Ser Leu Gln Asn Tyr Leu Asp Thr Pro
120      125

<210> 328
<211> 129
<212> PRT
<213> Corynebacterium glutamicum

<400> 328
Met Thr Ala Gly Glu Ala Ile Ala His Ser Val Arg Ala Ala Gln Ile
1      5      10      15

Ala Glu Glu His Asn Tyr Ala Arg Phe Trp Val Ala Glu His His Asn
20      25      30

Ser Glu Gly Leu Ala Ser Ser Ala Thr Thr Leu Leu Met Gly His Ile
35      40      45

Ala Gly His Thr Ser Arg Ile Arg Val Gly Ser Gly Gly Ile Met Met
50      55      60

Pro Asn His Ser Ala Leu His Val Ala Glu Glu Leu Gly Thr Leu Glu
65      70      75      80

Ala Ile Tyr Pro Gly Arg Ile Glu Ala Gly Leu Gly Arg Ala Pro Gly
85      90      95

Thr Asp Pro Met Thr Ala Arg Glu Leu Gly Arg Ala Ser Ser Leu Val

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100

105

110

Asp Asp Val Leu Ser Thr Ile Val Ser Leu Gln Asn Tyr Leu Asp Thr
 115 120 125

Pro

<210> 329

<211> 750

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(727)

<223> RXN00704

<400> 329

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ttacagcggtt tacagaattg aaaatgaaag gttcaaaagcc ttg acc att act ttt 115
 Leu Thr Ile Thr Phe
 1 5

agc cgc gtt gct ctg acc acc ctg gca gtc acc gca acc act ttg tcc 163
 Ser Arg Val Ala Leu Thr Thr Leu Ala Val Thr Thr Leu Ser
 10 15 20

ctg agc act gct gcg aat gca cag tct tcc ttg ttg gat aag act ctt 211
 Leu Ser Thr Ala Ala Asn Ala Gln Ser Ser Leu Leu Asp Lys Thr Leu
 25 30 35

gat gcc cgt cag tgc atc gat gca gac aac gtc tgg gtc tca gtt gac 259
 Asp Ala Arg Gln Cys Ile Asp Ala Asp Asn Val Trp Val Ser Val Asp
 40 45 50

tat ggt gca gat tcc gaa aaa gaa cca gag ggc gca tgt gcc acc gag 307
 Tyr Gly Ala Asp Ser Glu Lys Glu Pro Glu Gly Ala Cys Ala Thr Glu
 55 60 65

ttc act gat ggt gtt gta gct ctt gaa tct gct ggg ttc aaa ctg acc 355
 Phe Thr Asp Gly Val Val Ala Leu Glu Ser Ala Gly Phe Lys Leu Thr
 70 75 80 85

ttt gac gaa tct gaa atg ggc aaa tac atg acc ggt atc aac gga gtt 403
 Phe Asp Glu Ser Glu Met Gly Lys Tyr Met Thr Gly Ile Asn Gly Val
 90 95 100

gtt cct gat tgg gtt gaa act gga act tac tgg agt tac tac tct ggt 451
 Val Pro Asp Trp Val Glu Thr Gly Thr Tyr Trp Ser Tyr Tyr Ser Gly
 105 110 115

gaa gtc gca gat gat tac agc gtg gac tac acc tac tac gag gtt ggt 499
 Glu Val Ala Asp Asp Tyr Ser Val Asp Tyr Thr Tyr Tyr Glu Val Gly
 120 125 130

gca tct aat tct gaa cct gaa ggt gga act gtt gag gct tgg gtt gtt 547
 Ala Ser Asn Ser Glu Pro Glu Gly Gly Thr Val Glu Ala Trp Val Val
 135 140 145

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ggc acc ggc gag gaa aca cca gca ctc gag act ctt cct gaa act cca 595
Gly Thr Gly Glu Glu Thr Pro Ala Leu Glu Thr Leu Pro Glu Thr Pro
150 155 160 165

gca gca acc gga tct tct gaa gac ggc ggc tgg att gca gtc atc gca 643
Ala Ala Thr Gly Ser Ser Glu Asp Gly Gly Trp Ile Ala Val Ile Ala
170 175 180

ggt ctt ctc gca ctg atc ggt ggt gga gtt gca gct ttg tac cag ggc 691
Gly Leu Leu Ala Leu Ile Gly Gly Gly Val Ala Ala Leu Tyr Gln Gly
185 190 195

ttg atc act atc cca ggt ctg gtt ctg cct aag ttt taagcaacct 737
Leu Ile Thr Ile Pro Gly Leu Val Leu Pro Lys Phe
200 205

aacctaaagc ttc 750

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<210> 330

<211> 209

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 330

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Leu Thr Ile Thr Phe Ser Arg Val Ala Leu Thr Thr Leu Ala Val Thr
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Ala Thr Thr Leu Ser Leu Ser Thr Ala Ala Asn Ala Gln Ser Ser Leu
20 25 30

Leu Asp Lys Thr Leu Asp Ala Arg Gln Cys Ile Asp Ala Asp Asn Val
35 40 45

Trp Val Ser Val Asp Tyr Gly Ala Asp Ser Glu Lys Glu Pro Glu Gly
50 55 60

Ala Cys Ala Thr Glu Phe Thr Asp Gly Val Val Ala Leu Glu Ser Ala
65 70 75 80

Gly Phe Lys Leu Thr Phe Asp Glu Ser Glu Met Gly Lys Tyr Met Thr
85 90 95

Gly Ile Asn Gly Val Val Pro Asp Trp Val Glu Thr Gly Thr Tyr Trp
100 105 110

Ser Tyr Tyr Ser Gly Glu Val Ala Asp Asp Tyr Ser Val Asp Tyr Thr
115 120 125

Tyr Tyr Glu Val Gly Ala Ser Asn Ser Glu Pro Glu Gly Gly Thr Val
130 135 140

Glu Ala Trp Val Val Gly Thr Gly Glu Glu Thr Pro Ala Leu Glu Thr
145 150 155 160

Leu Pro Glu Thr Pro Ala Ala Thr Gly Ser Ser Glu Asp Gly Gly Trp
165 170 175

Ile Ala Val Ile Ala Gly Leu Leu Ala Leu Ile Gly Gly Gly Val Ala
180 185 190

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Ala Leu Tyr Gln Gly Leu Ile Thr Ile Pro Gly Leu Val Leu Pro Lys
 195 200 205

Phe

<210> 331
 <211> 636
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(613)
 <223> FRXA00704

<400> 331
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 ttacagcggt tacagaattg aaaatgaaag gttcaaagcc ttg acc att act ttt 115
 Leu Thr Ile Thr Phe
 1 5
 agc cgc gtt gct ctg acc acc ctg gca gtc acc gca acc act ttg tcc 163
 Ser Arg Val Ala Leu Thr Thr Leu Ala Val Thr Ala Thr Thr Leu Ser
 10 15 20
 ctg agc act gct gcg aat gca cag tct tcc ttg ttg gat aag act ctt 211
 Leu Ser Thr Ala Ala Asn Ala Gln Ser Ser Leu Leu Asp Lys Thr Leu
 25 30 35
 gat gcc cgt cag tgc atc gat gca gac aac gtc tgg gtc tca gtt gac 259
 Asp Ala Arg Gln Cys Ile Asp Ala Asp Asn Val Trp Val Ser Val Asp
 40 45 50
 tat ggt gca gat tcc gaa aaa gaa cca gag ggc gca tgt gcc acc gag 307
 Tyr Gly Ala Asp Ser Glu Lys Glu Pro Glu Gly Ala Cys Ala Thr Glu
 55 60 65
 ttc act gat ggt gtt gta gct ctt gaa tct gct ggg ttc aaa ctg acc 355
 Phe Thr Asp Gly Val Val Ala Leu Glu Ser Ala Gly Phe Lys Leu Thr
 70 75 80 85
 ttt gac gaa tct gaa atg ggc aaa tac atg acc ggt atc aac gga gtt 403
 Phe Asp Glu Ser Glu Met Gly Lys Tyr Met Thr Gly Ile Asn Gly Val
 90 95 100
 gtt cct gat tgg gtt gaa act gga act tac tgg agt tac tac tct ggt 451
 Val Pro Asp Trp Val Glu Thr Gly Thr Tyr Trp Ser Tyr Ser Gly
 105 110 115
 gaa gtc gca gat gat tac agc gtg gac tac acc tac tac gag gtt ggt 499
 Glu Val Ala Asp Asp Tyr Ser Val Asp Tyr Thr Tyr Tyr Glu Val Gly
 120 125 130
 gca tct aat tct gaa cct gaa ggt gga act gtt gag gct tgg gtt gtt 547
 Ala Ser Asn Ser Glu Pro Glu Gly Gly Thr Val Glu Ala Trp Val Val
 135 140 145

ggc acc ggc gag gaa aca cca gca ctc gag act ctt tct gaa act tca 595
 Gly Thr Gly Glu Glu Thr Pro Ala Leu Glu Thr Leu Ser Glu Thr Ser
 150 155 160 165

gca gca acc gga tct tct taagacggcg gctggattgc agt 636
 Ala Ala Thr Gly Ser Ser
 170

<210> 332

<211> 171

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 332

Leu Thr Ile Thr Phe Ser Arg Val Ala Leu Thr Thr Leu Ala Val Thr
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Ala Thr Thr Leu Ser Leu Ser Thr Ala Ala Asn Ala Gln Ser Ser Leu
 20 25 30

Leu Asp Lys Thr Leu Asp Ala Arg Gln Cys Ile Asp Ala Asp Asn Val
 35 40 45

Trp Val Ser Val Asp Tyr Gly Ala Asp Ser Glu Lys Glu Pro Glu Gly
 50 55 60

Ala Cys Ala Thr Glu Phe Thr Asp Gly Val Val Ala Leu Glu Ser Ala
 65 70 75 80

Gly Phe Lys Leu Thr Phe Asp Glu Ser Glu Met Gly Lys Tyr Met Thr
 85 90 95

Gly Ile Asn Gly Val Val Pro Asp Trp Val Glu Thr Gly Thr Tyr Trp
 100 105 110

Ser Tyr Tyr Ser Gly Glu Val Ala Asp Asp Tyr Ser Val Asp Tyr Thr
 115 120 125

Tyr Tyr Glu Val Gly Ala Ser Asn Ser Glu Pro Glu Gly Gly Thr Val
 130 135 140

Glu Ala Trp Val Val Gly Thr Gly Glu Glu Thr Pro Ala Leu Glu Thr
 145 150 155 160

Leu Ser Glu Thr Ser Ala Ala Thr Gly Ser Ser
 165 170

<210> 333

<211> 819

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(796)

<223> RXN00712

<400> 333

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Met	Ser	Leu	Arg	Lys	5												
1																	
aat	ctc	gcc	ctc	gga	agc	agc	aca	gta	cta	ctc	aca	gcc	gtg	cta	agc	163	
Asn	Leu	Ala	Leu	Gly	Ser	Ser	Thr	Val	Leu	Leu	Thr	Ala	Val	Leu	Ser		
10																	
15																	
ggg	tgt	gtt	tcc	ctt	gat	gag	cgc	tcc	act	gat	aca	tcc	acg	gag	aat	211	
Gly	Cys	Val	Ser	Leu	Asp	Glu	Arg	Ser	Thr	Asp	Thr	Ser	Thr	Glu	Asn		
25																	
30																	
35																	
gtc	acc	acg	gta	act	gcc	aca	ctc	act	tcc	acc	gcc	gca	gca	gaa	ccc	259	
Val	Thr	Thr	Val	Thr	Ala	Thr	Leu	Thr	Ser	Thr	Ala	Ala	Ala	Glu	Pro		
40																	
45																	
50																	
acc	act	aga	acg	act	gtg	caa	agt	gct	aca	gaa	gcc	tcc	act	act	gca	307	
Thr	Thr	Arg	Thr	Thr	Val	Gln	Ser	Ala	Thr	Glu	Ala	Ser	Thr	Thr	Ala		
55																	
60																	
65																	
cga	gtg	caa	tgc	aat	ttg	gat	ccc	cgt	acc	tcg	gat	ttt	ggg	cca	tat	355	
Pro	Val	Gln	Cys	Asn	Leu	Asp	Pro	Arg	Thr	Ser	Asp	Phe	Gly	Pro	Tyr		
70																	
75																	
80																	
85																	
ctt	gca	caa	tct	cgc	acc	ccg	gtt	ggc	gag	cta	gct	gga	tct	gca	gat	403	
Leu	Ala	Gln	Ser	Arg	Thr	Pro	Val	Gly	Glu	Leu	Ala	Gly	Ser	Ala	Asp		
90																	
95																	
tcc	gtc	gtg	cag	gtt	cct	gac	tgg	ttc	tat	cac	ttc	caa	atg	ggc	gac	451	
Ser	Val	Val	Gln	Val	Pro	Asp	Trp	Phe	Tyr	His	Phe	Gln	Met	Gly	Asp		
105																	
110																	
115																	
aac	ggc	tac	gat	tcc	tgt	tcc	aag	ctc	agc	tat	gtg	gtt	ctc	aac	ggc	499	
Asn	Gly	Tyr	Asp	Ser	Cys	Ser	Lys	Leu	Ser	Tyr	Val	Val	Leu	Asn	Gly		
120																	
125																	
130																	
tcc	aat	gga	gac	gcc	gaa	cgt	tct	act	gga	acg	ggc	gct	gcg	atc	gcc	547	
Ser	Asn	Gly	Asp	Ala	Glu												

tat ctg ctg tagcccccac taaaaactct tga
Tyr Leu Leu
230

819

<210> 334
<211> 232
<212> PRT
<213> Corynebacterium glutamicum

<400> 334
Met Ser Leu Arg Lys Asn Leu Ala Leu Gly Ser Ser Thr Val Leu Leu
1 5 10 15
Thr Ala Val Leu Ser Gly Cys Val Ser Leu Asp Glu Arg Ser Thr Asp
20 25 30
Thr Ser Thr Glu Asn Val Thr Thr Val Thr Ala Thr Leu Thr Ser Thr
35 40 45
Ala Ala Ala Glu Pro Thr Thr Arg Thr Thr Val Gln Ser Ala Thr Glu
50 55 60
Ala Ser Thr Thr Ala Pro Val Gln Cys Asn Leu Asp Pro Arg Thr Ser
65 70 75 80
Asp Phe Gly Pro Tyr Leu Ala Gln Ser Arg Thr Pro Val Gly Glu Leu
85 90 95
Ala Gly Ser Ala Asp Ser Val Val Gln Val Pro Asp Trp Phe Tyr His
100 105 110
Phe Gln Met Gly Asp Asn Gly Tyr Asp Ser Cys Ser Lys Leu Ser Tyr
115 120 125
Val Val Leu Asn Gly Ser Asn Gly Asp Ala Glu Arg Ser Thr Gly Thr
130 135 140
Gly Ala Ala Ile Ala Asp Val Val Val Leu Phe Ile Asp Gly His Met
145 150 155 160
Val Ala Arg Pro Ala Pro Phe Glu Met Lys Thr Val Glu Ser Val Thr
165 170 175
Arg Val Ser Asp Ser Glu Ile Gln Val Val Tyr Gly His Ala Gly Arg
180 185 190
Ser Thr Ala Glu Gly Val Thr Asp Tyr Phe Thr Phe Asn Phe Phe Val
195 200 205
Asp Asn Gly Val Leu Ser Gly Arg Gly Asp Leu Pro Glu His Ile Asp
210 215 220
Thr His Met Arg Leu Tyr Leu Leu
225 230

<210> 335
<211> 572
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(549)

<223> FRXA00712

<400> 335

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Ala Ala Glu Pro Thr Thr Arg Thr Val Gln Ser Ala Thr Glu Ala
1 5 10 15

tcc act act gca cca gtg caa tgc aat ttg gat ccc cgt acc tcg gat 96
Ser Thr Thr Ala Pro Val Gln Cys Asn Leu Asp Pro Arg Thr Ser Asp
20 25 30

ttt ggg cca tat ctt gca caa tct cgc acc ccg gtt ggt gag cta gct 144
Phe Gly Pro Tyr Leu Ala Gln Ser Arg Thr Pro Val Glu Leu Ala
35 40 45

gga tct gca gat tcc gtc gtg cag gtt cct gac tgg ttc tat cac ttc 192
Gly Ser Ala Asp Ser Val Val Gln Val Pro Asp Trp Phe Tyr His Phe
50 55 60

caa atg ggc gac aac ggc tac gat tcc tgt tcc aag ctc agc tat gtg 240
Gln Met Gly Asp Asn Gly Tyr Asp Ser Cys Ser Lys Leu Ser Tyr Val
65 70 75

gtt ctc aac ggt tcc aat gga gac gcc gaa cgt tct act gga acg ggt 288
Val Leu Asn Gly Ser Asn Gly Asp Ala Glu Arg Ser Thr Gly Thr Gly
85 90 95

gct gcg atc gcc gac gtg gtg gtg ctg ttt atc gac ggc cat atg gtt 336
Ala Ala Ile Ala Asp Val Val Val Leu Phe Ile Asp Gly His Met Val
100 105 110

gct cgt cct gct cct ttt gaa atg aag acc gtg gaa tcc gtc acc aga 384
Ala Arg Pro Ala Pro Phe Glu Met Lys Thr Val Glu Ser Val Thr Arg
115 120 125

gtg tca gat tca gaa atc caa gtt gtt tac gga cat gcc ggc cga tct 432
Val Ser Asp Ser Glu Ile Gln Val Val Tyr Gly His Ala Gly Arg Ser
130 135 140

act gcc gaa ggt gtt acg gac tat ttc acc ttt aac ttc ttc gtt gac 480
Thr Ala Glu Gly Val Thr Asp Tyr Phe Thr Phe Asn Phe Phe Val Asp
145 150 155 160

aac ggc gtt ctt tca gga cgc ggc gat ctc cca gaa cac atc gat act 528
Asn Gly Val Leu Ser Gly Arg Gly Asp Leu Pro Glu His Ile Asp Thr
165 170 175

cac atg cgt cta tat ctg ctg tagcccccac taaaaactct tga 572
His Met Arg Leu Tyr Leu Leu
180

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<210> 336

<211> 183

<212> PRT

<213> Corynebacterium glutamicum

<400> 336

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Ser Thr Thr Ala Pro Val Gln Cys Asn Leu Asp Pro Arg Thr Ser Asp
 20 25 30

Phe Gly Pro Tyr Leu Ala Gln Ser Arg Thr Pro Val Gly Glu Leu Ala
 35 40 45

Gly Ser Ala Asp Ser Val Val Gln Val Pro Asp Trp Phe Tyr His Phe
 50 55 60

Gln Met Gly Asp Asn Gly Tyr Asp Ser Cys Ser Lys Leu Ser Tyr Val
 65 70 75 80

Val Leu Asn Gly Ser Asn Gly Asp Ala Glu Arg Ser Thr Gly Thr Gly
 85 90 95

Ala Ala Ile Ala Asp Val Val Val Leu Phe Ile Asp Gly His Met Val
 100 105 110

Ala Arg Pro Ala Pro Phe Glu Met Lys Thr Val Glu Ser Val Thr Arg
 115 120 125

Val Ser Asp Ser Glu Ile Gln Val Val Tyr Gly His Ala Gly Arg Ser
 130 135 140

Thr Ala Glu Gly Val Thr Asp Tyr Phe Thr Phe Asn Phe Phe Val Asp
 145 150 155 160

Asn Gly Val Leu Ser Gly Arg Gly Asp Leu Pro Glu His Ile Asp Thr
 165 170 175

His Met Arg Leu Tyr Leu Leu
 180

<210> 337

<211> 789

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(766)

<223> RXN00720

<400> 337

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gtcgaagacc agcactccag attcaaggaa cttataaaac atg gca tca cgc cgc 115
 Met Ala Ser Pro Arg
 1 5

cgc cca cag gtt gca gca cca cgc atc aaa gaa ctt cgc cta aca ggc 163
 Arg Pro Gln Val Ala Ala Pro Arg Ile Lys Glu Leu Arg Leu Thr Gly
 10 15 20

ctt gac aac gct gac cct caa gac atc gaa tcg aat gag cag ata gag 211
 Leu Asp Asn Ala Asp Pro Gln Asp Ile Glu Ser Asn Glu Gln Ile Glu

	25	30	35	
tca tgc cgt ttt aac gag gcc gag ctt tcc gaa cgc gat ctt tct ggt	259			
Ser Cys Arg Phe Asn Glu Ala Glu Leu Ser Glu Arg Asp Leu Ser Gly				
40 45 50				
gct ggt ttc att gaa tgt gaa ttc ctt ggg ctg gaa gca cac gaa acc	307			
Ala Gly Phe Ile Glu Cys Glu Phe Leu Gly Leu Glu Ala His Glu Thr				
55 60 65				
gag cta cgc cgg gct caa ttc gtg gaa aca cgc atc gaa aga gcc aat	355			
Glu Leu Arg Arg Ala Gln Phe Val Glu Thr Arg Ile Glu Arg Ala Asn				
70 75 80 85				
gct cca tct ttt aag gca gcc cgc tcc atc tgg cgc aac gca acg att	403			
Ala Pro Ser Phe Lys Ala Ala Arg Ser Ile Trp Arg Asn Ala Thr Ile				
90 95 100				
tcc gac tcc cgc ttt ggt gcc gtc gaa atg tat gaa gca acc gtc caa	451			
Ser Asp Ser Arg Phe Gly Ala Val Glu Met Tyr Glu Ala Thr Val Gln				
105 110 115				
gct ttg aaa atc tct gat tct aag ctg tcg ttt gtc aat ctg cgg ggt	499			
Ala Leu Lys Ile Ser Asp Ser Lys Leu Ser Phe Val Asn Leu Arg Gly				
120 125 130				
gca tcg tta cgg gat gtg ctc ttt gag aac tgt gtc atc gac gag ctt	547			
Ala Ser Leu Arg Asp Val Leu Phe Glu Asn Cys Val Ile Asp Glu Leu				
135 140 145				
gat ctt ggc caa gcc aga gca gaa cgc atc gct ttt aaa gac tgc acg	595			
Asp Leu Gly Gln Ala Arg Ala Glu Arg Ile Ala Phe Lys Asp Cys Thr				
150 155 160 165				
gtg cat tcg ctc acc ttt gat cat gcc gtg ctc agc aat gtg gat ctt	643			
Val His Ser Leu Thr Phe Asp His Ala Val Leu Ser Asn Val Asp Leu				
170 175 180				
cgc ggt tta gat atc gag cgc atc agt ggc gtg gag tcc atg tcc gga	691			
Arg Gly Leu Asp Ile Glu Arg Ile Ser Gly Val Glu Ser Met Ser Gly				
185 190 195				
acc gtg atc tca tcc ctg cag gct gct gac ctg tcg gga gca ttt gca	739			
Thr Val Ile Ser Ser Leu Gln Ala Ala Asp Leu Ser Gly Ala Phe Ala				
200 205 210				
cgg cat tta gga att act gta aac gat tagaaatccg ctcttttgaa	786			
Arg His Leu Gly Ile Thr Val Asn Asp				
215 220				
caa	789			
<210> 338				
<211> 222				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 338				
Met Ala Ser Pro Arg Arg Pro Gln Val Ala Ala Pro Arg Ile Lys Glu				
1 5 10 15				

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Leu Arg Leu Thr Gly Leu Asp Asn Ala Asp Pro Gln Asp Ile Glu Ser
      20                      25                      30

Asn Glu Gln Ile Glu Ser Cys Arg Phe Asn Glu Ala Glu Leu Ser Glu
      35                      40                      45

Arg Asp Leu Ser Gly Ala Gly Phe Ile Glu Cys Glu Phe Leu Gly Leu
      50                      55                      60

Glu Ala His Glu Thr Glu Leu Arg Arg Ala Gln Phe Val Glu Thr Arg
      65                      70                      75                      80

Ile Glu Arg Ala Asn Ala Pro Ser Phe Lys Ala Ala Arg Ser Ile Trp
      85                      90                      95

Arg Asn Ala Thr Ile Ser Asp Ser Arg Phe Gly Ala Val Glu Met Tyr
      100                     105                     110

Glu Ala Thr Val Gln Ala Leu Lys Ile Ser Asp Ser Lys Leu Ser Phe
      115                     120                     125

Val Asn Leu Arg Gly Ala Ser Leu Arg Asp Val Leu Phe Glu Asn Cys
      130                     135                     140

Val Ile Asp Glu Leu Asp Leu Gly Gln Ala Arg Ala Glu Arg Ile Ala
      145                     150                     155                     160

Phe Lys Asp Cys Thr Val His Ser Leu Thr Phe Asp His Ala Val Leu
      165                     170                     175

Ser Asn Val Asp Leu Arg Gly Leu Asp Ile Glu Arg Ile Ser Gly Val
      180                     185                     190

Glu Ser Met Ser Gly Thr Val Ile Ser Ser Leu Gln Ala Ala Asp Leu
      195                     200                     205

Ser Gly Ala Phe Ala Arg His Leu Gly Ile Thr Val Asn Asp
      210                     215                     220

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<210> 339

<211> 789

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(766)

<223> FRXA00720

<400> 339

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gtcgaagacc agcactccag attcaaggaa cttataaaac atg gca tca ccg cgc 115
              Met Ala Ser Pro Arg
              1                      5

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cgc cca cag gtt gca gca cca cgc atc aaa gaa ctt cgc cta aca ggc 163
Arg Pro Gln Val Ala Ala Pro Arg Ile Lys Glu Leu Arg Leu Thr Gly
      10                      15                      20

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ctt gac aac gct gac cct caa gac atc gaa tcg aat gag cag ata gag 211
 Leu Asp Asn Ala Asp Pro Gln Asp Ile Glu Ser Asn Glu Gln Ile Glu
 25 30 35
 tca tgc cgt ttt aac gag gcc gag ctt tcc gaa cgc gat ctt tct ggt 259
 Ser Cys Arg Phe Asn Glu Ala Glu Leu Ser Glu Arg Asp Leu Ser Gly
 40 45 50
 gct ggt ttc att gaa tgt gaa ttc ctt ggg ctg gaa gca cac gaa acc 307
 Ala Gly Phe Ile Glu Cys Glu Phe Leu Gly Leu Glu Ala His Glu Thr
 55 60 65
 gag cta cgc cgg gct caa ttc gtg gaa aca cgc atc gaa aga gcc aat 355
 Glu Leu Arg Arg Ala Gln Phe Val Glu Thr Arg Ile Glu Arg Ala Asn
 70 75 80 85
 gct cca tct ttt aag gca gcc cgc tcc atc tgg cgc aac gca acg att 403
 Ala Pro Ser Phe Lys Ala Ala Arg Ser Ile Trp Arg Asn Ala Thr Ile
 90 95 100
 tcc gac tcc cgc ttt ggt gcc gtc gaa atg tat gaa gca acc gtc caa 451
 Ser Asp Ser Arg Phe Gly Ala Val Glu Met Tyr Glu Ala Thr Val Gln
 105 110 115
 gct ttg aaa atc tct gat tct aag ctg tcg ttt gtc aat ctg cgg ggt 499
 Ala Leu Lys Ile Ser Asp Ser Lys Leu Ser Phe Val Asn Leu Arg Gly
 120 125 130
 gca tcg tta cgg gat gtg ctc ttt gag aac tgt gtc atc gac gag ctt 547
 Ala Ser Leu Arg Asp Val Leu Phe Glu Asn Cys Val Ile Asp Glu Leu
 135 140 145
 gat ctt ggc caa gcc aga gca gaa cgc atc gct ttt aaa gac tgc acg 595
 Asp Leu Gly Gln Ala Arg Ala Glu Arg Ile Ala Phe Lys Asp Cys Thr
 150 155 160 165
 gtg cat tcg ctc acc ttt gat cat gcc gtg ctc agc aat gtg gat ctt 643
 Val His Ser Leu Thr Phe Asp His Ala Val Leu Ser Asn Val Asp Leu
 170 175 180
 cgc ggt tta gat atc gag cgc atc agt ggc gtg gag tcc atg tcc gga 691
 Arg Gly Leu Asp Ile Glu Arg Ile Ser Gly Val Glu Ser Met Ser Gly
 185 190 195
 acc gtg atc tca tcc ctg cag gct gct gac ctg tcg gga gca ttt gca 739
 Thr Val Ile Ser Ser Leu Gln Ala Ala Asp Leu Ser Gly Ala Phe Ala
 200 205 210
 cgg cat tta gga att act gta aac gat tagaaatcgg ctcttttgaa 786
 Arg His Leu Gly Ile Thr Val Asn Asp
 215 220
 caa 789

<210> 340

<211> 222

<212> PRT

<213> Corynebacterium glutamicum

<400> 340

Met Ala Ser Pro Arg Arg Pro Gln Val Ala Ala Pro Arg Ile Lys Glu
 1 5 10 15

Leu Arg Leu Thr Gly Leu Asp Asn Ala Asp Pro Gln Asp Ile Glu Ser
 20 25 30

Asn Glu Gln Ile Glu Ser Cys Arg Phe Asn Glu Ala Glu Leu Ser Glu
 35 40 45

Arg Asp Leu Ser Gly Ala Gly Phe Ile Glu Cys Glu Phe Leu Gly Leu
 50 55 60

Glu Ala His Glu Thr Glu Leu Arg Arg Ala Gln Phe Val Glu Thr Arg
 65 70 75 80

Ile Glu Arg Ala Asn Ala Pro Ser Phe Lys Ala Ala Arg Ser Ile Trp
 85 90 95

Arg Asn Ala Thr Ile Ser Asp Ser Arg Phe Gly Ala Val Glu Met Tyr
 100 105 110

Glu Ala Thr Val Gln Ala Leu Lys Ile Ser Asp Ser Lys Leu Ser Phe
 115 120 125

Val Asn Leu Arg Gly Ala Ser Leu Arg Asp Val Leu Phe Glu Asn Cys
 130 135 140

Val Ile Asp Glu Leu Asp Leu Gly Gln Ala Arg Ala Glu Arg Ile Ala
 145 150 155 160

Phe Lys Asp Cys Thr Val His Ser Leu Thr Phe Asp His Ala Val Leu
 165 170 175

Ser Asn Val Asp Leu Arg Gly Leu Asp Ile Glu Arg Ile Ser Gly Val
 180 185 190

Glu Ser Met Ser Gly Thr Val Ile Ser Ser Leu Gln Ala Ala Asp Leu
 195 200 205

Ser Gly Ala Phe Ala Arg His Leu Gly Ile Thr Val Asn Asp
 210 215 220

<210> 341

<211> 1088

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1065)

<223> RXN00722

<400> 341

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 Ala Val Leu Arg Glu Ala Gly Val Val Asp Ala Gly Gly Gln Gly Leu
 1 5 10 15

gtt att ctc ctg gag tcc ctg gcc gaa caa atc aac gga aac cca cct 96
 Val Ile Leu Leu Glu Ser Leu Ala Glu Gln Ile Asn Gly Asn Pro Pro

	20		25		30	
	cac cat cca tgc cac cac agt gaa cca gcc gaa gaa ccc tcc ttc cac	144				
	His His Pro Ser His His Ser Glu Pro Ala Glu Glu Pro Ser Phe His					
	35 40 45					
	ggc aaa acc ggc gac cta gaa gtg atg ttt tac att gca tgc gac tcc	192				
	Gly Lys Thr Gly Asp Leu Glu Val Met Phe Tyr Ile Ala Cys Asp Ser					
	50 55 60					
	gcg caa aca ctc gat gct ctc cac aac gaa ctt gaa aca cta ggc gac	240				
	Ala Gln Thr Leu Asp Ala Leu His Asn Glu Leu Glu Thr Leu Gly Asp					
	65 70 75 80					
	agc ctg ctc atc gcc cga gaa acc aat acc cgc ggc acc gtt cac atc	288				
	Ser Leu Leu Ile Ala Arg Glu Thr Asn Thr Arg Gly Thr Val His Ile					
	85 90 95					
	cat tgc cgc cgg gca gcc gag gtc atc caa aaa gca ttt gcc gca gga	336				
	His Ser Arg Arg Ala Gly Glu Val Ile Gln Lys Ala Phe Ala Ala Gly					
	100 105 110					
	gac gtc agc gaa ctc cgc ctt gaa atc ctc ccc gat act tcc ggc agc	384				
	Asp Val Ser Glu Leu Arg Leu Glu Ile Leu Pro Asp Thr Ser Gly Ser					
	115 120 125					
	ttc acg gaa gaa cca cgc cgg gtc ctc atg gct gtc gca cct gac ggc	432				
	Phe Thr Glu Glu Pro Arg Arg Val Leu Met Ala Val Ala Pro Asp Gly					
	130 135 140					
	ctg gtg gcg gag ctg tac cgc agc gct gga gtg aag gtg gtg gcc cgc	480				
	Leu Val Ala Glu Leu Tyr Arg Ser Ala Gly Val Lys Val Val Ala Arg					
	145 150 155 160					
	aac atc gcg caa tcc aag tct gat gat gtg gtg gca aag atc gtt tcc	528				
	Asn Ile Ala Gln Ser Lys Ser Asp Asp Val Val Ala Lys Ile Val Ser					
	165 170 175					
	atc gcg cgc aag tct ggt gcc gat gag gtg atc ttg ctg ccc aac ggt	576				
	Ile Ala Arg Lys Ser Gly Ala Asp Glu Val Ile Leu Leu Pro Asn Gly					
	180 185 190					
	ctt ttg acc aag cgt gag ctg gtt tcc att gag cgt tcc agc cat gct	624				
	Leu Leu Thr Lys Arg Glu Leu Val Ser Ile Glu Arg Ser Ser His Ala					
	195 200 205					
	ttt gag caa agt gtg gtt att ttg cct act gcc acg ttg gtt gca ggt	672				
	Phe Glu Gln Ser Val Val Ile Leu Pro Thr Ala Thr Leu Val Ala Gly					
	210 215 220					
	ctt gca gcg gtg tcc gtt cat gag cca gcg caa ccc ctg gcg gtg gat	720				
	Leu Ala Ala Val Ser Val His Glu Pro Ala Gln Pro Leu Ala Val Asp					
	225 230 235 240					
	tcc tat gcc atg gca gag gcc gcc ggt tcc atg cgc acg gcc acg atc	768				
	Ser Tyr Ala Met Ala Glu Ala Ala Gly Ser Met Arg Thr Ala Thr Ile					
	245 250 255					
	cgc gcc gcc acc agc gcc gcg ctc acc cag gcc ggc gca tgc tcc aag	816				
	Arg Ala Ala Thr Ser Ala Ala Leu Thr Gln Ala Gly Ala Cys Ser Lys					
	260 265 270					

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ggt gat cta tta agc ttc atc ggc cgg gag ata gct ctg gtc tcc gag      864
Gly Asp Leu Leu Ser Phe Ile Gly Pro Glu Ile Ala Leu Val Ser Glu
      275                      280                      285

gag ctc aac gac gcg cta tcg cgc acc gct tta agg ctt ctc gac ggc      912
Glu Leu Asn Asp Ala Leu Ser Arg Thr Ala Leu Arg Leu Leu Asp Gly
      290                      295                      300

tcc agc gag caa att acc ctt ctc ata gcg caa gac cgt cag tcc gcc      960
Ser Ser Glu Gln Ile Thr Leu Leu Ile Ala Gln Asp Arg Gln Ser Ala
      305                      310                      315

ttc gac gaa gat gtt ttc cgc cgt ggc ctg gga act cac acg gat gtg      1008
Phe Asp Glu Asp Val Phe Arg Arg Gly Leu Gly Thr His Thr Asp Val
      325                      330                      335

gag atc acg gtc tat cct gct act gga atg gag aat ctg gta gag atc      1056
Glu Ile Thr Val Tyr Pro Ala Thr Gly Met Glu Asn Leu Val Glu Ile
      340                      345                      350

gga gtg gag tagccacatg ttgggttggc atg      1088
Gly Val Glu
      355

<210> 342
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<212> PRT
<213> Corynebacterium glutamicum

<400> 342
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Val Ile Leu Leu Glu Ser Leu Ala Glu Gln Ile Asn Gly Asn Pro Pro
  20                      25                      30

His His Pro Ser His His Ser Glu Pro Ala Glu Glu Pro Ser Phe His
  35                      40                      45

Gly Lys Thr Gly Asp Leu Glu Val Met Phe Tyr Ile Ala Cys Asp Ser
  50                      55                      60

Ala Gln Thr Leu Asp Ala Leu His Asn Glu Leu Glu Thr Leu Gly Asp
  65                      70                      75                      80

Ser Leu Leu Ile Ala Arg Glu Thr Asn Thr Arg Gly Thr Val His Ile
  85                      90                      95

His Ser Arg Arg Ala Gly Glu Val Ile Gln Lys Ala Phe Ala Ala Gly
  100                      105                      110

Asp Val Ser Glu Leu Arg Leu Glu Ile Leu Pro Asp Thr Ser Gly Ser
  115                      120                      125

Phe Thr Glu Glu Pro Arg Arg Val Leu Met Ala Val Ala Pro Asp Gly
  130                      135                      140

Leu Val Ala Glu Leu Tyr Arg Ser Ala Gly Val Lys Val Val Ala Arg
  145                      150                      155                      160

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Asn Ile Ala Gln Ser Lys Ser Asp Asp Val Val Ala Lys Ile Val Ser
      165                      170                      175

Ile Ala Arg Lys Ser Gly Ala Asp Glu Val Ile Leu Leu Pro Asn Gly
      180                      185                      190

Leu Leu Thr Lys Arg Glu Leu Val Ser Ile Glu Arg Ser Ser His Ala
      195                      200                      205

Phe Glu Gln Ser Val Val Ile Leu Pro Thr Ala Thr Leu Val Ala Gly
      210                      215                      220

Leu Ala Ala Val Ser Val His Glu Pro Ala Gln Pro Leu Ala Val Asp
      225                      230                      235

Ser Tyr Ala Met Ala Glu Ala Ala Gly Ser Met Arg Thr Ala Thr Ile
      245                      250                      255

Arg Ala Ala Thr Ser Ala Ala Leu Thr Gln Ala Gly Ala Cys Ser Lys
      260                      265                      270

Gly Asp Leu Leu Ser Phe Ile Gly Pro Glu Ile Ala Leu Val Ser Glu
      275                      280                      285

Glu Leu Asn Asp Ala Leu Ser Arg Thr Ala Leu Arg Leu Leu Asp Gly
      290                      295                      300

Ser Ser Glu Gln Ile Thr Leu Leu Ile Ala Gln Asp Arg Gln Ser Ala
      305                      310                      315

Phe Asp Glu Asp Val Phe Arg Arg Gly Leu Gly Thr His Thr Asp Val
      325                      330                      335

Glu Ile Thr Val Tyr Pro Ala Thr Gly Met Glu Asn Leu Val Glu Ile
      340                      345                      350

Gly Val Glu
      355

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<210> 343

<211> 542

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (16)..(519)·

<223> FRXA00722

<400> 343

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      1                      5                      10

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gtt tcc att gag cgt tcc agc cat gct ttt gag caa agt gtg gtt att      99
Val Ser Ile Glu Arg Ser Ser His Ala Phe Glu Gln Ser Val Val Ile
      15                      20                      25

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ttg cct act gcc acg ttg gtt gca ggt ctt gca gcg gtg tcc gtt cat      147

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Leu Pro Thr Ala Thr Leu Val Ala Gly Leu Ala Ala Val Ser Val His
 30 35 40
 gag cca gcg caa ccc ctg gcg gtg gat tcc tat gcc atg gca gag gcc 195
 Glu Pro Ala Gln Pro Leu Ala Val Asp Ser Tyr Ala Met Ala Glu Ala
 45 50 55 60
 gcc ggt tcc atg cgc acg gcc acg atc cgc gcc acc agc gcc gcg 243
 Ala Gly Ser Met Arg Thr Ala Thr Ile Arg Ala Ala Thr Ser Ala Ala
 65 70 75
 ctc acc cag gcc ggc gca tgc tcc aag ggt gat cta tta agc ttc atc 291
 Leu Thr Gln Ala Gly Ala Cys Ser Lys Gly Asp Leu Leu Ser Phe Ile
 80 85 90
 ggc ccg gag ata gct ctg gtc tcc gag gag ctc aac gac gcg cta tcg 339
 Gly Pro Glu Ile Ala Leu Val Ser Glu Glu Leu Asn Asp Ala Leu Ser
 95 100 105
 cgc acc gct tta agg ctt ctc gac ggc tcc agc gag caa att acc ctt 387
 Arg Thr Ala Leu Arg Leu Leu Asp Gly Ser Ser Glu Gln Ile Thr Leu
 110 115 120
 ctc ata gcg caa gac cgt cag tcc gcc ttc gac gaa gat gtt ttc cgc 435
 Leu Ile Ala Gln Asp Arg Gln Ser Ala Phe Asp Glu Asp Val Phe Arg
 125 130 135 140
 cgt ggc ctg gga act cac acg gat gtg gag atc acg gtc tat cct gct 483
 Arg Gly Leu Gly Thr His Thr Asp Val Glu Ile Thr Val Tyr Pro Ala
 145 150 155
 act gga atg gag aat ctg gta gag atc gga gtg gag tagccacatg 529
 Thr Gly Met Glu Asn Leu Val Glu Ile Gly Val Glu
 160 165
 ttgggttggc atg 542
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 <211> 168
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 344
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 Arg Ser Ser His Ala Phe Glu Gln Ser Val Val Ile Leu Pro Thr Ala
 20 25 30
 Thr Leu Val Ala Gly Leu Ala Ala Val Ser Val His Glu Pro Ala Gln
 35 40 45
 Pro Leu Ala Val Asp Ser Tyr Ala Met Ala Glu Ala Ala Gly Ser Met
 50 55 60
 Arg Thr Ala Thr Ile Arg Ala Ala Thr Ser Ala Ala Leu Thr Gln Ala
 65 70 75 80
 Gly Ala Cys Ser Lys Gly Asp Leu Leu Ser Phe Ile Gly Pro Glu Ile
 85 90 95

Ala Leu Val Ser Glu Glu Leu Asn Asp Ala Leu Ser Arg Thr Ala Leu
100 105 110

Arg Leu Leu Asp Gly Ser Ser Glu Gln Ile Thr Leu Leu Ile Ala Gln
115 120

Asp Arg Gln Ser Ala Phe Asp Glu Asp Val Phe Arg Arg Gly Leu Gly
130 135 140

Thr His Thr Asp Val Glu Ile Thr Val Tyr Pro Ala Thr Gly Met Glu
145 150 155 160

Asn Leu Val Glu Ile Gly Val Glu
165

<210> 345

<211> 1101

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1078)

<223> RXN00729

<400> 345

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gcgttttggc agagcctaaa gaaagataat tggattacct atg agc gcc acc aac 115
Met Ser Ala Thr Asn
1 5

cct gat gcc cta gac gtg cag cac gtc tat ccc atc aag acg aaa aag 163
Pro Asp Ala Leu Asp Val Gln His Val Tyr Pro Ile Lys Thr Lys Lys
10 15 20

act cca ctt gcg gtg att ttc aac atc att agc ggt ggt ttg att gga 211
Thr Pro Leu Ala Val Ile Phe Asn Ile Ile Ser Gly Gly Leu Ile Gly
25 30 35

atg gcg gag ttg gtg cca gga att tcc ggc gga act gtc gct ttg gtt 259
Met Ala Glu Leu Val Pro Gly Ile Ser Gly Gly Thr Val Ala Leu Val
40 45 50

ctt gga att tat gag cgc gca ctg cac aac ggt gat ctc ctc att gat 307
Leu Gly Ile Tyr Glu Arg Ala Leu His Asn Gly Asp Leu Leu Ile Asp
55 60 65

ctg atc aag gtg ttg atc aag gac cgc tcg aag gtt aag gaa gct gcg 355
Leu Ile Lys Val Leu Ile Lys Asp Arg Ser Lys Val Lys Glu Ala Ala
70 75 80 85

gcg aaa atc gac tgg tgg ttc ctc ggc gct atc ggc gtt ggc atg gtc 403
Ala Lys Ile Asp Trp Trp Phe Leu Gly Ala Ile Gly Val Gly Met Val
90 95 100

gtg atg gtc ttc tcg atg tca tcg att ttg cat aca gtt gtt gag gac 451
Val Met Val Phe Ser Met Ser Ser Ile Leu His Thr Val Val Glu Asp
105 110 115

tac cca gag atc act cgc ggt ctg ttc ctt gga atg gtt gcc gtg tct 499
 Tyr Pro Glu Ile Thr Arg Gly Leu Phe Leu Gly Met Val Ala Val Ser
 120 125 130

atc ctt gtt ccg ttg gga atg atg gat atg cgg gat gcc aag aag cgc 547
 Ile Leu Val Pro Leu Gly Met Met Asp Met Arg Asp Ala Lys Lys Arg
 135 140 145

ctg gca atc gtc atc ccg cta ttt ata atc tgc gcc atg ctg gga ttc 595
 Leu Ala Ile Val Ile Pro Leu Phe Ile Ile Cys Ala Met Leu Gly Phe
 150 155 160 165

ttt gga aca tcc ttc act agt gcg cct cgc acc gat cct tca ctg atc 643
 Phe Gly Thr Ser Phe Thr Ser Ala Pro Arg Thr Asp Pro Ser Leu Ile
 170 175 180

ttt gtc ttc atc tgt gct gcg atc gct gtg tgt gct ctt gtt ctt cct 691
 Phe Val Phe Ile Cys Ala Ala Ile Ala Val Cys Ala Leu Leu Pro
 185 190 195

ggt gtt tca gga tca ttc ttc ttg ctg gcg gtc ggt atg tac gcg cca 739
 Gly Val Ser Gly Ser Phe Phe Leu Leu Ala Val Gly Met Tyr Ala Pro
 200 205 210

atc atg gaa tct ctg tcc aac cgt gac ttg tgc gtc atc gcc gtg ttc 787
 Ile Met Glu Ser Leu Ser Asn Arg Asp Leu Ser Val Ile Gly Val Phe
 215 220 225

ttg ctt ggc gcg ctc acc ggt gtg atc ttg ttt gtg aag gtt ttg tct 835
 Leu Leu Gly Ala Leu Thr Gly Val Ile Leu Phe Val Lys Val Leu Ser
 230 235 240 245

tat gtt ctc gag cac cac cgc acc atc acg ctg acc atc atg gct ggt 883
 Tyr Val Leu Glu His His Arg Thr Ile Thr Leu Thr Ile Met Ala Gly
 250 255 260

ctg atg ctg ggt tca ctt cgt gcg ctg tgg cct tgg cag gac ggt gac 931
 Leu Met Leu Gly Ser Leu Arg Ala Leu Trp Pro Trp Gln Asp Gly Asp
 265 270 275

gct aat cta ctt gct cct gcc gat aac gcc gtg atg att ttc agc atc 979
 Ala Asn Leu Leu Ala Pro Gly Asp Asn Ala Val Met Ile Phe Ser Ile
 280 285 290

atc att ctt ggt gcc gcg att gtc gct gct ttg atg ttt gct gag cgt 1027
 Ile Ile Leu Gly Gly Ala Ile Val Ala Ala Leu Met Phe Ala Glu Arg
 295 300 305

gtg tct tcc aag aac att gat tct gag acc gtg gca gaa gag cac ccg 1075
 Val Ser Ser Lys Asn Ile Asp Ser Glu Thr Val Ala Glu Glu His Pro
 310 315 320 325

cgc taaataagaa ctccacaag aaa 1101
 Arg

<210> 346

<211> 326

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 346

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Ile Lys Thr Lys Lys Thr Pro Leu Ala Val Ile Phe Asn Ile Ile Ser
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Gly Gly Leu Ile Gly Met Ala Glu Leu Val Pro Gly Ile Ser Gly Gly
 35             40             45

Thr Val Ala Leu Val Leu Gly Ile Tyr Glu Arg Ala Leu His Asn Gly
 50             55             60

Asp Leu Leu Ile Asp Leu Ile Lys Val Leu Ile Lys Asp Arg Ser Lys
 65             70             75             80

Val Lys Glu Ala Ala Lys Ile Asp Trp Trp Phe Leu Gly Ala Ile
 85             90             95

Gly Val Gly Met Val Val Met Val Phe Ser Met Ser Ser Ile Leu His
100             105             110

Thr Val Val Glu Asp Tyr Pro Glu Ile Thr Arg Gly Leu Phe Leu Gly
115             120             125

Met Val Ala Val Ser Ile Leu Val Pro Leu Gly Met Met Asp Met Arg
130             135             140

Asp Ala Lys Lys Arg Leu Ala Ile Val Ile Pro Leu Phe Ile Ile Cys
145             150             155             160

Ala Met Leu Gly Phe Phe Gly Thr Ser Phe Thr Ser Ala Pro Arg Thr
165             170             175

Asp Pro Ser Leu Ile Phe Val Phe Ile Cys Ala Ala Ile Ala Val Cys
180             185             190

Ala Leu Val Leu Pro Gly Val Ser Gly Ser Phe Phe Leu Leu Ala Val
195             200             205

Gly Met Tyr Ala Pro Ile Met Glu Ser Leu Ser Asn Arg Asp Leu Ser
210             215             220

Val Ile Gly Val Phe Leu Leu Gly Ala Leu Thr Gly Val Ile Leu Phe
225             230             235             240

Val Lys Val Leu Ser Tyr Val Leu Glu His His Arg Thr Ile Thr Leu
245             250             255

Thr Ile Met Ala Gly Leu Met Leu Gly Ser Leu Arg Ala Leu Trp Pro
260             265             270

Trp Gln Asp Gly Asp Ala Asn Leu Leu Ala Pro Gly Asp Asn Ala Val
275             280             285

Met Ile Phe Ser Ile Ile Ile Leu Gly Gly Ala Ile Val Ala Ala Leu
290             295             300

Met Phe Ala Glu Arg Val Ser Ser Lys Asn Ile Asp Ser Glu Thr Val

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<223> FRXA00729			
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 atg gtt gcc gtg tct atc ctt gtt ccg ttg gga atg atg gat atg cgg			
Met Val Ala Val Ser Ile Leu Val Pro Leu Gly Met Met Asp Met Arg			96
	20	25	30
 gat gcc aag aag cgc ctc gca atc gtc atc ccg cta ttt ata atc tgc			
Asp Ala Lys Lys Arg Leu Ala Ile Val Ile Pro Leu Phe Ile Ile Cys			144
	35	40	45
 gcc atg ctg gga ttc ttt gga aca tcc ttc act agt gcg cct cgc acc			
Ala Met Leu Leu Gly Phe Phe Gly Thr Ser Phe Thr Ser Ala Pro Arg Thr			192
	50	55	60
 gat cct tca ctg atc ttt gtc ttc atc tgt gct gcg atc gct gtg tgt			
Asp Pro Ser Leu Ile Phe Val Phe Ile Cys Ala Ala Ile Ala Val Cys			240
	65	70	75
 gct ctt gtt ctt cct ggt gtt tca gga tca ttc ttc ttg ctg gcg gtc			
Ala Leu Val Leu Pro Gly Val Ser Gly Ser Phe Phe Leu Leu Ala Val			288
	85	90	95
 ggt atg tac gcg cca atc atg gaa tct ctg tcc aac cgt gac ttg tgg			
Gly Met Tyr Ala Pro Ile Met Glu Ser Leu Ser Asn Arg Asp Leu Ser			336
	100	105	110
 gtc atc ggc gtg ttc ttg ctt ggc gcg ctc acc ggt gtg atc ttg ttt			
Val Ile Gly Val Phe Leu Leu Gly Ala Leu Thr Gly Val Ile Leu Phe			384
	115	120	125
 gtg aag gtt ttg tct tat gtt ctc gag cac cac cgc acc atc acg ctg			
Val Lys Val Val Leu Ser Tyr Val Leu Leu Glu His His Arg Thr Ile Thr Leu			432
	130	135	140
 acc atc atg gct ggt ctc atg ctg ggt tca ctt cgt gcg ctg tgg cct			
Thr Ile Met Ala Gly Leu Met Leu Gly Ser Leu Arg Ala Leu Trp Pro			480
	145	150	155
 tgg cag gac ggt gac gct aat cta ctt gct cct gcc gat aac gcc gtg			
Trp Gln Asp Gly Asp Ala Asn Leu Leu Ala Pro Gly Asp Asn Ala Val			528
	165	170	175

atg att ttc agc atc atc att ctt ggt ggc gcg att gtc gct gct ttg 576
Met Ile Phe Ser Ile Ile Ile Leu Gly Gly Ala Ile Val Ala Ala Leu
180 185 190

atg ttt gct gag cgt gtg tct tcc aag aac att gat tct gag acc gtg 624
Met Phe Ala Glu Arg Val Ser Ser Lys Asn Ile Asp Ser Glu Thr Val
195 200 205

gca gaa gag cac cgg cgc taaataagaa ctccacaaag aaa 665
Ala Glu Glu His Pro Arg
210

<210> 348

<211> 214

<212> PRT

<213> Corynebacterium glutamicum

<400> 348

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20 25 30

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35 40 45

Ala Met Leu Gly Phe Phe Gly Thr Ser Phe Thr Ser Ala Pro Arg Thr
50 55 60

Asp Pro Ser Leu Ile Phe Val Phe Ile Cys Ala Ala Ile Ala Val Cys
65 70 75 80

Ala Leu Val Leu Pro Gly Val Ser Gly Ser Phe Phe Leu Leu Ala Val
85 90 95

Gly Met Tyr Ala Pro Ile Met Glu Ser Leu Ser Asn Arg Asp Leu Ser
100 105 110

Val Ile Gly Val Phe Leu Leu Gly Ala Leu Thr Gly Val Ile Leu Phe
115 120 125

Val Lys Val Leu Ser Tyr Val Leu Glu His His Arg Thr Ile Thr Leu
130 135 140

Thr Ile Met Ala Gly Leu Met Leu Gly Ser Leu Arg Ala Leu Trp Pro
145 150 155 160

Trp Gln Asp Gly Asp Ala Asn Leu Leu Ala Pro Gly Asp Asn Ala Val
165 170 175

Met Ile Phe Ser Ile Ile Ile Leu Gly Gly Ala Ile Val Ala Ala Leu
180 185 190

Met Phe Ala Glu Arg Val Ser Ser Lys Asn Ile Asp Ser Glu Thr Val
195 200 205

Ala Glu Glu His Pro Arg
210

<210> 349
 <211> 706
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 <213> Corynebacterium glutamicum

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 <222> (101)..(706)
 <223> FRXA02867

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 Met Ser Ala Thr Asn
 1 5
 cct gat gcc cta gac gtg cag cac gtc tat ccc atc aag acg aaa aag 163
 Pro Asp Ala Leu Asp Val Gln His Val Tyr Pro Ile Lys Thr Lys Lys
 10 15 20
 act cca ctt gcg gtg att ttc aac atc att agc ggt ggt ttg att gga 211
 Thr Pro Leu Ala Val Ile Phe Asn Ile Ile Ser Gly Gly Leu Ile Gly
 25 30 35
 atg gcg gag ttg gtg cca gga att tcc gcc gga act gtc gct ttg gtt 259
 Met Ala Glu Leu Val Pro Gly Ile Ser Gly Gly Thr Val Ala Leu Val
 40 45 50
 ctt gga att tat gag cgc gca ctg cac aac ggt gat ctc ctc att gat 307
 Leu Gly Ile Tyr Glu Arg Ala Leu His Asn Gly Asp Leu Leu Ile Asp
 55 60 65
 ctg atc aag gtg ttg atc aag gac cgc tcg aag gtt aag gaa gct gcg 355
 Leu Ile Lys Val Leu Ile Lys Asp Arg Ser Lys Val Lys Glu Ala Ala
 70 75 80 85
 gcg aaa atc gac tgg tgg ttc ctc ggc gct atc ggc gtt ggc atg gtc 403
 Ala Lys Ile Asp Trp Trp Phe Leu Gly Ala Ile Gly Val Gly Met Val
 90 95 100
 gtg atg gtc ttc tcg atg tca tcg att ttg cat aca gtt gtt gag gac 451
 Val Met Val Phe Ser Met Ser Ser Ile Leu His Thr Val Val Glu Asp
 105 110 115
 tac cca gag atc act cgc ggt ctg ttc ctt gga atg gtt gcc gtg tct 499
 Tyr Pro Glu Ile Thr Arg Gly Leu Phe Leu Gly Met Val Ala Val Ser
 120 125 130
 atc ctt gtt ccg ttg gga atg atg gat atg cgg gat gcc aag aag cgc 547
 Ile Leu Val Pro Leu Gly Met Met Asp Met Arg Asp Ala Lys Lys Arg
 135 140 145
 ctc gca atc gtc atc ccg cta ttt ata atc tgc gcc atg ctg gga ttc 595
 Leu Ala Ile Val Ile Pro Leu Phe Ile Ile Cys Ala Met Leu Gly Phe
 150 155 160 165
 ttt gga aca tcc ttc act agt gcg cct cgc acc gat cct tca ctg atc 643
 Phe Gly Thr Ser Phe Thr Ser Ala Pro Arg Thr Asp Pro Ser Leu Ile
 170 175 180

ttt gtc ttc atc tgt gct gcg atc gct gtg tgt gct ctt gtt ctt cct 691
 Phe Val Phe Ile Cys Ala Ala Ile Ala Val Cys Ala Leu Val Leu Pro
 185 190 195

ggc gtt cag gat cac 706
 Gly Val Gln Asp His
 200

<210> 350

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 350

Met Ser Ala Thr Asn Pro Asp Ala Leu Asp Val Gln His Val Tyr Pro
 1 5 10 15

Ile Lys Thr Lys Lys Thr Pro Leu Ala Val Ile Phe Asn Ile Ile Ser
 20 25 30

Gly Gly Leu Ile Gly Met Ala Glu Leu Val Pro Gly Ile Ser Gly Gly
 35 40 45

Thr Val Ala Leu Val Leu Gly Ile Tyr Glu Arg Ala Leu His Asn Gly
 50 55 60

Asp Leu Leu Ile Asp Leu Ile Lys Val Leu Ile Lys Asp Arg Ser Lys
 65 70 75 80

Val Lys Glu Ala Ala Lys Ile Asp Trp Trp Phe Leu Gly Ala Ile
 85 90 95

Gly Val Gly Met Val Val Met Val Phe Ser Met Ser Ser Ile Leu His
 100 105 110

Thr Val Val Glu Asp Tyr Pro Glu Ile Thr Arg Gly Leu Phe Leu Gly
 115 120 125

Met Val Ala Val Ser Ile Leu Val Pro Leu Gly Met Met Asp Met Arg
 130 135 140

Asp Ala Lys Lys Arg Leu Ala Ile Val Ile Pro Leu Phe Ile Ile Cys
 145 150 155 160

Ala Met Leu Gly Phe Phe Gly Thr Ser Phe Thr Ser Ala Pro Arg Thr
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Asp Pro Ser Leu Ile Phe Val Phe Ile Cys Ala Ala Ile Ala Val Cys
 180 185 190

Ala Leu Val Leu Pro Gly Val Gln Asp His
 195 200

<210> 351

<211> 930

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(907)

<223> RXN00730

<400> 351

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atccggcatg ggctcgggag ggactttaaa ataaacagct atg tgc agc caa caa 115
Met Ser Ser Gln Gln
1 5

acg atc ttc atc att ttg ctc ttt gcc gca gtg att ctc att tcc ata 163
Thr Ile Phe Ile Ile Leu Leu Phe Ala Ala Val Ile Leu Ile Ser Ile
10 15 20

gta atg att aca gct gcc ttc aaa acc cgg aaa aag cgc ttt gcc gcg 211
Val Met Ile Thr Ala Ala Phe Lys Thr Arg Lys Lys Arg Phe Ala Ala
25 30 35

cgg gct gaa gga atg gcc aac cct aca att cct gcg cca act gtg ccg 259
Arg Ala Glu Gly Met Ala Asn Pro Thr Ile Pro Thr Val Pro
40 45 50

tgg cag cgc ttc gcc gga gca ctt gca gcc ttg tac gct agg cct gaa 307
Trp Gln Arg Phe Ala Gly Ala Leu Ala Ala Leu Tyr Ala Arg Pro Glu
55 60 65

tgg cac aag acc cgc gga gcg aaa cga gtg tac tca gct gaa cag act 355
Trp His Lys Thr Arg Gly Ala Lys Arg Val Tyr Ser Ala Glu Gln Thr
70 75 80 85

tat ttt ggg ttt gtc tca gca atg cca ctg ggg atg gtg caa aac atg 403
Tyr Phe Gly Phe Val Ser Ala Met Pro Leu Gly Met Val Gln Asn Met
90 95 100

ctg caa aca gac tgg ggt gtg aaa aag tct gag cat gca gtt gat cag 451
Leu Gln Thr Asp Trp Gly Val Lys Lys Ser Glu His Ala Val Asp Gln
105 110 115

ctt tct aaa gga gtg gaa gtg atc gtt ggg gta gcc gca ggc aac tgg 499
Leu Ser Lys Gly Val Glu Val Ile Val Gly Val Ala Ala Gly Asn Trp
120 125 130

cgt aaa aac gga gta tca ccc gca caa gtg gaa gag gca ggc cag cgg 547
Arg Lys Asn Gly Val Ser Pro Ala Gln Val Glu Ala Gly Gln Arg
135 140 145

tta gca gct gaa gga ttg gct cat cca cac ttt gtt gta ttc caa aag 595
Leu Ala Ala Glu Gly Leu Ala His Pro His Phe Val Val Phe Gln Lys
150 155 160 165

cag ctt caa cag gca gat cca aat gca gaa tat gat ctc gat gtg ctc 643
Gln Leu Gln Gln Ala Asp Pro Asn Ala Glu Tyr Asp Leu Asp Val Leu
170 175 180

gca ttt gat atc gca cgc gta gcc aac ctc ctt cgc tgg gct gct tat 691
Ala Phe Asp Ile Ala Arg Val Ala Asn Leu Leu Arg Trp Ala Ala Tyr
185 190 195

aca gat ctg ttg ctc cct gca gaa gcc cgt tgg ttc caa gac cag ctg 739

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Thr Asp Leu Leu Leu Pro Ala Glu Ala Arg Trp Phe Gln Asp Gln Leu
    200                205                210

gga att gcg gct gct gtg tcc ttt ggg agc tgg gaa gaa tac gga gag    787
Gly Ile Ala Ala Ala Val Ser Phe Gly Ser Trp Glu Glu Tyr Gly Glu
    215                220                225

cga tac gtc cgt gga cta cag aag aac ttc aag ggc gga aac aag cca    835
Arg Tyr Val Arg Gly Leu Gln Lys Asn Phe Lys Gly Gly Asn Lys Pro
    230                235                240                245

tat atc gaa gga gaa cgc tgg ctc aac act gag gct gaa agt cca tgg    883
Tyr Ile Glu Gly Glu Arg Trp Leu Asn Thr Glu Ala Glu Ser Pro Trp
    250                255                260

aag acc caa aag tgg att agc gcc taactgctca tgagctaagc ggc    930
Lys Thr Gln Lys Trp Ile Ser Ala
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<211> 269
<212> PRT
<213> Corynebacterium glutamicum

<400> 352
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Ile Leu Ile Ser Ile Val Met Ile Thr Ala Ala Phe Lys Thr Arg Lys
    20                25                30

Lys Arg Phe Ala Ala Arg Ala Glu Gly Met Ala Asn Pro Thr Ile Pro
    35                40                45

Ala Pro Thr Val Pro Trp Gln Arg Phe Ala Gly Ala Leu Ala Ala Leu
    50                55                60

Tyr Ala Arg Pro Glu Trp His Lys Thr Arg Gly Ala Lys Arg Val Tyr
    65                70                75                80

Ser Ala Glu Gln Thr Tyr Phe Gly Phe Val Ser Ala Met Pro Leu Gly
    85                90                95

Met Val Gln Asn Met Leu Gln Thr Asp Trp Gly Val Lys Lys Ser Glu
    100               105               110

His Ala Val Asp Gln Leu Ser Lys Gly Val Glu Val Ile Val Gly Val
    115               120               125

Ala Ala Gly Asn Trp Arg Lys Asn Gly Val Ser Pro Ala Gln Val Glu
    130               135               140

Glu Ala Gly Gln Arg Leu Ala Ala Glu Gly Leu Ala His Pro His Phe
    145               150               155               160

Val Val Phe Gln Lys Gln Leu Gln Gln Ala Asp Pro Asn Ala Glu Tyr
    165               170               175

Asp Leu Asp Val Leu Ala Phe Asp Ile Ala Arg Val Ala Asn Leu Leu
    180               185               190

```

```

Arg Trp Ala Ala Tyr Thr Asp Leu Leu Leu Pro Ala Glu Ala Arg Trp
   195                               200                               205

Phe Gln Asp Gln Leu Gly Ile Ala Ala Ala Val Ser Phe Gly Ser Trp
   210                               215                               220

Glu Glu Tyr Gly Glu Arg Tyr Val Arg Gly Leu Gln Lys Asn Phe Lys
   225                               230                               235                               240

Gly Gly Asn Lys Pro Tyr Ile Glu Gly Glu Arg Trp Leu Asn Thr Glu
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Ala Glu Ser Pro Trp Lys Thr Gln Lys Trp Ile Ser Ala
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<211> 356

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(333)

<223> FRXA00730

<400> 353

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cac ttt gtt gta ttc caa aag cag ctt caa cag gca gat cca aat gca 48
His Phe Val Val Phe Gln Lys Gln Leu Gln Gln Ala Asp Pro Asn Ala
   1                               5                               10                               15

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```

gaa tat gat ctc gat gtg ctc gca ttt gat atc gca cgc gta gcc aac 96
Glu Tyr Asp Leu Asp Val Leu Ala Phe Asp Ile Ala Arg Val Ala Asn
   20                               25                               30

```

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ctc ctt cgc tgg gct gct tat aca gat ctg ttg ctc cct gca gaa gcc 144
Leu Leu Arg Trp Ala Ala Tyr Thr Asp Leu Leu Leu Pro Ala Glu Ala
   35                               40                               45

```

```

cgt tgg ttc caa gac cag ctg gga att gcg gct gct gtg tcc ttt ggg 192
Arg Trp Phe Gln Asp Gln Leu Gly Ile Ala Ala Ala Val Ser Phe Gly
   50                               55                               60

```

```

agc tgg gaa gaa tac gga gag cga tac gtc cgt gga cta cag aag aac 240
Ser Trp Glu Glu Tyr Gly Glu Arg Tyr Val Arg Gly Leu Gln Lys Asn
   65                               70                               75                               80

```

```

ttc aag ggc gga aac aag cca tat atc gaa gga gaa cgc tgg ctc aac 288
Phe Lys Gly Gly Asn Lys Pro Tyr Ile Glu Gly Glu Arg Trp Leu Asn
   85                               90                               95

```

```

act gag gct gaa agt cca tgg aag acc caa aag tgg att agc gcc 333
Thr Glu Ala Glu Ser Pro Trp Lys Thr Gln Lys Trp Ile Ser Ala
   100                               105                               110

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taactgctca tgagctaagc ggc 356

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<210> 354

<211> 111

<212> PRT

<213> Corynebacterium glutamicum

<400> 354

His Phe Val Val Phe Gln Lys Gln Leu Gln Gln Ala Asp Pro Asn Ala
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Glu Tyr Asp Leu Asp Val Leu Ala Phe Asp Ile Ala Arg Val Ala Asn
 20 25 30

Leu Leu Arg Trp Ala Ala Tyr Thr Asp Leu Leu Leu Pro Ala Glu Ala
 35 40 45

Arg Trp Phe Gln Asp Gln Leu Gly Ile Ala Ala Ala Val Ser Phe Gly
 50 55 60

Ser Trp Glu Glu Tyr Gly Glu Arg Tyr Val Arg Gly Leu Gln Lys Asn
 65 70 75 80

Phe Lys Gly Gly Asn Lys Pro Tyr Ile Glu Gly Glu Arg Trp Leu Asn
 85 90 95

Thr Glu Ala Glu Ser Pro Trp Lys Thr Gln Lys Trp Ile Ser Ala
 100 105 110

<210> 355

<211> 2619

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(2596)

<223> RXN00731

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ttgattgggt tgccaagcgc ggccgattgc aggtttaaca atg aaa gac gct tca 115
 Met Lys Asp Ala Ser
 1 5

cag tcc tac tta tta ttc ggt ctg aga tgg ctg gcc agg tcc ctg cgt 163
 Gln Ser Tyr Leu Leu Phe Gly Leu Arg Trp Leu Gly Arg Ser Leu Arg
 10 15 20

ttc gca cag tta agc ctg ctc atg atc gtt gtc atg cgg ggt ttg agg 211
 Phe Ala Pro Leu Ser Leu Leu Met Ile Val Val Met Arg Gly Leu Arg
 25 30 35

gaa gtg ttt gcc gcc gaa gat ccc gca aat agc tct ttg gta gac aac 259
 Glu Val Phe Gly Ala Glu Asp Pro Ala Asn Ser Ser Leu Val Asp Asn
 40 45 50

ctt ggg ctc acc ctg ccg tgg tct ctt aat gat ccg cat ttt ctc acc 307
 Leu Gly Leu Thr Leu Pro Trp Ser Leu Asn Asp Pro His Phe Leu Thr
 55 60 65

gca ggg ttt agc gct tcc acc acc aca gca gcg ctc atg tcc acg ttg 355
 Ala Gly Phe Ser Ala Ser Thr Thr Thr Ala Ala Leu Met Ser Thr Leu

70	75	80	85	
tgg atc atc gtg ttt gcg gtg ccc tct gaa cgg att ctg ggc agc ctc	403			
Trp Ile Ile Val Phe Ala Val Pro Ser Glu Arg Ile Leu Gly Ser Leu				
90	95	100		
aaa ttc gcg atc aca gca gcg ctt atc cac atc act tcc att cgg ctg	451			
Lys Phe Ala Ile Thr Ala Ala Leu Ile His Ile Thr Ser Ile Pro Leu				
105	110	115		
ggc atc ggc atc gcc cac ctc atc gaa gaa gcc gat ctc aac cgc tgg	499			
Gly Ile Gly Ile Ala His Leu Ile Glu Glu Ala Asp Leu Asn Arg Trp				
120	125	130		
ggc aac aac atg ttg gcc gat gtg ctg ctc acc cca gat ttc tgg gtc	547			
Gly Asn Asn Met Leu Ala Asp Val Leu Leu Thr Pro Asp Phe Trp Val				
135	140	145		
ttc ggc gtc gcc gct ttc gca tcc gcc tcc atg cca ctg ctc tgg cga	595			
Phe Gly Val Ala Ala Phe Ala Ser Ala Ser Met Pro Leu Leu Trp Arg				
150	155	160		
cgg cgc acc cga ttg ttc ctc ttt act atc acc ttg acg ctg ctg ctt	643			
Arg Arg Thr Arg Leu Phe Leu Phe Thr Ile Thr Leu Leu Leu				
170	175	180		
tat acg ggc acg ctt gcc gac gtc acc atg ctc acc gcg acc atc atc	691			
Tyr Thr Gly Thr Leu Ala Asp Val Thr Met Leu Thr Ala Thr Ile Ile				
185	190	195		
ggc acc gtt gcc ggc gag ttg aac agg cat cgg aaa acc cca ggt ggc	739			
Gly Thr Val Ala Gly Glu Leu Asn Arg His Arg Lys Thr Pro Gly Gly				
200	205	210		
cgc tgg ctt ccc ggt tcc ctc acc gtg cgt gaa cgc cgc att atg acg	787			
Arg Trp Leu Pro Gly Ser Leu Thr Val Arg Glu Ala Arg Ile Met Thr				
215	220	225		
gcc att ttg gtc act gcc gta gca gca ggt cca gtg ctt gct gcg ctt	835			
Ala Ile Leu Val Thr Ala Val Ala Ala Gly Pro Val Leu Ala Ala Leu				
230	235	240		
aat cca ctc acc cac ggc cct ttt tcc agt gca acg aaa ttg atc tgg	883			
Asn Pro Leu Thr His Gly Pro Phe Ser Ser Ala Thr Lys Leu Ile Trp				
250	255	260		
cag ccc ctt gtc act gaa gaa cac atg cat cac ctc tgc cac aca gac	931			
Gln Pro Leu Val Thr Glu Glu His Met His His Leu Cys His Thr Asp				
265	270	275		
agc acc tct gat gca tgc caa ggt gcg ctt gat cag ctc caa cag cac	979			
Ser Thr Ser Asp Ala Cys Gln Gly Ala Leu Asp Gln Leu Gln Gln His				
280	285	290		
ggt gtt ggc cct tcc gtt gcc aac ctg att cca ctg atc ctc acc gtg	1027			
Gly Val Gly Pro Ser Val Ala Asn Leu Ile Pro Leu Ile Leu Thr Val				
295	300	305		
gtc ctt gcg atg ggg ctt agc cgc gga cgt cga ctt gca tgg att ttg	1075			
Val Leu Ala Met Gly Leu Ser Arg Gly Arg Arg Leu Ala Trp Ile Leu				
310	315	320		

gcg gtt ttg gcc cag ctc att tcc atc gca gtg ttg atg ttc cag ctg	1123
Ala Val Leu Ala Gln Leu Ile Ser Ile Ala Val Leu Met Phe Gln Leu	
330 335 340	
acc aaa cta tgc gct gat tcc acc gat ctt cta tgg tca gtc aat gcc	1171
Thr Lys Leu Ser Ala Asp Ser Thr Asp Leu Leu Trp Ser Val Asn Ala	
345 350 355	
ttt agc gtg atc gtt cct tgg ctg gtg gcg ctc gcc gtc ttg gtg ttt	1219
Phe Ser Val Ile Val Pro Trp Leu Val Ala Leu Ala Val Leu Val Phe	
360 365 370	
tcc cgc cgt gca ttc cag gtg aag att gat acc acc cgg att tct aaa	1267
Ser Arg Arg Ala Phe Gln Val Lys Ile Asp Thr Arg Ile Ser Lys	
375 380 385	
tcc tta ggc gct ctc atg gtt aca tgg ttg gca acg gca gca ttg tgg	1315
Ser Leu Gly Ala Leu Met Val Thr Trp Leu Ala Thr Ala Ala Leu Trp	
390 395 400 405	
atc ctt gcc aca ttg ttc ctg cca cac gca ttc cac cca cat cca aca	1363
Ile Leu Ala Thr Leu Phe Leu Pro His Ala Phe His Pro His Pro Thr	
410 415 420	
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Leu Gly Leu Ala Phe Lys Glu Leu Pro Phe Arg Tyr Leu Pro Pro Thr	
425 430 435	
atc gaa acg gtg tta agc cat caa ctc ttc ccc aga agc cct gct ggg	1459
Ile Glu Thr Val Leu Ser His Gln Leu Phe Pro Arg Ser Pro Ala Gly	
440 445 450	
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Trp Ala Val Phe Glu Trp Thr Gly Thr Leu Phe Trp Leu Val Val Ala	
455 460 465	
gca act ctt tat cat ctg ctc atg ggt gtg ccc agc aac aaa gcg cac	1555
Ala Thr Leu Tyr His Leu Leu Met Gly Val Pro Ser Asn Lys Ala His	
470 475 480 485	
gag gac caa gaa aac gca gcg act ctc ctg cgc tct gcc agc ggc gat	1603
Glu Asp Gln Glu Asn Ala Ala Thr Leu Leu Arg Ser Gly Ser Gly Asp	
490 495 500	
cac ttg tcc tgg atg acc att tgg ggt gcc aat acg tat tgg tgg gca	1651
His Leu Ser Trp Met Thr Ile Trp Gly Gly Asn Thr Tyr Trp Trp Ala	
505 510 515	
cca gaa aat gca gga tat gtg gcc tac cgc gtg aaa agg ggc atc gca	1699
Pro Glu Asn Ala Gly Tyr Val Ala Tyr Arg Val Lys Arg Gly Ile Ala	
520 525 530	
att aca ttg ggt gag cct att ctg ggt ccg gat tca tcc gtc tct aaa	1747
Ile Thr Leu Gly Glu Pro Ile Leu Gly Pro Asp Ser Ser Val Ser Lys	
535 540 545	
gca gag ctg gcc gca cag ttt gaa gaa ttt gcc agc aac caa ggc tgg	1795
Ala Glu Leu Ala Ala Gln Phe Glu Glu Phe Ala Ser Asn Gln Gly Trp	
550 555 560 565	

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 ile Val Ala Trp Tyr Ser Val Cys Glu Glu Phe Ser Lys Glu Arg Ile
 570 575 580

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 Asn Ala Gly His His Thr Leu Arg Val Ala Glu Glu Ala Val Leu Ser
 585 590 595

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 Ser Ala Asn Ala Asp Phe Lys Gly Lys His Phe Gln Asn Val Arg Thr
 600 605 610

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 Ala Arg Asn Arg Ala Ala Lys Glu Gly Val Ser Ile Trp Thr Thr
 615 620 625

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 630 635 640 645

gaa gaa tgg gtc tct gat aaa gct ctg ccg gag atg ggc ttc acg ctt 2083
 Glu Glu Trp Val Ser Asp Lys Ala Leu Pro Glu Met Gly Phe Thr Leu
 650 655 660

ggc act gtc aac gag ctc tca gat cca gat acc tat ctt ctt ctc gcg 2131
 Gly Thr Val Asn Glu Leu Ser Asp Pro Asp Thr Tyr Leu Leu Leu Ala
 665 670 675

att gat gag gaa gag cat ctg cac ggt gtg acc agt tgg ttg ccg gtc 2179
 Ile Asp Glu Glu Glu His Leu His Gly Val Thr Ser Trp Leu Pro Val
 680 685 690

tat gaa aaa gga cgc atc gtc ggc tac aca ctt gat gtg atg cgc cgt 2227
 Tyr Glu Lys Gly Arg Ile Val Gly Tyr Thr Leu Asp Val Met Arg Arg
 695 700 705

gat ccg caa ggc ttt aaa tct gtc atc gag ttt ctc att tcc gag gcc 2275
 Asp Pro Gln Gly Phe Lys Ser Val Ile Glu Phe Leu Ile Ser Glu Ala
 710 715 720 725

gtc gtt atc gca agg gat cac gat ctg gaa tgg atg tcg atg tcc gcc 2323
 Val Val Ile Ala Arg Asp His Asp Leu Glu Trp Met Ser Met Ser Gly
 730 735 740

gct cct ttg agt acg ccc cca ggt gtg gcc gac gac ggc acc atc gga 2371
 Ala Pro Leu Ser Thr Pro Pro Gly Val Ala Asp Asp Gly Thr Ile Gly
 745 750 755

caa att ttg gag ctt ttg ggc cga gca atg gag ccg ttc tac ggt ttc 2419
 Gln Ile Leu Glu Leu Leu Gly Arg Ala Met Glu Pro Phe Tyr Gly Phe
 760 765 770

cgt tcc ctc gct gcg tcc aag aac aaa ttc cac cca gaa cac cac ggt 2467
 Arg Ser Leu Ala Ala Ser Lys Asn Lys Phe His Pro Glu His His Gly
 775 780 785

tgg tac ttg tgt tac cgc gat gaa tta tcg tta cca agc att gcc ctt 2515
 Trp Tyr Leu Cys Tyr Arg Asp Glu Leu Ser Leu Pro Ser Ile Gly Leu
 790 795 800 805

gcc gtt gct gcc tgc tac ctc aac gag ttt ccg ctg ccg aat tgg ctg 2563

Ala Val Ala Ala Cys Tyr Leu Asn Glu Phe Pro Leu Pro Asn Trp Leu
810 815 820

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825 830

gtg

2619

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<211> 832

<212> PRT

<213> Corynebacterium glutamicum

<400> 356

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20 25 30

Met Arg Gly Leu Arg Glu Val Phe Gly Ala Glu Asp Pro Ala Asn Ser
35 40 45

Ser Leu Val Asp Asn Leu Gly Leu Thr Leu Pro Trp Ser Leu Asn Asp
50 55 60

Pro His Phe Leu Thr Ala Gly Phe Ser Ala Ser Thr Thr Thr Ala Ala
65 70 75 80

Leu Met Ser Thr Leu Trp Ile Ile Val Phe Ala Val Pro Ser Glu Arg
85 90 95

Ile Leu Gly Ser Leu Lys Phe Ala Ile Thr Ala Ala Leu Ile His Ile
100 105 110

Thr Ser Ile Pro Leu Gly Ile Gly Ile Ala His Leu Ile Glu Glu Ala
115 120 125

Asp Leu Asn Arg Trp Gly Asn Asn Met Leu Ala Asp Val Leu Leu Thr
130 135 140

Pro Asp Phe Trp Val Phe Gly Val Ala Ala Phe Ala Ser Ala Ser Met
145 150 155 160

Pro Leu Leu Trp Arg Arg Arg Thr Arg Leu Phe Leu Phe Thr Ile Thr
165 170 175

Leu Thr Leu Leu Leu Tyr Thr Gly Thr Leu Ala Asp Val Thr Met Leu
180 185 190

Thr Ala Thr Ile Ile Gly Thr Val Ala Gly Glu Leu Asn Arg His Arg
195 200 205

Lys Thr Pro Gly Gly Arg Trp Leu Pro Gly Ser Leu Thr Val Arg Glu
210 215 220

Ala Arg Ile Met Thr Ala Ile Leu Val Thr Ala Val Ala Ala Gly Pro
225 230 235 240

Val Leu Ala Ala Leu Asn Pro Leu Thr His Gly Pro Phe Ser Ser Ala
 245 250 255
 Thr Lys Leu Ile Trp Gln Pro Leu Val Thr Glu Glu His Met His His
 260 265 270
 Leu Cys His Thr Asp Ser Thr Ser Asp Ala Cys Gln Gly Ala Leu Asp
 275 280 285
 Gln Leu Gln Gln His Gly Val Gly Pro Ser Val Ala Asn Leu Ile Pro
 290 295 300
 Leu Ile Leu Thr Val Val Leu Ala Met Gly Leu Ser Arg Gly Arg Arg
 305 310 315 320
 Leu Ala Trp Ile Leu Ala Val Leu Ala Gln Leu Ile Ser Ile Ala Val
 325 330 335
 Leu Met Phe Gln Leu Thr Lys Leu Ser Ala Asp Ser Thr Asp Leu Leu
 340 345 350
 Trp Ser Val Asn Ala Phe Ser Val Ile Val Pro Trp Leu Val Ala Leu
 355 360 365
 Ala Val Leu Val Phe Ser Arg Arg Ala Phe Gln Val Lys Ile Asp Thr
 370 375 380
 Thr Arg Ile Ser Lys Ser Leu Gly Ala Leu Met Val Thr Trp Leu Ala
 385 390 395 400
 Thr Ala Ala Leu Trp Ile Leu Ala Thr Leu Phe Leu Pro His Ala Phe
 405 410 415
 His Pro His Pro Thr Leu Gly Leu Ala Phe Lys Glu Leu Pro Phe Arg
 420 425 430
 Tyr Leu Pro Pro Thr Ile Glu Thr Val Leu Ser His Gln Leu Phe Pro
 435 440 445
 Arg Ser Pro Ala Gly Trp Ala Val Phe Glu Trp Thr Gly Thr Leu Phe
 450 455 460
 Trp Leu Val Val Ala Ala Thr Leu Tyr His Leu Leu Met Gly Val Pro
 465 470 475 480
 Ser Asn Lys Ala His Glu Asp Gln Glu Asn Ala Ala Thr Leu Leu Arg
 485 490 495
 Ser Gly Ser Gly Asp His Leu Ser Trp Met Thr Ile Trp Gly Gly Asn
 500 505 510
 Thr Tyr Trp Trp Ala Pro Glu Asn Ala Gly Tyr Val Ala Tyr Arg Val
 515 520 525
 Lys Arg Gly Ile Ala Ile Thr Leu Gly Glu Pro Ile Leu Gly Pro Asp
 530 535 540
 Ser Ser Val Ser Lys Ala Glu Leu Ala Ala Gln Phe Glu Glu Phe Ala
 545 550 555 560
 Ser Asn Gln Gly Trp Ile Val Ala Trp Tyr Ser Val Cys Glu Glu Phe

565										570										575																																			
Ser	Lys	Glu	Arg	Ile	Asn	Ala	Gly	His	His	Thr	Leu	Arg	Val	Ala	Glu																																								
			580																				585																																
Glu	Ala	Val	Leu	Ser	Ser	Ala	Asn	Ala	Asp	Phe	Lys	Gly	Lys	His	Phe																																								
			595																				600																																
Gln	Asn	Val	Arg	Thr	Ala	Arg	Asn	Arg	Ala	Ala	Lys	Glu	Gly	Val	Ser																																								
			610																				615																																
Ser	Ile	Trp	Thr	Thr	Trp	Ala	Asp	Leu	Ser	Ala	Glu	Met	Gln	His	Lys																																								
			625																				630																																
Ile	Ile	Thr	Leu	Ser	Glu	Glu	Trp	Val	Ser	Asp	Lys	Ala	Leu	Pro	Glu																																								
			645																				650																																
Met	Gly	Phe	Thr	Leu	Gly	Thr	Val	Asn	Glu	Leu	Ser	Asp	Pro	Asp	Thr																																								
			660																				665																																
Tyr	Leu	Leu	Leu	Ala	Ile	Asp	Glu	Glu	Glu	His	Leu	His	Gly	Val	Thr																																								
			675																				680																																
Ser	Trp	Leu	Pro	Val	Tyr	Glu	Lys	Gly	Arg	Ile	Val	Gly	Tyr	Thr	Leu																																								
			690																				695																																
Asp	Val	Met	Arg	Arg	Asp	Pro	Gln	Gly	Phe	Lys	Ser	Val	Ile	Glu	Phe																																								
			705																				710																																
Leu	Ile	Ser	Glu	Ala	Val	Val	Ile	Ala	Arg	Asp	His	Asp	Leu	Glu	Trp																																								
			725																				730																																
Met	Ser	Met	Ser	Gly	Ala	Pro	Leu	Ser	Thr	Pro	Pro	Gly	Val	Ala	Asp																																								
			740																				745																																
Asp	Gly	Thr	Ile	Gly	Gln	Ile	Leu	Glu	Leu	Leu	Gly	Arg	Ala	Met	Glu																																								
			755																				760																																
Pro	Phe	Tyr	Gly	Phe	Arg	Ser	Leu	Ala	Ala	Ser	Lys	Asn	Lys	Phe	His																																								
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Pro	Glu	His	His	Gly	Trp	Tyr	Leu	Cys	Tyr	Arg	Asp	Glu	Leu	Ser	Leu																																								
			785																				790																																
Pro	Ser	Ile	Gly	Leu	Ala	Val	Ala	Ala	Cys	Tyr	Leu	Asn	Glu	Phe	Pro																																								
			805																				810																																
Leu	Pro	Asn	Trp	Leu	Lys	Lys	Thr	Ala	Thr	Ser	Ala	Pro	Ser	His	Ser																																								
			820																				825																																

<210> 357

<211> 2495

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(2472)

<223> FRXA00731

<400> 357

tta tta ttc ggt ctg aga tgg ctg ggc agg tcc ctg cgt ttc gca ccg	48
Leu Leu Phe Gly Leu Arg Trp Leu Gly Arg Ser Leu Arg Phe Ala Pro	
1 5 10 15	
tta agc ctg ctc atg atc gtt gtc atg cgg ggt ttg agg gaa gtg ttt	96
Leu Ser Leu Leu Met Ile Val Val Met Arg Gly Leu Arg Glu Val Phe	
20 25 30	
ggc gcc gaa gat ccc gca aat agc tct ttg gta gac aac ctt ggg ctc	144
Gly Ala Glu Asp Pro Ala Asn Ser Ser Leu Val Asp Asn Leu Gly Leu	
35 40 45	
acc ctg ccg tgg tct ctt aat gat ccg cat ttt ctc acc gca ggg ttt	192
Thr Leu Pro Trp Ser Leu Asn Asp Pro His Phe Leu Thr Ala Gly Phe	
50 55 60	
agc gct tcc acc acc aca gca gcg ctc atg tcc acg ttg tgg atc atc	240
Ser Ala Ser Thr Thr Ala Ala Leu Met Ser Thr Leu Trp Ile Ile	
65 70 75 80	
gtg ttt gcg gtg ccc tct gaa cgg att ctg ggc agc ctc aaa ttc gcg	288
Val Phe Ala Val Pro Ser Glu Arg Ile Leu Gly Ser Leu Lys Phe Ala	
85 90 95	
atc aca gca gcg ctt atc cac atc act tcc att ccg ctg ggc atc ggc	336
Ile Thr Ala Ala Leu Ile His Ile Thr Ser Ile Pro Leu Gly Ile Gly	
100 105 110	
atc gcc cac ctc atc gaa gaa gcc gat ctc aac cgc tgg ggc aac aac	384
Ile Ala His Leu Ile Glu Glu Ala Asp Leu Asn Arg Trp Gly Asn Asn	
115 120 125	
atg ttg gcc gat gtg ctg ctc acc cca gat ttc tgg gtc ttc ggc gtc	432
Met Leu Ala Asp Val Leu Leu Thr Pro Asp Phe Trp Val Phe Gly Val	
130 135 140	
gcc gct ttc gca tcc gcc tcc atg cca ctg ctc tgg cga cgg cgc acc	480
Ala Ala Phe Ala Ser Met Pro Leu Leu Trp Arg Arg Arg Thr	
145 150 155 160	
cga ttg ttc ctc ttt act atc acc ttg acg ctg ctg ctt tat acg ggc	528
Arg Leu Phe Leu Phe Thr Ile Thr Leu Thr Leu Leu Leu Tyr Thr Gly	
165 170 175	
acg ctt gcc gac gtc acc atg ctc acc gcg acc atc atc ggc acc gtt	576
Thr Leu Ala Asp Val Thr Met Leu Thr Ala Thr Ile Ile Gly Thr Val	
180 185 190	
gcc gcc gag ttg aac agg cat cgg aaa acc cca ggt ggc cgc tgg ctt	624
Ala Gly Glu Leu Asn Arg His Arg Lys Thr Pro Gly Gly Arg Trp Leu	
195 200 205	
ccc ggt tcc ctc acc gtg cgt gaa gcg cgc att atg acg gcc att ttg	672
Pro Gly Ser Leu Thr Val Arg Glu Ala Arg Ile Met Thr Ala Ile Leu	
210 215 220	
gtc act gcc gta gca gca ggt cca gtg ctt gct gcg ctt aat cca ctc	720

Val Thr Ala Val Ala Ala Gly Pro Val Leu Ala Ala Leu Asn Pro Leu	
225 230 235 240	
acc cac ggc cct ttt tcc agt gca acg aaa ttg atc tgg cag ccc ctt	768
Thr His Gly Pro Phe Ser Ser Ala Thr Lys Leu Ile Trp Gln Pro Leu	
245 250 255	
gtc act gaa gaa cac atg cat cac ctc tgc cac aca gac agc acc tct	816
Val Thr Glu Glu His Met His His Leu Cys His Thr Asp Ser Thr Ser	
260 265 270	
gat gca tgc caa ggt gcg ctt gat cag ctc caa cag cac ggt gtt ggc	864
Asp Ala Cys Gln Gly Ala Leu Asp Gln Leu Gln Gln His Gly Val Gly	
275 280 285	
cct tcc gtt gcc aac ctg att cca ctg atc ctc acc gtg gtc ctt gcg	912
Pro Ser Val Ala Asn Leu Ile Pro Leu Ile Leu Thr Val Val Leu Ala	
290 295 300	
atg ggg ctt agc cgc gga cgt cga ctt gca tgg att ttg gcg gtt ttg	960
Met Gly Leu Ser Arg Gly Arg Arg Leu Ala Trp Ile Leu Ala Val Leu	
305 310 315 320	
gcc cag ctc att tcc atc gca gtg ttg atg ttc cag ctg acc aaa cta	1008
Ala Gln Leu Ile Ser Ile Ala Val Leu Met Phe Gln Leu Thr Lys Leu	
325 330 335	
tgc gct gat tcc acc gat ctt cta tgg tca gtc aat gcc ttt agc gtg	1056
Ser Ala Asp Ser Thr Asp Leu Trp Ser Val Asn Ala Phe Ser Val	
340 345 350	
atc gtt cct tgg ctg gtg gcg ctc gcc gtc ttg gtg ttt tcc cgc cgt	1104
Ile Val Pro Trp Leu Val Ala Leu Ala Val Leu Val Phe Ser Arg Arg	
355 360 365	
gca ttc cag gtg aag att gat acc acc cgg att tct aaa tcc tta ggc	1152
Ala Phe Gln Val Lys Ile Asp Thr Thr Arg Ile Ser Lys Ser Leu Gly	
370 375 380	
gct ctc atg gtt aca tgg ttg gca acg gca gca ttg tgg atc ctt gcc	1200
Ala Leu Met Val Thr Trp Leu Ala Thr Ala Ala Leu Trp Ile Leu Ala	
385 390 395 400	
aca ttg ttc ctg cca cac gca ttc cac cca cat cca aca ttg ggg ctg	1248
Thr Leu Phe Leu Pro His Ala Phe His Pro His Pro Thr Leu Gly Leu	
405 410 415	
get ttc aaa gaa ctc ccc ttc cgc tat ctc cca cca act atc gaa acg	1296
Ala Phe Lys Glu Leu Pro Phe Arg Tyr Leu Pro Pro Thr Ile Glu Thr	
420 425 430	
gtg tta agc cat caa ctc ttc ccc aga agc cct gct ggg tgg gca gtg	1344
Val Leu Ser His Gln Leu Phe Pro Arg Ser Pro Ala Gly Trp Ala Val	
435 440 445	
ttt gaa tgg act gga acg cta ttc tgg ctg gtc gta gca gca act ctt	1392
Phe Glu Trp Thr Gly Thr Phe Thr Trp Leu Val Val Ala Ala Thr Leu	
450 455 460	
tat cat ctg ctc atg ggt gtg ccc agc aac aaa gcg cac gag gac caa	1440
Tyr His Leu Leu Met Gly Val Pro Ser Asn Lys Ala His Glu Asp Gln	

465	470	475	480	
gaa aac gca gcg act ctc ctg cgc tct ggc agc ggc gat cac ttg tcc				1488
Glu Asn Ala Ala Thr Leu Leu Arg Ser Gly Ser His Leu Ser	485	490	495	
tgg atg acc att tgg ggt ggc aat acg tat tgg tgg gca cca gaa aat				1536
Trp Met Thr Ile Trp Gly Gly Asn Thr Tyr Trp Trp Ala Pro Glu Asn	500	505	510	
gca gga tat gtg gcc tac cgc gtg aaa agg ggc atc gca att aca ttg				1584
Ala Gly Tyr Val Ala Tyr Arg Val Lys Arg Gly Ile Ala Ile Thr Leu	515	520	525	
ggt gag cct att ctg ggt ccg gat tca tcc gtc tct aaa gca gag ctg				1632
Gly Glu Pro Ile Leu Gly Pro Asp Ser Ser Val Ser Lys Ala Glu Leu	530	535	540	
gcc gca cag ttt gaa gaa ttt gcc agc aac caa ggc tgg att gtt gcg				1680
Ala Ala Gln Phe Glu Glu Phe Ala Ser Asn Gln Gly Trp Ile Val Ala	545	550	555	560
tgg tat tcc gtt tgt gaa gaa ttc tca aag gaa cgc atc aac gct ggc				1728
Trp Tyr Ser Val Cys Glu Glu Phe Ser Lys Glu Arg Ile Asn Ala Gly	565	570	575	
cac cac aca ctt cgt gtg gct gag gaa gca gtc tta agc tca gct aat				1776
His His Thr Leu Arg Val Ala Glu Glu Ala Val Leu Ser Ser Ala Asn	580	585	590	
gcg gat ttc aaa ggt aag cac ttc caa aat gtc cgc acc gcc cga aac				1824
Ala Asp Phe Lys Gly Lys His Phe Gln Asn Val Arg Thr Ala Arg Asn	595	600	605	
cgc gcg gcc aaa gag gcc gta agt tcc atc tgg aca acc tgg gct gat				1872
Arg Ala Ala Lys Glu Gly Val Ser Ser Ile Trp Thr Thr Trp Ala Asp	610	615	620	
ttg agt gcc gaa atg cag cac aag atc atc acg ctg tgg gaa gaa tgg				1920
Leu Ser Ala Glu Met Gln His Lys Ile Thr Leu Ser Glu Glu Trp	625	630	635	640
gtc tct gat aaa gct ctg ccg gag atg ggc ttc acg ctt ggc act gtc				1968
Val Ser Asp Lys Ala Leu Pro Glu Met Gly Phe Thr Leu Gly Thr Val	645	650	655	
aac gag ctc tca gat cca gat acc tat ctt ctt ctc gcg att gat gag				2016
Asn Glu Leu Ser Asp Pro Asp Thr Tyr Leu Leu Leu Ala Ile Asp Glu	660	665	670	
gaa gag cat ctg cac ggt gtg acc agt tgg ttg ccg gtc tat gaa aaa				2064
Glu Glu His Leu His Gly Val Thr Ser Trp Leu Pro Val Tyr Glu Lys	675	680	685	
gga cgc atc gtc gcc tac aca ctt gat gtg atg cgc cgt gat ccg caa				2112
Gly Arg Ile Val Gly Tyr Thr Leu Asp Val Met Arg Arg Asp Pro Gln	690	695	700	
ggc ttt aaa tct gtc atc gag ttt ctc att tcc gag gcc gtc gtt atc				2160
Gly Phe Lys Ser Val Ile Glu Phe Leu Ile Ser Glu Ala Val Val Ile	705	710	715	720

gca agg gat cac gat ctg gaa tgg atg tcg atg tcc ggc gct cct ttg 2208
 Ala Arg Asp His Asp Leu Glu Trp Met Ser Met Ser Gly Ala Pro Leu
 725 730 735

agt acg ccc cca ggt gtg gcc gac gac ggc acc atc gga caa att ttg 2256
 Ser Thr Pro Pro Gly Val Ala Asp Asp Gly Thr Ile Gly Gln Ile Leu
 740 745 750

gag ctt ttg ggc cga gca atg gag ccg ttc tac ggt ttc cgt tcc ctc 2304
 Glu Leu Leu Gly Arg Ala Met Glu Pro Phe Tyr Gly Phe Arg Ser Leu
 755 760 765

gct gcg tcc aag aac aaa ttc cac cca gaa cac cac ggt tgg tac ttg 2352
 Ala Ala Ser Lys Asn Lys Phe His Pro Glu His His Gly Trp Tyr Leu
 770 775 780

tgt tac cgc gat gaa tta tgg tta cca agc att ggc ctt gcc gtt gct 2400
 Cys Tyr Arg Asp Glu Leu Ser Leu Pro Ser Ile Gly Leu Ala Val Ala
 785 790 795 800

gcc tgc tac ctc aac gag ttt ccg ctg ccg aat tgg ctg aaa aag acc 2448
 Ala Cys Tyr Leu Asn Glu Phe Pro Leu Pro Asn Trp Leu Lys Lys Thr
 805 810 815

gcc act tcc gcc cca agc cac agc tagaaaaacg cgtaaccttg gtg 2495
 Ala Thr Ser Ala Pro Ser His Ser
 820

<210> 358
 <211> 824
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 358
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Leu Ser Leu Leu Met Ile Val Val Met Arg Gly Leu Arg Glu Val Phe
 20 25 30

Gly Ala Glu Asp Pro Ala Asn Ser Ser Leu Val Asp Asn Leu Gly Leu
 35 40 45

Thr Leu Pro Trp Ser Leu Asn Asp Pro His Phe Leu Thr Ala Gly Phe
 50 55 60

Ser Ala Ser Thr Thr Thr Ala Ala Leu Met Ser Thr Leu Trp Ile Ile
 65 70 75 80

Val Phe Ala Val Pro Ser Glu Arg Ile Leu Gly Ser Leu Lys Phe Ala
 85 90 95

Ile Thr Ala Ala Leu Ile His Ile Thr Ser Ile Pro Leu Gly Ile Gly
 100 105 110

Ile Ala His Leu Ile Glu Glu Ala Asp Leu Asn Arg Trp Gly Asn Asn
 115 120 125

Met Leu Ala Asp Val Leu Leu Thr Pro Asp Phe Trp Val Phe Gly Val

130					135					140						
Ala	Ala	Phe	Ala	Ser	Ala	Ser	Met	Pro	Leu	Leu	Trp	Arg	Arg	Arg	Thr	
145					150					155						160
Arg	Leu	Phe	Leu	Phe	Thr	Ile	Thr	Leu	Thr	Leu	Leu	Leu	Tyr	Thr	Gly	
				165					170						175	
Thr	Leu	Ala	Asp	Val	Thr	Met	Leu	Thr	Ala	Thr	Ile	Ile	Gly	Thr	Val	
			180					185					190			
Ala	Gly	Glu	Leu	Asn	Arg	His	Arg	Lys	Thr	Pro	Gly	Gly	Arg	Trp	Leu	
		195						200					205			
Pro	Gly	Ser	Leu	Thr	Val	Arg	Glu	Ala	Arg	Ile	Met	Thr	Ala	Ile	Leu	
			210				215				220					
Val	Thr	Ala	Val	Ala	Ala	Gly	Pro	Val	Leu	Ala	Ala	Leu	Asn	Pro	Leu	
225						230					235				240	
Thr	His	Gly	Pro	Phe	Ser	Ser	Ala	Thr	Lys	Leu	Ile	Trp	Gln	Pro	Leu	
				245					250					255		
Val	Thr	Glu	Glu	His	Met	His	His	Leu	Cys	His	Thr	Asp	Ser	Thr	Ser	
				260				265						270		
Asp	Ala	Cys	Gln	Gly	Ala	Leu	Asp	Gln	Leu	Gln	Gln	His	Gly	Val	Gly	
			275				280						285			
Pro	Ser	Val	Ala	Asn	Leu	Ile	Pro	Leu	Ile	Leu	Thr	Val	Val	Leu	Ala	
			290				295						300			
Met	Gly	Leu	Ser	Arg	Gly	Arg	Arg	Leu	Ala	Trp	Ile	Leu	Ala	Val	Leu	
305						310					315				320	
Ala	Gln	Leu	Ile	Ser	Ile	Ala	Val	Leu	Met	Phe	Gln	Leu	Thr	Lys	Leu	
				325					330						335	
Ser	Ala	Asp	Ser	Thr	Asp	Leu	Leu	Trp	Ser	Val	Asn	Ala	Phe	Ser	Val	
			340					345						350		
Ile	Val	Pro	Trp	Leu	Val	Ala	Leu	Ala	Val	Leu	Val	Phe	Ser	Arg	Arg	
				355			360							365		
Ala	Phe	Gln	Val	Lys	Ile	Asp	Thr	Thr	Arg	Ile	Ser	Lys	Ser	Leu	Gly	
				370			375				380					
Ala	Leu	Met	Val	Thr	Trp	Leu	Ala	Thr	Ala	Ala	Leu	Trp	Ile	Leu	Ala	
385						390					395				400	
Thr	Leu	Phe	Leu	Pro	His	Ala	Phe	His	Pro	His	Pro	Thr	Leu	Gly	Leu	
				405					410					415		
Ala	Phe	Lys	Glu	Leu	Pro	Phe	Arg	Tyr	Leu	Pro	Pro	Thr	Ile	Glu	Thr	
				420				425						430		
Val	Leu	Ser	His	Gln	Leu	Phe	Pro	Arg	Ser	Pro	Ala	Gly	Trp	Ala	Val	
			435				440						445			
Phe	Glu	Trp	Thr	Gly	Thr	Leu	Phe	Trp	Leu	Val	Val	Ala	Ala	Thr	Leu	
				450			455							460		

Tyr His Leu Leu Met Gly Val Pro Ser Asn Lys Ala His Glu Asp Gln
 465 470 475 480
 Glu Asn Ala Ala Thr Leu Leu Arg Ser Gly Ser Gly Asp His Leu Ser
 485 490 495
 Trp Met Thr Ile Trp Gly Gly Asn Thr Tyr Trp Trp Ala Pro Glu Asn
 500 505 510
 Ala Gly Tyr Val Ala Tyr Arg Val Lys Arg Gly Ile Ala Ile Thr Leu
 515 520 525
 Gly Glu Pro Ile Leu Gly Pro Asp Ser Ser Val Ser Lys Ala Glu Leu
 530 535 540
 Ala Ala Gln Phe Glu Glu Phe Ala Ser Asn Gln Gly Trp Ile Val Ala
 545 550 555 560
 Trp Tyr Ser Val Cys Glu Glu Phe Ser Lys Glu Arg Ile Asn Ala Gly
 565 570 575
 His His Thr Leu Arg Val Ala Glu Glu Ala Val Leu Ser Ser Ala Asn
 580 585 590
 Ala Asp Phe Lys Gly Lys His Phe Gln Asn Val Arg Thr Ala Arg Asn
 595 600 605
 Arg Ala Ala Lys Glu Gly Val Ser Ser Ile Trp Thr Thr Trp Ala Asp
 610 615 620
 Leu Ser Ala Glu Met Gln His Lys Ile Ile Thr Leu Ser Glu Glu Trp
 625 630 635 640
 Val Ser Asp Lys Ala Leu Pro Glu Met Gly Phe Thr Leu Gly Thr Val
 645 650 655
 Asn Glu Leu Ser Asp Pro Asp Thr Tyr Leu Leu Leu Ala Ile Asp Glu
 660 665 670
 Glu Glu His Leu His Gly Val Thr Ser Trp Leu Pro Val Tyr Glu Lys
 675 680 685
 Gly Arg Ile Val Gly Tyr Thr Leu Asp Val Met Arg Arg Asp Pro Gln
 690 695 700
 Gly Phe Lys Ser Val Ile Glu Phe Leu Ile Ser Glu Ala Val Val Ile
 705 710 715 720
 Ala Arg Asp His Asp Leu Glu Trp Met Ser Met Ser Gly Ala Pro Leu
 725 730 735
 Ser Thr Pro Pro Gly Val Ala Asp Asp Gly Thr Ile Gly Gln Ile Leu
 740 745 750
 Glu Leu Leu Gly Arg Ala Met Glu Pro Phe Tyr Gly Phe Arg Ser Leu
 755 760 765
 Ala Ala Ser Lys Asn Lys Phe His Pro Glu His His Gly Trp Tyr Leu
 770 775 780

Cys Tyr Arg Asp Glu Leu Ser Leu Pro Ser Ile Gly Leu Ala Val Ala
785 790 795 800

Ala Cys Tyr Leu Asn Glu Phe Pro Leu Pro Asn Trp Leu Lys Lys Thr
805 810 815

Ala Thr Ser Ala Pro Ser His Ser
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<210> 359

<211> 386

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(363)

<223> RXN00738

<400> 359

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Cys Gln Glu Glu Thr Asp Gly Phe Phe Asp Phe Gly Arg Asp Met Arg
1 5 10 15

ccc ggt gag cgc cgg tcg tat ggc act ttg ctt aac gac gcc acg acg 96
Pro Gly Glu Arg Arg Ser Tyr Gly Thr Leu Leu Asn Asp Ala Thr Thr
20 25 30

cag gtg tcg cac atc ctc ggc aat gcc ttc acc cga tct ggg ctc aac 144
Gln Val Ser His Ile Leu Gly Asn Ala Phe Thr Arg Ser Gly Leu Asn
35 40 45

gct gag tac gcg aat ctt tat ggt cag gcg ttg gtg ggc atg gtg tcg 192
Ala Glu Tyr Ala Asn Leu Tyr Gly Gln Ala Leu Val Gly Met Val Ser
50 55 60

atg acg gcg caa tgg tgg ttg gat gag cgc act ccg ccg aag gaa gaa 240
Met Thr Ala Gln Trp Trp Leu Asp Glu Arg Thr Pro Pro Lys Glu Glu
65 70 75 80

gtt gcc gca cat att gtt aat ctt tgt tgg aat ggt ttg acg ggg atg 288
Val Ala Ala His Ile Val Asn Leu Cys Trp Asn Gly Leu Thr Gly Met
85 90 95

gaa gcc gat ccg aag tta act ccc atc agt tct gct gag ggt gcg att 336
Glu Ala Asp Pro Lys Leu Thr Pro Ile Ser Ser Ala Glu Gly Ala Ile
100 105 110

ttt ggt caa gaa aag gag agt gaa gcg tgacacctat gctcgcgggg 383
Phe Gly Gln Glu Lys Glu Ser Glu Ala
115 120

ctg 386

<210> 360

<211> 121

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 360

Cys Gln Glu Glu Thr Asp Gly Phe Phe Asp Phe Gly Arg Asp Met Arg
 1 5 10 15

Pro Gly Glu Arg Arg Ser Tyr Gly Thr Leu Leu Asn Asp Ala Thr Thr
 20 25 30

Gln Val Ser His Ile Leu Gly Asn Ala Phe Thr Arg Ser Gly Leu Asn
 35 40 45

Ala Glu Tyr Ala Asn Leu Tyr Gly Gln Ala Leu Val Gly Met Val Ser
 50 55 60

Met Thr Ala Gln Trp Trp Leu Asp Glu Arg Thr Pro Pro Lys Glu Glu
 65 70 75 80

Val Ala Ala His Ile Val Asn Leu Cys Trp Asn Gly Leu Thr Gly Met
 85 90 95

Glu Ala Asp Pro Lys Leu Thr Pro Ile Ser Ser Ala Glu Gly Ala Ile
 100 105 110

Phe Gly Gln Glu Lys Glu Ser Glu Ala
 115 120

<210> 361

<211> 388

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (78)..(365)

<223> FRXA00738

<400> 361

catgcccccta ttagacggat ggcttttttg attttgggcg cgatatgctgg cccggtgagc 60

gccggtcgta tggcactttg ctt aac gac gcc acg acg cag gtg tgg cac atc 113
 Leu Leu Asn Asp Ala Thr Thr Gln Val Ser His Ile
 1 5 10

ctc ggc aat gcc ttc acc cga tct ggg ctc aac gct gag tac gcg aat 161
 Leu Gly Asn Ala Phe Thr Arg Ser Gly Leu Asn Ala Glu Tyr Ala Asn
 15 20 25

ctt tat ggt cag gcg ttg gtg ggc atg gtg tgg atg acg gcg caa tgg 209
 Leu Tyr Gly Gln Ala Leu Val Gly Met Val Ser Met Thr Ala Gln Trp
 30 35 40

tgg ttg gat gag cgc act ccg ccg aag gaa gaa gtt gcc gca cat att 257
 Trp Leu Asp Glu Arg Thr Pro Pro Lys Glu Glu Val Ala Ala His Ile
 45 50 55 60

gtt aat ctt tgt tgg aat ggt ttg acg ggg atg gaa gcc gat ccg aag 305
 Val Asn Leu Cys Trp Asn Gly Leu Thr Gly Met Glu Ala Asp Pro Lys
 65 70 75

tta act ccc atc agt tct gct gag ggt gcg att ttt ggt caa gaa aag 353
 Leu Thr Pro Ile Ser Ser Ala Glu Gly Ala Ile Phe Gly Gln Glu Lys

80

85

90

gag agt gaa gcg tgacacctat gctcgcgggg ctg
 Glu Ser Glu Ala
 95

388

<210> 362

<211> 96

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 362

Leu Leu Asn Asp Ala Thr Thr Gln Val Ser His Ile Leu Gly Asn Ala
 1 5 10 15

Phe Thr Arg Ser Gly Leu Asn Ala Glu Tyr Ala Asn Leu Tyr Gly Gln
 20 25 30

Ala Leu Val Gly Met Val Ser Met Thr Ala Gln Trp Trp Leu Asp Glu
 35 40 45

Arg Thr Pro Pro Lys Glu Glu Val Ala Ala His Ile Val Asn Leu Cys
 50 55 60

Trp Asn Gly Leu Thr Gly Met Glu Ala Asp Pro Lys Leu Thr Pro Ile
 65 70 75 80

Ser Ser Ala Glu Gly Ala Ile Phe Gly Gln Glu Lys Glu Ser Glu Ala
 85 90 95

<210> 363

<211> 561

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(538)

<223> RXN00750

<400> 363

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cactaacacc ccaccagaaa ataacacctc gaccgaacct atg gac tgg tcg atc 115
 Met Asp Trp Ser Ile
 1 5

att att aat gtg ctt gcc gtt got act gtc gtg ata ctc acc ctt atc 163
 Ile Ile Asn Val Leu Ala Val Ala Thr Val Val Ile Leu Thr Leu Ile
 10 15 20

atc gca gct gca tta tat agg ggt ttc aca cgc aac aaa ata aaa aaa 211
 Ile Ala Ala Ala Leu Tyr Arg Gly Phe Thr Arg Asn Lys Ile Lys Lys
 25 30 35

ctt gaa gct ata cga gaa gcc cag caa cac gaa cgc gac aat ccc act 259

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Leu Glu Ala Ile Arg Glu Ala Gln Gln His Glu Arg Asp Asn Pro Thr
    40                      45                      50

atc cgc att gct gat ctt cgc ggc atc atg gat act cac cac tac atc 307
Ile Arg Ile Ala Asp Leu Arg Gly Ile Met Asp Thr His His Tyr Ile
    55                      60                      65

tac acc gac gtc atg gtt aca cgt gca cat gaa ctc atg att act gca 355
Tyr Thr Asp Val Met Val Thr Arg Ala His Glu Leu Met Ile Thr Ala
    70                      75                      80                      85

ccc gca ttc ttt gat gtc act ctc ccc gaa gca gtg ctc tac gaa gat 403
Pro Ala Phe Phe Asp Val Thr Leu Pro Glu Ala Val Leu Tyr Glu Asp
    90                      95                      100

act aaa cgt gct gct cat gat gcc ctt aac ggc tat aaa gac acc act 451
Thr Lys Arg Ala Ala His Asp Ala Leu Asn Gly Tyr Lys Asp Thr Thr
    105                      110                      115

gtc gct agt gca gag aag atc atg ctt gta gat gca gtc acc gca gca 499
Val Ala Ser Ala Glu Lys Ile Met Leu Val Asp Ala Val Thr Ala Ala
    120                      125                      130

tgg act ctc tat tcc aca aaa gca aac acc gga tcc acg tgatccgaga 548
Trp Thr Leu Tyr Ser Thr Lys Ala Asn Thr Gly Ser Thr
    135                      140                      145

gccgagtacc gct 561

<210> 364
<211> 146
<212> PRT
<213> Corynebacterium glutamicum

<400> 364
Met Asp Trp Ser Ile Ile Ile Asn Val Leu Ala Val Ala Thr Val Val
  1           5           10          15

Ile Leu Thr Leu Ile Ile Ala Ala Ala Leu Tyr Arg Gly Phe Thr Arg
    20           25           30

Asn Lys Ile Lys Lys Leu Glu Ala Ile Arg Glu Ala Gln His Glu
    35           40           45

Arg Asp Asn Pro Thr Ile Arg Ile Ala Asp Leu Arg Gly Ile Met Asp
    50           55           60

Thr His His Tyr Ile Tyr Thr Asp Val Met Val Thr Arg Ala His Glu
    65           70           75           80

Leu Met Ile Thr Ala Pro Ala Phe Phe Asp Val Thr Leu Pro Glu Ala
    85           90           95

Val Leu Tyr Glu Asp Thr Lys Arg Ala Ala His Asp Ala Leu Asn Gly
    100          105          110

Tyr Lys Asp Thr Thr Val Ala Ser Ala Glu Lys Ile Met Leu Val Asp
    115          120          125

Ala Val Thr Ala Ala Trp Thr Leu Tyr Ser Thr Lys Ala Asn Thr Gly

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130

135

140

Ser Thr

145

<210> 365

<211> 561

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(538)

<223> FRXA00750

<400> 365

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cactaacacc ccaccagaaa ataacacctc gaccgaacct atg gac tgg tgg atc 115
 Met Asp Trp Ser Ile
 1 5

att att aat gtg ctt gcc gtt gct act gtc gtg ata ctc acc ctt atc 163
 Ile Ile Asn Val Leu Ala Val Ala Thr Val Val Ile Leu Thr Leu Ile
 10 15 20

atc gca gct gca tta tat agg ggt ttc aca cgc gca aac aaa ata aaa aaa 211
 Ile Ala Ala Ala Leu Tyr Arg Gly Phe Thr Arg Asn Lys Ile Lys Lys
 25 30 35

ctt gaa gct ata cga gaa gcc cag caa cac gaa cgc gac aat ccc act 259
 Leu Glu Ala Ile Arg Glu Ala Gln Gln His Glu Arg Asp Asn Pro Thr
 40 45 50

atc cgc att gct gat ctt cgc ggc atc atg gat act cac cac tac atc 307
 Ile Arg Ile Ala Asp Leu Arg Gly Ile Met Asp Thr His His Tyr Ile
 55 60 65

tac acc gac gtc atg gtt aca cgt gca cat gaa ctc atg att act gca 355
 Tyr Thr Asp Val Met Val Thr Arg Ala His Glu Leu Met Ile Thr Ala
 70 75 80 85

ccc gca ttc ttt gat gtc act ctc ccc gaa gca gtg ctc tac gaa gat 403
 Pro Ala Phe Phe Asp Val Thr Leu Pro Glu Ala Val Leu Tyr Glu Asp
 90 95 100

act aaa cgt gct gct cat gat gcc ctt aac ggc tat aaa gac acc act 451
 Thr Lys Arg Ala Ala His Asp Ala Leu Asn Gly Tyr Lys Asp Thr Thr
 105 110 115

gtc gct agt gca gag aag atc atg ctt gta gat gca gtc acc gca gca 499
 Val Ala Ser Ala Glu Lys Ile Met Leu Val Asp Ala Val Thr Ala Ala
 120 125 130

tgg act ctc tat tcc aca aaa gca aac acc gga tcc acg tgatccgaga 548
 Trp Thr Leu Tyr Ser Thr Lys Ala Asn Thr Gly Ser Thr
 135 140 145

gccgagtacc gct 561

<210> 366
 <211> 146
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 366
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 Ile Leu Thr Leu Ile Ile Ala Ala Ala Leu Tyr Arg Gly Phe Thr Arg
 20 25 30
 Asn Lys Ile Lys Lys Leu Glu Ala Ile Arg Glu Ala Gln Gln His Glu
 35 40 45
 Arg Asp Asn Pro Thr Ile Arg Ile Ala Asp Leu Arg Gly Ile Met Asp
 50 55 60
 Thr His His Tyr Ile Tyr Thr Asp Val Met Val Thr Arg Ala His Glu
 65 70 75 80
 Leu Met Ile Thr Ala Pro Ala Phe Phe Asp Val Thr Leu Pro Glu Ala
 85 90 95
 Val Leu Tyr Glu Asp Thr Lys Arg Ala Ala His Asp Ala Leu Asn Gly
 100 105 110
 Tyr Lys Asp Thr Thr Val Ala Ser Ala Glu Lys Ile Met Leu Val Asp
 115 120 125
 Ala Val Thr Ala Ala Trp Thr Leu Tyr Ser Thr Lys Ala Asn Thr Gly
 130 135 140
 Ser Thr
 145

<210> 367
 <211> 999
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(976)
 <223> RXN00762

<400> 367
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 gttcctgcga gagattcaaa cttggggcta acctggggac atg aat act tcc gat 115
 Met Asn Thr Ser Asp
 1 5
 cgt att aaa agc act caa atc gcg ctg gat cgt gac ctc cgt gag cag 163
 Arg Ile Lys Ser Thr Gln Ile Ala Leu Asp Arg Asp Leu Arg Glu Gln
 10 15 20
 gca cta ttg ctt ttg aag gag gtt cgc gca gtt gat ggc gtg gat gct 211
 Ala Leu Leu Leu Leu Lys Glu Val Arg Ala Val Asp Gly Val Asp Ala

25										30					35					
tta	tca	gaa	caa	ttt	gtc	cgt	ggg	ctt	gca	gaa	ccc	gga	ctt	gtt	cac	259				
Leu	Ser	Glu	Gln	Phe	Val	Arg	Gly	Leu	Ala	Glu	Pro	Gly	Leu	Val	His					
40 45 50																				
tcc	cat	tta	ata	gtc	acg	ctc	aat	agc	gag	ctg	gtt	ggc	ctc	gcg	gcc	307				
Ser	His	Leu	Ile	Val	Thr	Leu	Asn	Ser	Glu	Leu	Val	Gly	Leu	Ala	Ala					
55 60 65																				
gcg	gat	gag	gaa	acc	acg	gaa	ctg	gct	gtc	cac	ccg	gcg	cac	agg	cgt	355				
Ala	Asp	Glu	Glu	Thr	Thr	Glu	Leu	Ala	Val	His	Pro	Ala	His	Arg	Arg					
70 75 80 85																				
cag	gga	atc	ggt	aag	gcg	ctt	atc	gac	gcc	gcc	ccc	acc	tca	tca	atc	403				
Gln	Gly	Ile	Gly	Lys	Ala	Leu	Ile	Asp	Ala	Ala	Pro	Thr	Ser	Ser	Ile					
90 95 100																				
tgg	gcg	cat	gga	aat	aca	gca	ggt	gca	caa	gcg	ttg	gca	tcc	acc	ctg	451				
Trp	Ala	His	Gly	Asn	Thr	Ala	Gly	Ala	Gln	Ala	Leu	Ala	Ser	Thr	Leu					
105 110 115																				
cgt	atg	aag	aag	act	cgc	gag	ctt	ctg	gtg	atg	gag	att	tcc	gac	agg	499				
Arg	Met	Lys	Lys	Thr	Arg	Glu	Leu	Leu	Val	Met	Glu	Ile	Ser	Asp	Arg					
120 125 130																				
gcg	ctc	gat	gac	tct	gca	gca	tac	aaa	gat	cca	gat	gga	att	aca	cac	547				
Ala	Leu	Asp	Asp	Ser	Ala	Ala	Tyr	Lys	Asp	Pro	Asp	Gly	Ile	Thr	His					
135 140 145																				
agt	agt	ttg	gcg	aat	gcc	cct	gtg	gag	aaa	tca	gta	gct	gag	gct	aaa	595				
Ser	Ser	Leu	Ala	Asn	Ala	Pro	Val	Glu	Lys	Ser	Val	Ala	Glu	Ala	Lys					
150 155 160 165																				
tgg	ctt	caa	tcc	aac	aac	gaa	gca	ttc	gac	tgg	cat	ccc	gag	cag	ggc	643				
Trp	Leu	Gln	Ser	Asn	Asn	Glu	Ala	Phe	Asp	Trp	His	Pro	Glu	Gln	Gly					
170 175 180																				
gga	tgg	aca	act	cat	cgg	ttg	gcg	cag	gct	cag	aaa	gcc	gat	tgg	tac	691				
Gly	Trp	Thr	Thr	His	Arg	Leu	Ala	Gln	Ala	Gln	Lys	Ala	Asp	Trp	Tyr					
185 190 195																				
aag	gac	tct	gac	gtg	tta	ttc	ctc	tgg	gac	ggc	gaa	gag	atc	gtt	ggc	739				
Lys	Asp	Ser	Asp	Val	Leu	Phe	Leu	Trp	Asp	Gly	Glu	Glu	Ile	Val	Gly					
200 205 210																				
ttc	cac	tgg	gta	aag	cag	cac	agt	cca	gaa	tta	caa	gag	att	tac	gta	787				
Phe	His	Trp	Val	Lys	Gln	His	Ser	Pro	Glu	Leu	Gln	Glu	Ile	Tyr	Val					
215 220 225																				
gtt	ggc	ctt	tct	tca	gcc	tac	cgt	ggt	cgc	ggc	ttg	gga	gat	ccg	ctt	835				
Val	Gly	Leu	Ser	Ser	Ala	Tyr	Arg	Gly	Arg	Gly	Leu	Gly	Asp	Pro	Leu					
230 235 240 245																				
gtt	cgc	ctc	gga	ctg	cat	cac	atg	agg	gct	cat	ggt	gct	cga	aaa	gtg	883				
Val	Arg	Leu	Gly	Leu	His	His	Met	Arg	Ala	His	Gly	Ala	Arg	Lys	Val					
250 255 260 265																				
att	ctt	tat	gtg	gaa	gct	ggc	aac	act	ccg	gca	gtc	gcg	gca	tac	gaa	931				
Ile	Leu	Tyr	Val	Glu	Ala	Gly	Asn	Thr	Pro	Ala	Val	Ala	Ala	Tyr	Glu					
265 270 275																				

aaa ctg gga ttc act gtc gcg gaa agc cac gta gtt tac gaa aag 976
 Lys Leu Gly Phe Thr Val Ala Glu Ser His Val Val Tyr Glu Lys
 280 285 290

taaaaaagag acttgctaaa aac 999

<210> 368

<211> 292

<212> PRT

<213> Corynebacterium glutamicum

<400> 368

Met Asn Thr Ser Asp Arg Ile Lys Ser Thr Gln Ile Ala Leu Asp Arg
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Asp Leu Arg Glu Gln Ala Leu Leu Leu Lys Glu Val Arg Ala Val
 20 25 30

Asp Gly Val Asp Ala Leu Ser Glu Gln Phe Val Arg Gly Leu Ala Glu
 35 40 45

Pro Gly Leu Val His Ser His Leu Ile Val Thr Leu Asn Ser Glu Leu
 50 55 60

Val Gly Leu Ala Ala Ala Asp Glu Glu Thr Thr Glu Leu Ala Val His
 65 70 75 80

Pro Ala His Arg Arg Gln Gly Ile Gly Lys Ala Leu Ile Asp Ala Ala
 85 90 95

Pro Thr Ser Ser Ile Trp Ala His Gly Asn Thr Ala Gly Ala Gln Ala
 100 105 110

Leu Ala Ser Thr Leu Arg Met Lys Lys Thr Arg Glu Leu Leu Val Met
 115 120 125

Glu Ile Ser Asp Arg Ala Leu Asp Asp Ser Ala Ala Tyr Lys Asp Pro
 130 135 140

Asp Gly Ile Thr His Ser Ser Leu Ala Asn Ala Pro Val Glu Lys Ser
 145 150 155 160

Val Ala Glu Ala Lys Trp Leu Gln Ser Asn Asn Glu Ala Phe Asp Trp
 165 170 175

His Pro Glu Gln Gly Gly Trp Thr Thr His Arg Leu Ala Gln Ala Gln
 180 185 190

Lys Ala Asp Trp Tyr Lys Asp Ser Asp Val Leu Phe Leu Trp Asp Gly
 195 200 205

Glu Glu Ile Val Gly Phe His Trp Val Lys Gln His Ser Pro Glu Leu
 210 215 220

Gln Glu Ile Tyr Val Val Gly Leu Ser Ser Ala Tyr Arg Gly Arg Gly
 225 230 235 240

Leu Gly Asp Pro Leu Val Arg Leu Gly Leu His His Met Arg Ala His
 245 250 255

Gly Ala Arg Lys Val Ile Leu Tyr Val Glu Ala Gly Asn Thr Pro Ala
 260 265 270

Val Ala Ala Tyr Glu Lys Leu Gly Phe Thr Val Ala Glu Ser His Val
 275 280 285

Val Tyr Glu Lys
 290

<210> 369
 <211> 1242
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1219)
 <223> RXN00768

<400> 369
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cacttgcgct ttggaagga ataacccttc ctgtcagatt gtg ggt act atc gaa 115
 Val Gly Thr Ile Glu 5

gac gtg gct aac gaa caa atc gag gtc gcg aac aac act gat cag att 163
 Asp Val Ala Asn Glu Gln Ile Glu Val Ala Asn Asn Thr Asp Gln Ile 10 15 20

cct gca gga tac aag tcc cct ctt ctt tct aga agt ggt gcg gca gaa 211
 Pro Ala Gly Tyr Lys Ser Pro Leu Leu Ser Arg Ser Gly Ala Ala Glu 25 30 35

gcg cag ggc gct gct gct caa gca ggt act gaa ggt gtc gcg tgg cat 259
 Ala Gln Gly Ala Ala Ala Gln Ala Gly Thr Glu Gly Val Ala Trp His 40 45 50

tac ggt tcc cct ctc gtc gag caa cgc atc ttc gaa act ggc acg ggc 307
 Tyr Gly Ser Pro Leu Val Glu Gln Arg Ile Phe Glu Thr Gly Thr Gly 55 60 65

tta gtt gac cgt tct aat cgc aag gtg atc aaa gtc gaa ggg cct gat 355
 Leu Val Asp Arg Ser Asn Arg Lys Val Ile Lys Val Glu Gly Pro Asp 70 75 80 85

gcc ccc acg ttc ctc aat aat att ttg tcc caa aag gtt gat tcc gtt 403
 Ala Pro Thr Phe Leu Asn Asn Ile Leu Ser Gln Lys Val Asp Ser Val 90 95 100

gaa aac ggc ttt act gcc ggt gcc ctg gat ttg gat gcg cag ggt cgt 451
 Glu Asn Gly Phe Thr Ala Gly Ala Leu Asp Leu Asp Ala Gln Gly Arg 105 110 115

att caa cac aca atg cag gta act gtc gtc gat ggg gtt ttc tac ctc 499
 Ile Gln His Thr Met Gln Val Thr Val Val Asp Gly Val Phe Tyr Leu 120 125 130

gac acg tcc gcg gcg gag ttt gat acc ctc atc ggt ttc ttg acc aag 547

Asp Thr Ser Ala Ala Glu Phe Asp Thr Leu Ile Gly Phe Leu Thr Lys	
135 140 145	
atg att ttc tgg tcg gaa gtc acc gtc cag gaa gcc gat ctg gcg atc	595
Met Ile Phe Trp Ser Glu Val Thr Val Gln Glu Ala Asp Leu Ala Ile	
150 155 160 165	
atc act ctg ctc ggc cag gaa att gcc ctt ccg gac gcg gtc ttt gcc	643
Ile Thr Leu Leu Gly Gln Glu Ile Ala Leu Pro Asp Ala Val Phe Ala	
170 175 180	
cgt agg gtc gat tgg aat ggg cca tcg cgt atc gac gtc gcc atc cgg	691
Arg Arg Val Asp Trp Asn Gly Pro Ser Arg Ile Asp Val Ala Ile Arg	
185 190 195	
cgt gaa aac ctg gag gag ggc gtc gac aag ctc tta gaa gct ggc gca	739
Arg Glu Asn Leu Glu Glu Gly Val Asp Lys Leu Leu Glu Ala Gly Ala	
200 205 210	
aag ctc acc ggt ctc atg gct tac acg gcc gag cgc gtg aag gcg ttg	787
Lys Leu Thr Gly Leu Met Ala Tyr Thr Ala Glu Arg Val Lys Ala Leu	
215 220 225	
gag ccc gct gcg ggc gtg gat ttg gat gat aag acc att ccc cat gaa	835
Glu Pro Ala Ala Gly Val Asp Leu Asp Asp Lys Thr Ile Pro His Glu	
230 235 240 245	
atc ccc cat tgg att ggc cgt ggc gaa cat tta ggc gct gtg cat ttg	883
Ile Pro His Trp Ile Gly Arg Gly Glu His Leu Gly Ala Val His Leu	
250 255 260	
acc aag ggt tgc tac cgc ggg cag gaa act gtc gcg cgc gtt gat aat	931
Thr Lys Gly Cys Tyr Arg Gly Gln Glu Thr Val Ala Arg Val Asp Asn	
265 270 275	
ctt ggg cgt tcc ccg cgc gtg ctg gtt ctg ctt cat ctt gac ggt tcc	979
Leu Gly Arg Ser Pro Arg Val Leu Val Leu Leu His Leu Asp Gly Ser	
280 285 290	
gca ccg ctg gat cct gtg act ggc gct gaa atc aag gcc ggt gcg cgc	1027
Ala Pro Leu Asp Pro Val Thr Gly Ala Glu Ile Lys Ala Gly Ala Arg	
295 300 305	
acc gtt ggt cgt ctg ggc acc gtt gtc cat gac gcc gat tac ggg ccg	1075
Thr Val Gly Arg Leu Gly Thr Val Val His Asp Ala Asp Tyr Gly Pro	
310 315 320 325	
atc gct ctc ggg ctg gtt aag cgc agc gct ttg gat aaa gaa ctt cac	1123
Ile Ala Leu Gly Leu Val Lys Arg Ser Ala Leu Asp Lys Glu Leu His	
330 335 340	
atc gat gat gtc tct gta aac gtc gac cgc gat ctg ctt cct gcg gag	1171
Ile Asp Asp Val Ser Val Asn Val Asp Arg Asp Leu Leu Pro Ala Glu	
345 350 355	
gaa agt gaa caa cgc gga cgc gca gcg atc aat aag ctc aag ggt ctt	1219
Glu Ser Glu Gln Arg Gly Arg Ala Ala Ile Asn Lys Leu Lys Gly Leu	
360 365 370	
taactaaaac gatttatagc gaa	1242

<210> 370
 <211> 373
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 370
 Val Gly Thr Ile Glu Asp Val Ala Asn Glu Gln Ile Glu Val Ala Asn
 1 5 10 15
 Asn Thr Asp Gln Ile Pro Ala Gly Tyr Lys Ser Pro Leu Leu Ser Arg
 20 25 30
 Ser Gly Ala Ala Glu Ala Gln Gly Ala Ala Ala Gln Ala Gly Thr Glu
 35 40 45
 Gly Val Ala Trp His Tyr Gly Ser Pro Leu Val Glu Gln Arg Ile Phe
 50 55 60
 Glu Thr Gly Thr Gly Leu Val Asp Arg Ser Asn Arg Lys Val Ile Lys
 65 70 75 80
 Val Glu Gly Pro Asp Ala Pro Thr Phe Leu Asn Asn Ile Leu Ser Gln
 85 90 95
 Lys Val Asp Ser Val Glu Asn Gly Phe Thr Ala Gly Ala Leu Asp Leu
 100 105 110
 Asp Ala Gln Gly Arg Ile Gln His Thr Met Gln Val Thr Val Val Asp
 115 120 125
 Gly Val Phe Tyr Leu Asp Thr Ser Ala Ala Glu Phe Asp Thr Leu Ile
 130 135 140
 Gly Phe Leu Thr Lys Met Ile Phe Trp Ser Glu Val Thr Val Gln Glu
 145 150 155 160
 Ala Asp Leu Ala Ile Ile Thr Leu Leu Gly Gln Glu Ile Ala Leu Pro
 165 170 175
 Asp Ala Val Phe Ala Arg Arg Val Asp Trp Asn Gly Pro Ser Arg Ile
 180 185 190
 Asp Val Ala Ile Arg Arg Glu Asn Leu Glu Glu Gly Val Asp Lys Leu
 195 200 205
 Leu Glu Ala Gly Ala Lys Leu Thr Gly Leu Met Ala Tyr Thr Ala Glu
 210 215 220
 Arg Val Lys Ala Leu Glu Pro Ala Ala Gly Val Asp Leu Asp Asp Lys
 225 230 235 240
 Thr Ile Pro His Glu Ile Pro His Trp Ile Gly Arg Gly Glu His Leu
 245 250 255
 Gly Ala Val His Leu Thr Lys Gly Cys Tyr Arg Gly Gln Glu Thr Val
 260 265 270
 Ala Arg Val Asp Asn Leu Gly Arg Ser Pro Arg Val Leu Val Leu Leu
 275 280 285

His Leu Asp Gly Ser Ala Pro Leu Asp Pro Val Thr Gly Ala Glu Ile
 290 295 300

Lys Ala Gly Ala Arg Thr Val Gly Arg Leu Gly Thr Val Val His Asp
 305 310 315 320

Ala Asp Tyr Gly Pro Ile Ala Leu Gly Leu Val Lys Arg Ser Ala Leu
 325 330 335

Asp Lys Glu Leu His Ile Asp Asp Val Ser Val Asn Val Asp Arg Asp
 340 345 350

Leu Leu Pro Ala Glu Glu Ser Glu Gln Arg Gly Arg Ala Ala Ile Asn
 355 360 365

Lys Leu Lys Gly Leu
 370

<210> 371
 <211> 567
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(544)
 <223> FRXA00768

<400> 371
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 gcaaagctca ccggtctcat ggcttacacg gcccgagcgc gtg aag gcg ttg gag 115
 Val Lys Ala Leu Glu
 1 5

ccc gct gcg gcc gtg gat ttg gat gat aag acc att ccc cat gaa atc 163
 Pro Ala Ala Gly Val Asp Leu Asp Asp Lys Thr Ile Pro His Glu Ile
 10 15 20

ccc cat tgg att gcc cgt gcc gaa cat tta gcc gct gtg cat ttg acc 211
 Pro His Trp Ile Gly Arg Gly Glu His Leu Gly Ala Val His Leu Thr
 25 30 35

aag ggt tgc tac cgc ggg cag gaa act gtc gcg cgc gtt gat aat ctt 259
 Lys Gly Cys Tyr Arg Gly Gln Glu Thr Val Ala Arg Val Asp Asn Leu
 40 45 50

ggg cgt tcc ccg cgc gtg ctg gtt ctg ctt cat ctt gac ggt tcc gca 307
 Gly Arg Ser Pro Arg Val Leu Val Leu Leu His Leu Asp Gly Ser Ala
 55 60 65

ccg ctg gat cct gtg act gcc gct gaa atc aag gcc ggt gcg cgc acc 355
 Pro Leu Asp Pro Val Thr Gly Ala Glu Ile Lys Ala Gly Ala Arg Thr
 70 75 80 85

gtt ggt cgt ctg gcc acc gtt gtc cat gac gcc gat tac ggg ccg atc 403
 Val Gly Arg Leu Gly Thr Val Val His Asp Ala Asp Tyr Gly Pro Ile
 90 95 100

gct ctc ggg ctg gtt aag cgc agc gct ttg gat aaa gaa ctt cac atc 451

Ala Leu Gly Leu Val Lys Arg Ser Ala Leu Asp Lys Glu Leu His Ile
 105 110 115

gat gat gtc tct gta aac gtc gac cgc gat ctg ctt cct gcg gag gaa 499
 Asp Asp Val Ser Val Asn Val Asp Arg Asp Leu Leu Pro Ala Glu Glu
 120 125 130

agt gaa caa cgc gga cgc gca gcg atc aat aag ctc aag ggt ctt 544
 Ser Glu Gln Arg Gly Arg Ala Ala Ile Asn Lys Leu Lys Gly Leu
 135 140 145

taactaaaac gatttatagc gaa 567

<210> 372
 <211> 148
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 372
 Val Lys Ala Leu Glu Pro Ala Ala Gly Val Asp Leu Asp Asp Lys Thr
 1 5 10 15

Ile Pro His Glu Ile Pro His Trp Ile Gly Arg Gly Glu His Leu Gly
 20 25 30

Ala Val His Leu Thr Lys Gly Cys Tyr Arg Gly Gln Glu Thr Val Ala
 35 40 45

Arg Val Asp Asn Leu Gly Arg Ser Pro Arg Val Leu Val Leu Leu His
 50 55 60

Leu Asp Gly Ser Ala Pro Leu Asp Pro Val Thr Gly Ala Glu Ile Lys
 65 70 75 80

Ala Gly Ala Arg Thr Val Gly Arg Leu Gly Thr Val Val His Asp Ala
 85 90 95

Asp Tyr Gly Pro Ile Ala Leu Gly Leu Val Lys Arg Ser Ala Leu Asp
 100 105 110

Lys Glu Leu His Ile Asp Asp Val Ser Val Asn Val Asp Arg Asp Leu
 115 120 125

Leu Pro Ala Glu Glu Ser Glu Gln Arg Gly Arg Ala Ala Ile Asn Lys
 130 135 140

Leu Lys Gly Leu
 145

<210> 373
 <211> 837
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(814)
 <223> FRXA00767

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cactttgcgct ttggaagga ataacccttc ctgtcagatt																115
Val Gly Thr Ile Glu 1 5																
gac gtg gct aac gaa caa atc gag gtc gcg aac aac act gat cag att																163
Asp Val Ala Asn Glu Gln Ile Glu Val Ala Asn Asn Thr Asp Gln Ile 10 15 20																
cct gca gga tac aag tcc cct ctt ctt aga agt ggt gcg gca gaa																211
Pro Ala Gly Tyr Lys Ser Pro Leu Leu Ser Arg Ser Gly Ala Ala Glu 25 30 35																
gcg cag gcc gct gct gct caa gca ggt act gaa ggt gtc gcg tgg cat																259
Ala Gln Gly Ala Ala Ala Gln Ala Gly Thr Glu Gly Val Ala Trp His 40 45 50																
tac ggt tcc cct ctc gtc gag caa cgc atc ttc gaa act ggc acg gcc																307
Tyr Gly Ser Pro Leu Val Glu Gln Arg Ile Phe Glu Thr Gly Thr Gly 55 60 65																
tta gtt gac cgt tct aat cgc aag gtg atc aaa gtc gaa ggg cct gat																355
Leu Val Asp Arg Ser Asn Arg Lys Val Ile Lys Val Glu Gly Pro Asp 70 75 80 85																
gcc ccc acg ttc ctc aat aat att ttg tcc caa aag gtt gat tcc gtt																403
Ala Pro Thr Phe Leu Asn Asn Ile Leu Ser Gln Lys Val Asp Ser Val 90 95 100																
gaa aac gcc ttt act gcc ggt gcc ctg gat ttg gat gcg cag ggt cgt																451
Glu Asn Gly Phe Thr Ala Gly Ala Leu Asp Leu Asp Ala Gln Gly Arg 105 110 115																
att caa cac aca atg cag gta act gtc gtc gat ggg gtt ttc tac ctc																499
Ile Gln His Thr Met Gln Val Thr Val Val Asp Gly Val Phe Tyr Leu 120 125 130																
gac acg tcc gcg gcg gag ttt gat acc ctc atc ggt ttc ttg acc aag																547
Asp Thr Ser Ala Ala Glu Phe Asp Thr Leu Ile Gly Phe Leu Thr Lys 135 140 145																
atg att ttc tgg tgg gaa gtc acc gtc cag gaa gcc gat ctg gcg atc																595
Met Ile Phe Trp Ser Glu Val Thr Val Gln Glu Ala Asp Leu Ala Ile 150 155 160 165																
atc act ctg ctc gcc cag gaa att gcc ctt ccg gac gcg gtc ttt gcc																643
Ile Thr Leu Leu Gly Gln Glu Ile Ala Leu Pro Asp Ala Val Phe Ala 170 175 180																
cgt agg gtc gat tgg aat ggg cca tcg cgt atc gac gtc gcc atc cgg																691
Arg Arg Val Asp Trp Asn Gly Pro Ser Arg Ile Asp Val Ala Ile Arg 185 190 195																
cgt gaa aac ctg gag gag gcc gtc aag ctc tta gaa gct ggc gca																739
Arg Glu Asn Leu Glu Glu Gly Val Asp Lys Leu Leu Glu Ala Gly Ala 200 205 210																
aag ctc acc ggt ctc atg gct tac acg gcc cga gcg cgt gaa ggc gtt																787
Lys Leu Thr Gly Leu Met Ala Tyr Thr Ala Arg Ala Arg Glu Gly Val 215 220 225 230 235																

215	220	225	
gga gcc cgc tgc ggg cgt gga ttt gga tgataagacc attccccatg			834
Gly Ala Arg Cys Gly Arg Gly Phe Gly			
230	235		
aaa			837
 <210> 374			
<211> 238			
<212> PRT			
<213> Corynebacterium glutamicum			
 <400> 374			
Val Gly Thr Ile Glu Asp Val Ala Asn Glu Gln Ile Glu Val Ala Asn			
1	5	10	15
Asn Thr Asp Gln Ile Pro Ala Gly Tyr Lys Ser Pro Leu Leu Ser Arg			
	20	25	30
Ser Gly Ala Ala Glu Ala Gln Gly Ala Ala Ala Gln Ala Gly Thr Glu			
	35	40	45
Gly Val Ala Trp His Tyr Gly Ser Pro Leu Val Glu Gln Arg Ile Phe			
	50	55	60
Glu Thr Gly Thr Gly Leu Val Asp Arg Ser Asn Arg Lys Val Ile Lys			
	65	70	75
Val Glu Gly Pro Asp Ala Pro Thr Phe Leu Asn Asn Ile Leu Ser Gln			
	85	90	95
Lys Val Asp Ser Val Glu Asn Gly Phe Thr Ala Gly Ala Leu Asp Leu			
	100	105	110
Asp Ala Gln Gly Arg Ile Gln His Thr Met Gln Val Thr Val Val Asp			
	115	120	125
Gly Val Phe Tyr Leu Asp Thr Ser Ala Ala Glu Phe Asp Thr Leu Ile			
	130	135	140
Gly Phe Leu Thr Lys Met Ile Phe Trp Ser Glu Val Thr Val Gln Glu			
	145	150	155
Ala Asp Leu Ala Ile Ile Thr Leu Leu Gly Gln Glu Ile Ala Leu Pro			
	165	170	175
Asp Ala Val Phe Ala Arg Arg Val Asp Trp Asn Gly Pro Ser Arg Ile			
	180	185	190
Asp Val Ala Ile Arg Arg Glu Asn Leu Glu Glu Gly Val Asp Lys Leu			
	195	200	205
Leu Glu Ala Gly Ala Lys Leu Thr Gly Leu Met Ala Tyr Thr Ala Arg			
	210	215	220
Ala Arg Glu Gly Val Gly Ala Arg Cys Gly Arg Gly Phe Gly			
225	230	235	

<210> 375
 <211> 336
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(313)
 <223> RXN00769

<400> 375
 ggctattgtg tctatcagga atacagttaa tacatcttga aaagcccatg ggccatccga 60
 attccccagga tcggcccgct cactccaagg gggtoaggca atg ggt cgc ggt cgc 115
 Met Gly Arg Gly Arg
 1 5
 gcg aag gca aaa cag acc aaa gtt gct cgc cag ttg aag tac agc tct 163
 Ala Lys Ala Lys Gln Thr Lys Val Ala Arg Gln Leu Lys Tyr Ser Ser
 10 15 20
 cca gac atg gat ctc gat tcg ctg cag cgg gag ctg gct aac cag tct 211
 Pro Asp Met Asp Leu Asp Ser Leu Gln Arg Glu Leu Ala Asn Gln Ser
 25 30 35
 cot agg cgt tcc tac tcc gat acc cct gat gat gag gac cag tac gca 259
 Pro Arg Arg Ser Tyr Ser Asp Thr Pro Asp Asp Glu Asp Gln Tyr Ala
 40 45 50
 gag tat gcg gac tgg gat gag gac gac acc gac aat cgt gcc tac ggc 307
 Glu Tyr Ala Asp Trp Asp Glu Asp Asp Thr Asp Asn Arg Ala Tyr Gly
 55 60 65
 aca aac tgatttcgtg tgtccttaac tct 336
 Thr Asn
 70

<210> 376
 <211> 71
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 376
 Met Gly Arg Gly Ala Lys Ala Lys Gln Thr Lys Val Ala Arg Gln
 1 5 10 15
 Leu Lys Tyr Ser Ser Pro Asp Met Asp Leu Asp Ser Leu Gln Arg Glu
 20 25 30
 Leu Ala Asn Gln Ser Pro Arg Arg Ser Tyr Ser Asp Thr Pro Asp Asp
 35 40 45
 Glu Asp Gln Tyr Ala Glu Tyr Ala Asp Trp Asp Glu Asp Asp Thr Asp
 50 55 60
 Asn Arg Ala Tyr Gly Thr Asn
 65 70

<210> 377

<211> 336
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> {101}..{313}
 <223> FRXA00769

<400> 377
 ggtctattgtg tctatcagga atacagttaa tacatottga aaagcccatg ggccatccga 60
 attcccagga tcggcccgc tctccaagg gggtcaggca atg ggt cgc ggt cgc 115
 Met Gly Arg Gly Arg
 1 5
 gcg aag gca aaa cag acc aaa gtt gct cgc cag ttg aag tac agc tct 163
 Ala Lys Ala Lys Gln Thr Lys Val Ala Arg Gln Leu Lys Tyr Ser Ser
 10 15 20
 cca gac atg gat ctc gat tcg ctg cag cgg gag ctg gct aac cag tct 211
 Pro Asp Met Asp Leu Asp Ser Leu Gln Arg Glu Leu Ala Asn Gln Ser
 25 30 35
 cct agg cgt tcc tac tcc gat acc cct gat gat gag gac cag tac gca 259
 Pro Arg Arg Ser Tyr Ser Asp Thr Pro Asp Asp Glu Asp Gln Tyr Ala
 40 45 50
 gag tat gcg gac tgg gat gag gac gac acc gac aat cgt gcc tac ggc 307
 Glu Tyr Ala Asp Trp Asp Glu Asp Asp Thr Asp Asn Arg Ala Tyr Gly
 55 60 65
 aca aac tgatttcgtg tgtccttaac tct 336
 Thr Asn
 70

<210> 378
 <211> 71
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 378
 Met Gly Arg Gly Arg Ala Lys Ala Lys Gln Thr Lys Val Ala Arg Gln
 1 5 10 15
 Leu Lys Tyr Ser Ser Pro Asp Met Asp Leu Asp Ser Leu Gln Arg Glu
 20 25 30
 Leu Ala Asn Gln Ser Pro Arg Arg Ser Tyr Ser Asp Thr Pro Asp Asp
 35 40 45
 Glu Asp Gln Tyr Ala Glu Tyr Ala Asp Trp Asp Glu Asp Asp Thr Asp
 50 55 60
 Asn Arg Ala Tyr Gly Thr Asn
 65 70

<210> 379
 <211> 942

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(919)

<223> RXN00771

<400> 379

taccocctgtt ttggagaatg ctccgagcca ggggtacttt tcttttcctc acacacagta 60

gctgctgaga aaaatgaaga ccttttgta ggttggagt atg acc aac cca tac 115
 Met Thr Asn Pro Tyr
 1 5

gag gcc ttc ata cgc ctc aag cat cgt acg ggg att gaa ccc gag cac 163
 Glu Ala Phe Ile Pro Leu Lys His Arg Thr Gly Ile Glu Pro Glu His
 10 15 20

acc ttt tgg gaa tgg gaa aac aaa agg gtt cac att gca agg aga cgt 211
 Thr Phe Trp Glu Trp Glu Asn Lys Arg Val His Ile Ala Arg Arg Arg
 25 30 35

cga gaa gcg ccc gtc cgc gtt atc gtg gtg cat ggg cta ggc acc cat 259
 Arg Glu Ala Pro Val Arg Val Ile Val Val His Gly Leu Gly Thr His
 40 45 50

agt ggc gcc ctc tgg ccc ctc gtc gcg gcc att gag ggc gcg gac ctc 307
 Ser Gly Ala Leu Trp Pro Leu Val Ala Ala Ile Glu Gly Ala Asp Leu
 55 60 65

gcc gcg atc gac ctg cct aaa act ccg ctt tac gac gat tgg ctg cgc 355
 Ala Ala Ile Asp Leu Pro Lys Thr Pro Leu Tyr Asp Asp Trp Leu Arg
 70 75 80 85

ctt tta gaa tct ttc atc tcg tcc gaa gac gac ggt cgg cca ctc atc 403
 Leu Leu Glu Ser Phe Ile Ser Ser Glu Asp Asp Gly Arg Pro Leu Ile
 90 95 100

ctg atc ggt gca ggc acc gga ggc ttg ctt tgc gca gaa gct gca cac 451
 Leu Ile Gly Ala Gly Thr Gly Gly Leu Leu Cys Ala Glu Ala Ala His
 105 110 115

cgc aca gga ctg gtc gca cac gtc att gcc acc tgc ctg ctc aac ccc 499
 Arg Thr Gly Leu Val Ala His Val Ile Ala Thr Cys Leu Leu Asn Pro
 120 125 130

tcc gac cag ccg acg cgc cgg gca ctg ttc agg ttt tca ccg ctg act 547
 Ser Asp Gln Pro Thr Arg Arg Ala Leu Phe Arg Phe Ser Pro Leu Thr
 135 140 145

cgg ttg atc caa ggc cgc ttg cgc aac cgc gaa att ccc gtg acc aga 595
 Arg Leu Ile Gln Gly Arg Leu Arg Asn Arg Glu Ile Pro Val Thr Arg
 150 155 160 165

gtg ttg aac ttc agc aaa atc agc cgc agc cca gcc ctg agc aaa ttg 643
 Val Leu Asn Phe Ser Lys Ile Ser Arg Ser Pro Ala Leu Ser Lys Leu
 170 175 180

tgc gcg gcc gat gaa ttt agc gga gca tcc aaa ata acc tgg ggt ttc 691
 Cys Ala Ala Asp Glu Phe Ser Gly Ala Ser Lys Ile Thr Trp Gly Phe

185	190	195	
ctc gcg tca tat gtg caa cac aag gcc aaa ctg ggt gca gtt ccc gtc			739
Leu Ala Ser Tyr Val Gln His Lys Ala Lys Leu Gly Ala Val Pro Val			
200	205	210	
act ctg atg cac cct gac cac gac ctt ctg act ccc gtt gag ctc agt			787
Thr Leu Met His Pro Asp His Asp Leu Leu Thr Pro Val Glu Leu Ser			
215	220	225	
ctg cgt acg ctt tgc cgc ctc aaa gcg ccc act gac gtg gtt atg ctc			835
Leu Arg Thr Leu Ser Arg Leu Lys Ala Pro Thr Asp Val Val Met Leu			
230	235	240	245
aag gac tgc ggg cat ttt ccc atc gaa gaa ccc ggc ttc acc acc atg			883
Lys Asp Cys Gly His Phe Pro Ile Glu Glu Pro Gly Phe Thr Thr Met			
250	255	260	
ctc gaa acc gtc aca tca gtt atc gcg cgg aat agt tagcggggcgc			929
Leu Glu Thr Val Thr Ser Val Ile Ala Arg Asn Ser			
265	270		
atgtggttgg gat			942
<210> 380			
<211> 273			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 380			
Met Thr Asn Pro Tyr Glu Ala Phe Ile Pro Leu Lys His Arg Thr Gly			
1	5	10	15
Ile Glu Pro Glu His Thr Phe Trp Glu Trp Glu Asn Lys Arg Val His			
20	25	30	
Ile Ala Arg Arg Arg Arg Glu Ala Pro Val Arg Val Ile Val Val His			
35	40	45	
Gly Leu Gly Thr His Ser Gly Ala Leu Trp Pro Leu Val Ala Ala Ile			
50	55	60	
Glu Gly Ala Asp Leu Ala Ala Ile Asp Leu Pro Lys Thr Pro Leu Tyr			
65	70	75	80
Asp Asp Trp Leu Arg Leu Leu Glu Ser Phe Ile Ser Ser Glu Asp Asp			
85	90	95	
Gly Arg Pro Leu Ile Leu Ile Gly Ala Gly Thr Gly Gly Leu Leu Cys			
100	105	110	
Ala Glu Ala Ala His Arg Thr Gly Leu Val Ala His Val Ile Ala Thr			
115	120	125	
Cys Leu Leu Asn Pro Ser Asp Gln Pro Thr Arg Arg Ala Leu Phe Arg			
130	135	140	
Phe Ser Pro Leu Thr Arg Leu Ile Gln Gly Arg Leu Arg Asn Arg Glu			
145	150	155	160

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Ile Pro Val Thr Arg Val Leu Asn Phe Ser Lys Ile Ser Arg Ser Pro
      165                      170                      175

Ala Leu Ser Lys Leu Cys Ala Ala Asp Glu Phe Ser Gly Ala Ser Lys
      180                      185                      190

Ile Thr Trp Gly Phe Leu Ala Ser Tyr Val Gln His Lys Ala Lys Leu
      195                      200                      205

Gly Ala Val Pro Val Thr Leu Met His Pro Asp His Asp Leu Leu Thr
      210                      215                      220

Pro Val Glu Leu Ser Leu Arg Thr Leu Ser Arg Leu Lys Ala Pro Thr
      225                      230                      235                      240

Asp Val Val Met Leu Lys Asp Cys Gly His Phe Pro Ile Glu Glu Pro
      245                      250                      255

Gly Phe Thr Thr Met Leu Glu Thr Val Thr Ser Val Ile Ala Arg Asn
      260                      265                      270

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Ser

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<210> 381
<211> 801
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(778)
<223> FRXA00771

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<400> 381
taccacctgtt ttggagaatg ctccgagcca ggggtacttt tcttttctct acacacagta 60

gctgctgaga aaaatgaaga ccttttggtta ggttgggagt atg acc aac cca tac 115
                                         Met Thr Asn Pro Tyr
                                         1                               5

gag gcc ttc ata cgc ctc aag cat cgt acg ggg att gaa ccc gag cac 163
Glu Ala Phe Ile Pro Leu Lys His Arg Thr Gly Ile Glu Pro Glu His
      10                      15                      20

acc ttt tgg gaa tgg gaa aac aaa agg gtt cac att gca agg aga cgt 211
Thr Phe Trp Glu Trp Glu Asn Lys Arg Val His Ile Ala Arg Arg Arg
      25                      30                      35

cga gaa gcg ccc gtc cgc gtt atc gtg gtg cat ggg cta ggc acc cat 259
Arg Glu Ala Pro Val Arg Val Ile Val Val His Gly Leu Gly Thr His
      40                      45                      50

agt ggc gcc ctc tgg ccc ctc gtc gcg gcc att gag ggc gcg gac ctc 307
Ser Gly Ala Leu Trp Pro Leu Val Ala Ala Ile Glu Gly Ala Asp Leu
      55                      60                      65

gcc gcg atc gac ctg cct aaa act ccg ctt tac gac gat tgg ctg cgc 355
Ala Ala Ile Asp Leu Pro Lys Thr Pro Leu Tyr Asp Asp Trp Leu Arg
      70                      75                      80                      85

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ctt tta gaa tct ttc atc tcg tcc gaa gac gac ggt cgg cca ctc atc 403
 Leu Leu Glu Ser Phe Ile Ser Ser Glu Asp Asp Gly Arg Pro Leu Ile
 90 95 100

ctg atc ggt gca ggc acc gga ggc ttg ctt tgc gca gaa gct gca cac 451
 Leu Ile Gly Ala Gly Thr Gly Gly Leu Leu Cys Ala Glu Ala Ala His
 105 110 115

cgc aca gga ctg gtc gca cac gtc att gcc acc tgc ctg ctc aac ccc 499
 Arg Thr Gly Leu Val Ala His Val Ile Ala Thr Cys Leu Leu Asn Pro
 120 125 130

tcc gac cag ccg acg cgc cgg gca ctg ttc agg ttt tca ccg ctg act 547
 Ser Asp Gln Pro Thr Arg Arg Ala Leu Phe Arg Phe Ser Pro Leu Thr
 135 140 145

cgg ttg atc caa ggc cgc ttg cgc aac cgc gaa att ccc gtg acc aga 595
 Arg Leu Ile Gln Gly Arg Leu Arg Asn Arg Glu Ile Pro Val Thr Arg
 150 155 160 165

gtg ttg aac ttc agc aaa atc agc cgc agc cca gcc ctg agc aaa ttg 643
 Val Leu Asn Phe Ser Lys Ile Ser Arg Ser Pro Ala Leu Ser Lys Leu
 170 175 180

tgc gcg gcc gat gaa ttt aac gga gca ttc aaa ata acc tgg ggt ttc 691
 Cys Ala Ala Asp Glu Phe Asn Gly Ala Phe Lys Ile Thr Trp Gly Phe
 185 190 195

ctg gcg tca tat gtg caa cac aag gcc aaa ctg ggt gca gtt ccc ctc 739
 Leu Ala Ser Tyr Val Gln His Lys Ala Lys Leu Gly Ala Val Pro Leu
 200 205 210

act ctg atg cac cct gac cac gac ctt ttt gac tcc cgt tgagctcaaaa 788
 Thr Leu Met His Pro Asp His Asp Leu Phe Asp Ser Arg
 215 220 225

tctgcgtacg ctt 801

<210> 382

<211> 226

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 382

 Met Thr Asn Pro Tyr Glu Ala Phe Ile Pro Leu Lys His Arg Thr Gly
 1 5 10 15

 Ile Glu Pro Glu His Thr Phe Trp Glu Trp Glu Asn Lys Arg Val His
 20 25 30

 Ile Ala Arg Arg Arg Arg Glu Ala Pro Val Arg Val Ile Val Val His
 35 40 45

 Gly Leu Gly Thr His Ser Gly Ala Leu Trp Pro Leu Val Ala Ala Ile
 50 55 60

 Gly Gly Ala Asp Leu Ala Ala Ile Asp Leu Pro Lys Thr Pro Leu Tyr
 65 70 75 80

Asp Asp Trp Leu Arg Leu Leu Glu Ser Phe Ile Ser Ser Glu Asp Asp
 85 90 95
 Gly Arg Pro Leu Ile Leu Ile Gly Ala Gly Thr Gly Gly Leu Leu Cys
 100 105 110
 Ala Glu Ala Ala His Arg Thr Gly Leu Val Ala His Val Ile Ala Thr
 115 120 125
 Cys Leu Leu Asn Pro Ser Asp Gln Pro Thr Arg Arg Ala Leu Phe Arg
 130 135 140
 Phe Ser Pro Leu Thr Arg Leu Ile Gln Gly Arg Leu Arg Asn Arg Glu
 145 150 155 160
 Ile Pro Val Thr Arg Val Leu Asn Phe Ser Lys Ile Ser Arg Ser Pro
 165 170 175
 Ala Leu Ser Lys Leu Cys Ala Ala Asp Glu Phe Asn Gly Ala Phe Lys
 180 185 190
 Ile Thr Trp Gly Phe Leu Ala Ser Tyr Val Gln His Lys Ala Lys Leu
 195 200 205
 Gly Ala Val Pro Leu Thr Leu Met His Pro Asp His Asp Leu Phe Asp
 210 215 220
 Ser Arg
 225

<210> 383

<211> 680

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(657)

<223> RXN00785

<400> 383

atc atc gct act ctc ggt gtg acc ttg ctg gtt gag gcc cgc gga tta 48
 Ile Ile Ala Thr Leu Gly Val Thr Leu Leu Val Glu Ala Arg Gly Leu
 1 5 10 15

ttc ttg acg gtt gcg tcc att ccc att ctg ttt ggt att ttc aca cca 96
 Phe Leu Thr Val Ala Ser Ile Pro Ile Leu Phe Gly Ile Phe Thr Pro
 20 25 30

ctg act tcg tgg ttt gtg tcc caa caa ggc gtg gct gcg aat gtg tcc 144
 Leu Thr Ser Trp Phe Val Ser Gln Gln Gly Val Ala Ala Asn Val Ser
 35 40 45

cct ggt gtt tcc gtc acg gaa atc ctc acg gct gtt tat cct ttg gcg 192
 Pro Gly Val Ser Val Thr Glu Ile Leu Thr Ala Val Tyr Pro Leu Ala
 50 55 60

cag ttg ttc ccc acc ctg atc atg gtc act ttg gtg gcg gca ttg atc 240
 Gln Leu Phe Pro Thr Leu Ile Met Val Thr Leu Val Ala Ala Leu Ile
 65 70 75 80

gct gtg gtg cgg att att ctg ctg cgc agg aac cag gaa tct cgt cag 288
Ala Val Val Arg 85 Ile Leu Leu Arg Arg Asn Gln Glu Ser Arg Gln 95

gtt tct ggg gaa ctt acc cgg cgc gcg cag cgt gag gct gag gaa gct 336
Val Ser Gly Glu Leu Thr Arg Arg Ala Gln Arg Glu Ala Glu Glu Ala 100 105 110

aat cag aat gct gct cgt cgt gct cgc gca cag agc acg agg gta caa 384
Asn Gln Asn Ala Ala Arg Arg Ala Arg Ala Gln Ser Thr Arg Val Gln 115 120 125

agt tct aaa aca cgt aac cgt cgc gcg caa cca acc ggc gat acc ggt 432
Ser Ser Lys Thr Arg Asn Arg Arg Ala Gln Pro Thr Gly Asp Thr Gly 130 135 140

tca caa gtc acg gtt gat gag ttg atc agg cgt agc cag gag cgc cgg 480
Ser Gln Val Thr Val Asp 150 Glu Leu Ile Arg Arg Ser Gln Glu Arg Arg 145 155 160

caa act gtt gcg cag cgc caa act gag cgc ggt gtg ccg ttt act cca 528
Gln Thr Val Ala Gln Arg Gln Thr Glu Arg Gly Val Pro Phe Thr Pro 165 170 175

act ccg ggt cct gtg gtg gcc ccc aag ccg cgc ccg agc gcc cct gag 576
Thr Pro Gly Pro Val Val Ala Pro Lys Pro Arg Pro Ser Ala Pro Glu 180 185 190

gcg ccg gct cct acg gat gtg ggt gag cgt cga caa gca gcc cct aaa 624
Ala Pro Ala Pro Thr Asp Val Gly Glu Arg Arg Gln Ala Ala Pro Lys 195 200 205

gcg cgc acc tcg ctc gac gat gat ctg tac agc taaaaaatcc ccgctcatgt 677
Arg Arg Thr Ser Leu Asp Asp Asp Leu Tyr Ser 210 215

ggc 680

<210> 384

<211> 219

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 384

Ile Ile Ala Thr Leu Gly Val Thr Leu Leu Val Glu Ala Arg Gly Leu
1 5 10 15

Phe Leu Thr Val Ala Ser Ile Pro Ile Leu Phe Gly Ile Phe Thr Pro
20 25 30

Leu Thr Ser Trp Phe Val Ser Gln Gln Gly Val Ala Ala Asn Val Ser
35 40 45

Pro Gly Val Ser Val Thr Glu Ile Leu Thr Ala Val Tyr Pro Leu Ala
50 55 60

Gln Leu Phe Pro Thr Leu Ile Met Val Thr Leu Val Ala Ala Leu Ile
65 70 75 80

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Ala Val Val Arg Ile Ile Leu Leu Arg Arg Asn Gln Glu Ser Arg Gln
                        85                      90                      95

Val Ser Gly Glu Leu Thr Arg Arg Ala Gln Arg Glu Ala Glu Glu Ala
                        100                     105                     110

Asn Gln Asn Ala Ala Arg Arg Ala Arg Ala Gln Ser Thr Arg Val Gln
                        115                     120                     125

Ser Ser Lys Thr Arg Asn Arg Arg Ala Gln Pro Thr Gly Asp Thr Gly
                        130                     135                     140

Ser Gln Val Thr Val Asp Glu Leu Ile Arg Arg Ser Gln Glu Arg Arg
                        145                     150                     155                     160

Gln Thr Val Ala Gln Arg Gln Thr Glu Arg Gly Val Pro Phe Thr Pro
                        165                     170                     175

Thr Pro Gly Pro Val Val Ala Pro Lys Pro Arg Pro Ser Ala Pro Glu
                        180                     185                     190

Ala Pro Ala Pro Thr Asp Val Gly Glu Arg Arg Gln Ala Ala Pro Lys
                        195                     200                     205

Arg Arg Thr Ser Leu Asp Asp Asp Leu Tyr Ser
                        210                     215

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<210> 385
<211> 621
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (1)..(621)
<223> FRXA00785

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<400> 385
atc atc gct act ctc ggt gtg acc ttg ctg gtt gag gcc cgc gga tta 48
Ile Ile Ala Thr Leu Gly Val Thr Leu Leu Val Glu Ala Arg Gly Leu
1 5 10 15

ttc ttg acg gtt gcg tcc att ccc att ctg ttt ggt att ttc aca cca 96
Phe Leu Thr Val Ala Ser Ile Pro Ile Leu Phe Gly Ile Phe Thr Pro
20 25 30

ctg act tcg tgg ttt gtg tcc caa caa ggc gtg gct gcg aat gtg tcc 144
Leu Thr Ser Trp Phe Val Ser Gln Gly Val Ala Ala Asn Val Ser
35 40 45

cct ggt gtt tcc gtc acg gaa atc ctc acg gct gtt tat cct ttg gcg 192
Pro Gly Val Ser Val Thr Glu Ile Leu Thr Ala Val Tyr Pro Leu Ala
50 55 60

cag ttg ttc ccc acc ctg atc atg gtc act ttg gtg gcg gca ttg atc 240
Gln Leu Phe Pro Thr Leu Ile Met Val Thr Leu Val Ala Ala Leu Ile
65 70 75 80

gct gtg gtg cgg att att ctg ctg cgc agg aac cag gaa tct cgt cag 288
Ala Val Val Arg Ile Ile Leu Leu Arg Arg Asn Gln Glu Ser Arg Gln

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	85	90	95	
gtt tct ggg gaa ctt acc cgg cgc gcg cag cgt gag gct gag gaa gct				336
Val Ser Gly Glu Leu Thr Arg Arg Ala Gln Arg Glu Ala Glu Ala				
	100	105	110	
aat cag aat gct gct cgt cgt gct cgc gca cag agc acg agg gta caa				384
Asn Gln Asn Ala Ala Arg Arg Ala Arg Ala Gln Ser Thr Arg Val Gln				
	115	120	125	
agt tct aaa aca cgt aac cgt cgc gcg caa cca acc ggc gat acc ggt				432
Ser Ser Lys Thr Arg Asn Arg Arg Ala Gln Pro Thr Gly Asp Thr Gly				
	130	135	140	
tca caa gtc acg gtt gat gag ttg atc agg cgt agc cag gag cgc cgg				480
Ser Gln Val Thr Val Asp Glu Leu Ile Arg Arg Ser Gln Glu Arg Arg				
	145	150	155	160
caa act gtt gcg cag cgc caa act gag cgc ggt gtg cgg ttt act cca				528
Gln Thr Val Ala Gln Arg Gln Thr Glu Arg Gly Val Pro Phe Thr Pro				
	165	170	175	
act cgg ggt cct gtg gtg gcc ccc aag cgg cgc ccg agc gcc cct gag				576
Thr Pro Gly Pro Val Val Ala Pro Lys Pro Arg Pro Ser Ala Pro Glu				
	180	185	190	
gcg ccg gct cct acg gat gtg ggt gag cgt cga caa gca gcc cct				621
Ala Pro Ala Pro Thr Asp Val Gly Glu Arg Arg Gln Ala Ala Pro				
	195	200	205	
<210> 386				
<211> 207				
<212> PRT				
<213> <i>Corynebacterium glutamicum</i>				
<400> 386				
Ile Ile Ala Thr Leu Gly Val Thr Leu Leu Val Glu Ala Arg Gly Leu				
	1	5	10	15
Phe Leu Thr Val Ala Ser Ile Pro Ile Leu Phe Gly Ile Phe Thr Pro				
	20	25	30	
Leu Thr Ser Trp Phe Val Ser Gln Gln Gly Val Ala Ala Asn Val Ser				
	35	40	45	
Pro Gly Val Ser Val Thr Glu Ile Leu Thr Ala Val Tyr Pro Leu Ala				
	50	55	60	
Gln Leu Phe Pro Thr Leu Ile Met Val Thr Leu Val Ala Ala Leu Ile				
	65	70	75	80
Ala Val Val Arg Ile Ile Leu Leu Arg Arg Asn Gln Glu Ser Arg Gln				
	85	90	95	
Val Ser Gly Glu Leu Thr Arg Arg Ala Gln Arg Glu Ala Glu Glu Ala				
	100	105	110	
Asn Gln Asn Ala Ala Arg Arg Ala Arg Ala Gln Ser Thr Arg Val Gln				
	115	120	125	

Ser Ser Lys Thr Arg Asn Arg Arg Ala Gln Pro Thr Gly Asp Thr Gly
 130 135
 Ser Gln Val Thr Val Asp Glu Leu Ile Arg Arg Ser Gln Glu Arg Arg
 145 150 155 160
 Gln Thr Val Ala Gln Arg Gln Thr Glu Arg Gly Val Pro Phe Thr Pro
 165 170 175
 Thr Pro Gly Pro Val Val Ala Pro Lys Pro Arg Pro Ser Ala Pro Glu
 180 185 190
 Ala Pro Ala Pro Thr Asp Val Gly Glu Arg Arg Gln Ala Ala Pro
 195 200 205

<210> 387

<211> 651

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(628)

<223> RXN00795

<400> 387

tttggattct ggacacccaa aagggggttt cgtaccaaac tcgtgacata ctaggcgggt 60
 ggctgagaaa cgaccgaaaa tttttgatgg cagtcgagac atg att atc tcg ttg 115
 Met Ile Ile Ser Leu
 1 5
 gta gtc tcc gcg atc atc atg ttg gta gcg gtg gga ttc acg gga atg 163
 Val Val Ser Ala Ile Ile Met Leu Val Ala Val Gly Phe Thr Gly Met
 10 15 20
 tgt tct ttc aat aca gga tcc cct gaa aat ggg cag gta cct gaa gtt 211
 Cys Ser Phe Asn Thr Gly Ser Pro Glu Asn Gly Gln Val Pro Glu Val
 25 30 35
 gat gct tcc act ttt atg tca atg gaa gcg cgc gca atg act gat cat 259
 Asp Ala Ser Thr Phe Met Ser Met Glu Ala Arg Ala Met Thr Asp His
 40 45 50
 gca act agg ttg ccg gaa act cct gaa ggc tgg acc aca aat tca gct 307
 Ala Thr Arg Leu Pro Glu Thr Pro Glu Gly Trp Thr Thr Asn Ser Ala
 55 60 65
 cga cgc acc atg gtg gat gac acc ccg gca tct gta gtt gga tat gtc 355
 Arg Arg Thr Met Val Asp Asp Thr Pro Ala Ser Val Val Gly Tyr Val
 70 75 80 85
 acc gca gat gag ggc tat att cag ctc act caa act ggt gaa acc gtt 403
 Thr Ala Asp Glu Gly Tyr Ile Gln Leu Thr Gln Thr Gly Glu Thr Val
 90 95 100
 gag gat gct gtg gct ggt tat gat act cgc tgg cgt gat ctt tct gag 451
 Glu Asp Ala Val Ala Gly Tyr Asp Thr Arg Trp Arg Asp Leu Ser Glu
 105 110 115

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tct tat gat ctt gat ggc cac gac gtg gga att tac acc tca cag gaa 499
Ser Tyr Asp Leu Asp Gly His Asp Val Gly Ile Tyr Thr Ser Gln Glu
120 125 130

tct gat gtg cgt gat ctg cgt gtg atg gat ctg ggc gat gcc cgc gtc 547
Ser Asp Val Arg Asp Leu Arg Val Met Asp Leu Gly Asp Ala Arg Val
135 140 145

atg gtc tcg ggt gct gct acc gat gaa gaa ttc aat gat ctg ctt cgc 595
Met Val Ser Gly Ala Ala Thr Asp Glu Glu Phe Asn Asp Leu Leu Arg
150 155 160 165

gca gtt gcg aat tcg gag cca ctg cct acc aat taagaattgg tcgaaccacc 648
Ala Val Ala Asn Ser Glu Pro Leu Pro Thr Asn
170 175

aaa 651

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<210> 388

<211> 176

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 388

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Met Ile Ile Ser Leu Val Val Ser Ala Ile Ile Met Leu Val Ala Val
1 5 10 15

Gly Phe Thr Gly Met Cys Ser Phe Asn Thr Gly Ser Pro Glu Asn Gly
20 25 30

Gln Val Pro Glu Val Asp Ala Ser Thr Phe Met Ser Met Glu Ala Arg
35 40 45

Ala Met Thr Asp His Ala Thr Arg Leu Pro Glu Thr Pro Glu Gly Trp
50 55 60

Thr Thr Asn Ser Ala Arg Arg Thr Met Val Asp Asp Thr Pro Ala Ser
65 70 75 80

Val Val Gly Tyr Val Thr Ala Asp Glu Gly Tyr Ile Gln Leu Thr Gln
85 90 95

Thr Gly Glu Thr Val Glu Asp Ala Val Ala Gly Tyr Asp Thr Arg Trp
100 105 110

Arg Asp Leu Ser Glu Ser Tyr Asp Leu Asp Gly His Asp Val Gly Ile
115 120 125

Tyr Thr Ser Gln Glu Ser Asp Val Arg Asp Leu Arg Val Met Asp Leu
130 135 140

Gly Asp Ala Arg Val Met Val Ser Gly Ala Ala Thr Asp Glu Glu Phe
145 150 155 160

Asn Asp Leu Leu Arg Ala Val Ala Asn Ser Glu Pro Leu Pro Thr Asn
165 170 175

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<210> 389
 <211> 651
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(628)
 <223> FRXA00795

<400> 389
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 ggctgagaaa cgaccgaaaa tttttgatgg cagtcgagac atg att atc tcg ttg 115
 Met Ile Ile Ser Leu
 1 5
 gta gtc tcc gcg atc atc atg ttg gta gcg gtg gga ttc acg gga atg 163
 Val Val Ser Ala Ile Ile Met Leu Val Ala Val Gly Phe Thr Gly Met
 10 15 20
 tgt tct ttc aat aca gga tcc cct gaa aat ggg cag gta cct gaa gtt 211
 Cys Ser Phe Asn Thr Gly Ser Pro Glu Asn Gly Gln Val Pro Glu Val
 25 30 35
 gat gct tcc act ttt atg tca atg gaa gcg cgc gca atg act gat cat 259
 Asp Ala Ser Thr Phe Met Ser Met Glu Ala Arg Ala Met Thr Asp His
 40 45 50
 gca act agg ttg ccg gaa act cct gaa ggc tgg acc aca aat tca gct 307
 Ala Thr Arg Leu Pro Glu Thr Pro Glu Gly Trp Thr Thr Asn Ser Ala
 55 60 65
 cga cgc acc atg gtg gat gac acc ccg gca tct gta gtt gga tat gtc 355
 Arg Arg Thr Met Val Asp Asp Thr Pro Ala Ser Val Val Gly Tyr Val
 70 75 80 85
 acc gca gat gag ggc tat att cag etc act caa act ggt gaa acc gtt 403
 Thr Ala Asp Glu Gly Tyr Ile Gln Leu Thr Gln Thr Gly Thr Leu Val
 90 95 100
 gag gat gct gtg gct ggt tat gat act cgc tgg cgt gat ctt tct gag 451
 Glu Asp Ala Val Ala Gly Tyr Asp Thr Arg Trp Arg Asp Leu Ser Glu
 105 110 115
 tct tat gat ctt gat ggc cac gac gtg gga att tac acc tca cag gaa 499
 Ser Tyr Asp Leu Asp Gly His Asp Val Gly Ile Tyr Thr Ser Gln Glu
 120 125 130
 tct gat gtg cgt gat ctg cgt gtg atg gat ctg ggc gat gcc cgc gtc 547
 Ser Asp Val Arg Asp Leu Arg Val Met Asp Leu Gly Asp Ala Arg Val
 135 140 145
 atg gtc tcg ggt gct gct acc gat gaa gaa ttc aat gat ctg ctt cgc 595
 Met Val Ser Gly Ala Ala Thr Asp Glu Glu Phe Asn Asp Leu Leu Arg
 150 155 160 165
 gca gtt gcg aat tcg gag cca ctg cct acc aat taagaattgg tcgaaccacc 648
 Ala Val Ala Asn Ser Glu Pro Leu Pro Thr Asn
 170 175

aaa

651

<210> 390

<211> 176

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 390

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 1 5 10 15

Gly Phe Thr Gly Met Cys Ser Phe Asn Thr Gly Ser Pro Glu Asn Gly
 20 25 30

Gln Val Pro Glu Val Asp Ala Ser Thr Phe Met Ser Met Glu Ala Arg
 35 40 45

Ala Met Thr Asp His Ala Thr Arg Leu Pro Glu Thr Pro Glu Gly Trp
 50 55 60

Thr Thr Asn Ser Ala Arg Arg Thr Met Val Asp Asp Thr Pro Ala Ser
 65 70 75 80

Val Val Gly Tyr Val Thr Ala Asp Glu Gly Tyr Ile Gln Leu Thr Gln
 85 90 95

Thr Gly Glu Thr Val Glu Asp Ala Val Ala Gly Tyr Asp Thr Arg Trp
 100 105 110

Arg Asp Leu Ser Glu Ser Tyr Asp Leu Asp Gly His Asp Val Gly Ile
 115 120 125

Tyr Thr Ser Gln Glu Ser Asp Val Arg Asp Leu Arg Val Met Asp Leu
 130 135 140

Gly Asp Ala Arg Val Met Val Ser Gly Ala Ala Thr Asp Glu Glu Phe
 145 150 155 160

Asn Asp Leu Leu Arg Ala Val Ala Asn Ser Glu Pro Leu Pro Thr Asn
 165 170 175

<210> 391

<211> 825

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}..{802}

<223> RXN00831

<400> 391

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atgatgagca tggctgcctg atttaggttag cctgggtggga atg agt gca ctt gag 115

	Met	Ser	Ala	Leu	Glu	
	1				5	
aca ttg caa tgg cag gac tgg tca agc gtc tta att gtg gta gct cac						163
Thr Leu Gln Trp Gln Asp Trp Ser Ser Val Leu Ile Val Val Ala His						
	10				20	
cca gat gat ccg gag tat ggg ctt tcc gcg gct gtt aaa gaa tgg aca						211
Pro Asp Asp Pro Glu Tyr Gly Leu Ser Ala Ala Val Lys Glu Trp Thr						
	25				35	
gac gcc ggg gtg gag gtg tct tac ctg ctg ctc acc cac ggg gag gca						259
Asp Ala Gly Val Glu Val Ser Tyr Leu Leu Leu Thr His Gly Glu Ala						
	40				50	
ggc atc caa ggt tta gac cct aaa gaa acc ggg tca ttg cgc gca gcg						307
Gly Ile Gln Gly Leu Asp Pro Lys Glu Thr Gly Ser Leu Arg Ala Ala						
	55				65	
gaa cag cgg gct gca tgt gat gtg gta gga gtt aga aat ctc acc att						355
Glu Gln Arg Ala Ala Cys Asp Val Val Gly Val Arg Asn Leu Thr Ile						
	70				80	
ttg aat cac cca gat tcc atg ttg gtg tac aat ctg gta ctg cgc aaa						403
Leu Asn His Pro Asp Ser Met Leu Val Tyr Asn Leu Val Leu Arg Lys						
	90				100	
gat att gct ccg gaa atc cgg atc cgt aaa cca aat gct gtg gta						451
Asp Ile Ala Arg Glu Ile Arg Ile Arg Lys Pro Asn Ala Val Val Val						
	105				115	
tcc aat ttt gat gta gag gcc tac ggt ggt ttg aac cag gcg gat cac						499
Ser Asn Phe Asp Val Glu Ala Tyr Gly Gly Leu Asn Gln Ala Asp His						
	120				130	
cgc gtg gcg gga tta gcc gca att gat gcg acc cgc gat gcc gct aat						547
Arg Val Ala Gly Leu Ala Ala Ile Asp Ala Thr Arg Asp Ala Ala Asn						
	135				145	
ccg tgg gcg cag cca gag ctg ttg cag gag gat ctg cag ccg tgg gga						595
Pro Trp Ala Gln Pro Glu Leu Leu Gln Glu Asp Leu Gln Pro Trp Gly						
	150				160	
gct gaa gtc atc atc att gcc gga cac cca gag ccc acc cac acc atg						643
Ala Glu Val Ile Ile Ile Ala Gly His Pro Glu Pro Thr His Thr Met						
	170				180	
gat ctg gct aaa gat tct gtt gat gcc gga gtt gca tcc ctt caa gct						691
Asp Leu Ala Lys Asp Ser Val Asp Ala Gly Val Ala Ser Leu Gln Ala						
	185				195	
cac aag gaa tac ttg gcc gct ctt cca gat ccc ccg aag ccg gag gag						739
His Lys Glu Tyr Leu Ala Ala Leu Pro Asp Pro Lys Pro Glu Glu						
	200				210	
ttc att ccg gcg ttt ctc gag gta gag ggc ggt tac gca gcg gcc ttc						787
Phe Ile Pro Ala Phe Leu Glu Val Glu Gly Gly Tyr Ala Ala Ala Phe						
	215				225	
cga gtt ttc gga ccg taagcagggc gatacgtgat agg						825
Arg Val Phe Gly Arg						

230

<210> 392

<211> 234

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 392

Met Ser Ala Leu Glu Thr Leu Gln Trp Gln Asp Trp Ser Ser Val Leu
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Ile Val Val Ala His Pro Asp Asp Pro Glu Tyr Gly Leu Ser Ala Ala
 20 25 30

Val Lys Glu Trp Thr Asp Ala Gly Val Glu Val Ser Tyr Leu Leu Leu
 35 40 45

Thr His Gly Glu Ala Gly Ile Gln Gly Leu Asp Pro Lys Glu Thr Gly
 50 55 60

Ser Leu Arg Ala Ala Glu Gln Arg Ala Ala Cys Asp Val Val Gly Val
 65 70 75 80

Arg Asn Leu Thr Ile Leu Asn His Pro Asp Ser Met Leu Val Tyr Asn
 85 90 95

Leu Val Leu Arg Lys Asp Ile Ala Arg Glu Ile Arg Ile Arg Lys Pro
 100 105 110

Asn Ala Val Val Val Ser Asn Phe Asp Val Glu Ala Tyr Gly Gly Leu
 115 120 125

Asn Gln Ala Asp His Arg Val Ala Gly Leu Ala Ala Ile Asp Ala Thr
 130 135 140

Arg Asp Ala Ala Asn Pro Trp Ala Gln Pro Glu Leu Leu Gln Glu Asp
 145 150 155 160

Leu Gln Pro Trp Gly Ala Glu Val Ile Ile Ile Ala Gly His Pro Glu
 165 170 175

Pro Thr His Thr Met Asp Leu Ala Lys Asp Ser Val Asp Ala Gly Val
 180 185 190

Ala Ser Leu Gln Ala His Lys Glu Tyr Leu Ala Ala Leu Pro Asp Pro
 195 200 205

Pro Lys Pro Glu Glu Phe Ile Pro Ala Phe Leu Glu Val Glu Gly Gly
 210 215 220

Tyr Ala Ala Ala Phe Arg Val Phe Gly Arg
 225 230

<210> 393

<211> 825

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(802)

<223> FRXA00831

<400> 393

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atgatgagca tgttcgcctg atttaggtag cctgggtggga atg agt gca ctt gag 115
                                     Met Ser Ala Leu Glu
                                     1 5

aca ttg caa tgg cag gac tgg tca agc gtc tta att gtg gta gct cac 163
Thr Leu Gln Trp Gln Asp Trp Ser Ser Val Leu Ile Val Val Ala His
                                     10 15 20

cca gat gat ccg gag tat ggg ctt tcc gcg gct gtt aaa gaa tgg aca 211
Pro Asp Asp Pro Glu Tyr Gly Leu Ser Ala Ala Val Lys Glu Trp Thr
                                     25 30 35

gac gcc ggg gtg gag gtg tct tac ctg ctg ctc acc cac ggg gag gca 259
Asp Ala Gly Val Glu Val Ser Tyr Leu Leu Leu Thr His Gly Glu Ala
                                     40 45 50

ggg atc caa ggt tta gac cct aaa gaa acc ggg tca ttg cgc gca gcg 307
Gly Ile Gln Gly Leu Asp Pro Lys Glu Thr Gly Ser Leu Arg Ala Ala
                                     55 60 65

gaa cag cgg gct gca tgt gat gtg gta gga gtt aga aat ctc acc att 355
Glu Gln Arg Ala Ala Cys Asp Val Val Gly Val Arg Asn Leu Thr Ile
                                     70 75 80 85

ttg aat cac cca gat tcc atg ttg gtg tac aat ctg gta ctg cgc aaa 403
Leu Asn His Pro Asp Ser Met Leu Val Tyr Asn Leu Val Leu Arg Lys
                                     90 95 100

gat att gct cgg gaa atc cgg atc cgt aaa cca aat gct gtg gtg gta 451
Asp Ile Ala Arg Glu Ile Arg Ile Arg Lys Pro Asn Ala Val Val
                                     105 110 115

tcc aat ttt gat gta gag gcc tac ggt ggt ttg aac cag gcg gat cac 499
Ser Asn Phe Asp Val Glu Ala Tyr Gly Gly Leu Asn Gln Ala Asp His
                                     120 125 130

cgc gtg gcg gga tta gcc gca att gat gcg acc cgc gat gcc gct aat 547
Arg Val Ala Gly Leu Ala Ala Ile Asp Ala Thr Arg Asp Ala Ala Asn
                                     135 140 145

ccg tgg gcg cag cca gag ctg ttg cag gag gat ctg cag ccg tgg gga 595
Pro Trp Ala Gln Pro Glu Leu Leu Gln Glu Asp Leu Gln Pro Trp Gly
                                     150 155 160 165

gct gaa gtc atc atc att gcc gga cac cca gag ccc acc cac acc atg 643
Ala Glu Val Ile Ile Ile Ala Gly His Pro Glu Pro Thr His Thr Met
                                     170 175 180

gat ctg gct aaa gat tct gtt gat gcc gga gtt gca tcc ctt caa gct 691
Asp Leu Ala Lys Asp Ser Val Asp Ala Gly Val Ala Ser Leu Gln Ala
                                     185 190 195

cac aag gaa tac ttg gcc gct ctt cca gat ccc ccg aag ccg gag gag 739
His Lys Glu Tyr Leu Ala Ala Leu Pro Asp Pro Pro Lys Pro Glu Glu

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200 205 210
 ttc att cgc gcg ttt ctc gag gta gag ggc ggt tac gca gcg gcc ttc 787
 Phe Ile Pro Ala Phe Leu Glu Val Glu Gly Gly Tyr Ala Ala Ala Phe
 215 220 225
 cga gtt ttc gga cgg taagcagggc gatacgtgat agg 825
 Arg Val Phe Gly Arg
 230

 <210> 394
 <211> 234
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 394
 Met Ser Ala Leu Glu Thr Leu Gln Trp Gln Asp Trp Ser Ser Val Leu
 1 5 10 15
 Ile Val Val Ala His Pro Asp Asp Pro Glu Tyr Gly Leu Ser Ala Ala
 20 25 30
 Val Lys Glu Trp Thr Asp Ala Gly Val Glu Val Ser Tyr Leu Leu Leu
 35 40 45
 Thr His Gly Glu Ala Gly Ile Gln Gly Leu Asp Pro Lys Glu Thr Gly
 50 55 60
 Ser Leu Arg Ala Ala Glu Gln Arg Ala Ala Cys Asp Val Val Gly Val
 65 70 75 80
 Arg Asn Leu Thr Ile Leu Asn His Pro Asp Ser Met Leu Val Tyr Asn
 85 90 95
 Leu Val Leu Arg Lys Asp Ile Ala Arg Glu Ile Arg Ile Arg Lys Pro
 100 105 110
 Asn Ala Val Val Val Ser Asn Phe Asp Val Glu Ala Tyr Gly Gly Leu
 115 120 125
 Asn Gln Ala Asp His Arg Val Ala Gly Leu Ala Ala Ile Asp Ala Thr
 130 135 140
 Arg Asp Ala Ala Asn Pro Trp Ala Gln Pro Glu Leu Leu Gln Glu Asp
 145 150 155 160
 Leu Gln Pro Trp Gly Ala Glu Val Ile Ile Ile Ala Gly His Pro Glu
 165 170 175
 Pro Thr His Thr Met Asp Leu Ala Lys Asp Ser Val Asp Ala Gly Val
 180 185 190
 Ala Ser Leu Gln Ala His Lys Glu Tyr Leu Ala Ala Leu Pro Asp Pro
 195 200 205
 Pro Lys Pro Glu Glu Phe Ile Pro Ala Phe Leu Glu Val Glu Gly Gly
 210 215 220
 Tyr Ala Ala Ala Phe Arg Val Phe Gly Arg
 225 230

<210> 395

<211> 1077

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> {101}..{1054}

<223> RXN00835

<400> 395

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gatttgtaag cactaccocct tctotacaaa ggagtcotca atg gcc ggt gga ttg 115
 Met Ala Gly Gly Leu
 1 5

gca gca cta tta gac gat gtc gca gca att act cga gcg gct gca gcc 163
 Ala Ala Leu Leu Asp Val Ala Ala Ile Thr Arg Ala Ala Ala Ala
 10 15 20

agc ctc gat gat gtc acg gcg atg gct gga aaa acc agc gtt aaa gcc 211
 Ser Leu Asp Asp Val Thr Ala Met Ala Gly Lys Thr Ser Val Lys Ala
 25 30 35

gca ggc gtg gtt gta gat gac acg gca gtt acc ccg caa tat gtt caa 259
 Ala Gly Val Val Val Asp Asp Thr Ala Val Thr Pro Gln Tyr Val Gln
 40 45 50

ggt gtc aaa cct gca cgc gaa ctg ccc atg att tgg cgg atc gct aag 307
 Gly Val Lys Pro Ala Arg Glu Leu Pro Met Ile Trp Arg Ile Ala Lys
 55 60 65

ggc tct ttg gta aac aag atc atc atc att ttg ccc atc gcg ttg ctt 355
 Gly Ser Leu Val Asn Lys Ile Ile Ile Ile Leu Pro Ile Ala Leu Leu
 70 75 80 85

ctt tcc gcg ttt gct ccg tgg got ctc aca cca att ttg atg ctg ggc 403
 Leu Ser Ala Phe Ala Pro Trp Ala Leu Thr Pro Ile Leu Met Leu Gly
 90 95 100

ggc tcc tac ctg tgc ttc gaa ggt gca gaa aag atc tgg cac tcc ctc 451
 Gly Ser Tyr Leu Cys Phe Glu Gly Ala Glu Lys Ile Trp His Ser Leu
 105 110 115

cac agg cgc atc aaa ggt gaa cag cac agc acc gaa ccc aag tcg cag 499
 His Arg Arg Ile Lys Gly Glu Gln His Ser Thr Glu Pro Lys Ser Gln
 120 125 130

gaa agc cca aag tca gag gat cag ctg gtc aaa agt gcc atc aca act 547
 Glu Ser Pro Lys Ser Glu Asp Gln Leu Val Lys Ser Ala Ile Thr Thr
 135 140 145

gac ctc atc ctt tcc gca gag atc atg gtt att tca ctc aat cag att 595
 Asp Leu Ile Leu Ser Ala Glu Ile Met Val Ile Ser Leu Asn Gln Ile
 150 155 160 165

gca gat caa act atc tgg atg cag gct gcg gtt ctt ttc gtc gta ggt 643
 Ala Asp Gln Thr Ile Trp Met Gln Ala Ala Val Leu Phe Val Val Gly

	170	175	180	
	att ggc atc acc gcg ctc gtg tac ggc gta gtc ggt gtt ctt gtg aaa			691
	Ile Gly Ile Thr Ala Leu Val Tyr Gly Val Val Gly Val Leu Val Lys			
	185	190	195	
	atg gat gac gtc gga ctt aca ctt tca aag cgt gac tcc gca ggt atc			739
	Met Asp Asp Val Gly Leu Thr Leu Ser Lys Arg Asp Ser Ala Gly Ile			
	200	205	210	
	cag aaa ttt ggc cgc ggc ttg gtc aaa gcg atg ccc atc gtt ctt caa			787
	Gln Lys Phe Gly Arg Gly Leu Val Lys Ala Met Pro Ile Val Leu Gln			
	215	220	225	
	gtt att tct gtt gtc ggc gtt ttt gcc atg ctg tgg gtt ggt ggc cac			835
	Val Ile Ser Val Val Gly Val Phe Ala Met Leu Trp Val Gly Gly His			
	230	235	240	245
	atc atg gtc gtt gga act gaa gag tta gga tgg gaa ctt ccc tac cac			883
	Ile Met Val Val Gly Thr Glu Glu Leu Gly Trp Glu Leu Pro Tyr His			
	250	255	260	
	ctt gtt cac gga cta gag tcc tgg gct aac ggt atc gga ggc agt gct			931
	Leu Val His Gly Leu Glu Ser Trp Ala Asn Gly Ile Gly Gly Ser Ala			
	265	270	275	
	ctg gga tgg gtt ggc aat act ttc ggg tca ctt gtg ttc ggc ctc att			979
	Leu Gly Trp Val Gly Asn Thr Phe Gly Ser Leu Val Phe Gly Leu Ile			
	280	285	290	
	tgg ggc gcg att atc acc gtt gtg gtc agt gtg atc aag aag ttc att			1027
	Trp Gly Ala Ile Ile Thr Val Val Val Ser Val Ile Lys Lys Phe Ile			
	295	300	305	
	cca cag cgt gcg caa aac tcg tct cat tagtggagag ttgttcgctg			1074
	Pro Gln Arg Ala Gln Asn Ser Ser His			
	310	315		
	taa			1077
	<210> 396			
	<211> 318			
	<212> PRT			
	<213> Corynebacterium glutamicum			
	<400> 396			
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	Arg Ala Ala Ala Ala Ser Leu Asp Asp Val Thr Ala Met Ala Gly Lys			
	20	25	30	
	Thr Ser Val Lys Ala Ala Gly Val Val Asp Asp Thr Ala Val Thr			
	35	40	45	
	Pro Gln Tyr Val Gln Gly Val Lys Pro Ala Arg Glu Leu Pro Met Ile			
	50	55	60	
	Trp Arg Ile Ala Lys Gly Ser Leu Val Asn Lys Ile Ile Ile Ile Leu			
	65	70	75	80

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Pro Ile Ala Leu Leu Leu Ser Ala Phe Ala Pro Trp Ala Leu Thr Pro
      85                      90                      95

Ile Leu Met Leu Gly Gly Ser Tyr Leu Cys Phe Glu Gly Ala Glu Lys
      100                      105                      110

Ile Trp His Ser Leu His Arg Arg Ile Lys Gly Glu Gln His Ser Thr
      115                      120                      125

Glu Pro Lys Ser Gln Glu Ser Pro Lys Ser Glu Asp Gln Leu Val Lys
      130                      135                      140

Ser Ala Ile Thr Thr Asp Leu Ile Leu Ser Ala Glu Ile Met Val Ile
      145                      150                      155                      160

Ser Leu Asn Gln Ile Ala Asp Gln Thr Ile Trp Met Gln Ala Ala Val
      165                      170                      175

Leu Phe Val Val Gly Ile Gly Ile Thr Ala Leu Val Tyr Gly Val Val
      180                      185                      190

Gly Val Leu Val Lys Met Asp Asp Val Gly Leu Thr Leu Ser Lys Arg
      195                      200                      205

Asp Ser Ala Gly Ile Gln Lys Phe Gly Arg Gly Leu Val Lys Ala Met
      210                      215                      220

Pro Ile Val Leu Gln Val Ile Ser Val Val Gly Val Phe Ala Met Leu
      225                      230                      235                      240

Trp Val Gly Gly His Ile Met Val Val Gly Thr Glu Glu Leu Gly Trp
      245                      250                      255

Glu Leu Pro Tyr His Leu Val His Gly Leu Glu Ser Trp Ala Asn Gly
      260                      265                      270

Ile Gly Gly Ser Ala Leu Gly Trp Val Gly Asn Thr Phe Gly Ser Leu
      275                      280                      285

Val Phe Gly Leu Ile Trp Gly Ala Ile Ile Thr Val Val Ser Val
      290                      295                      300

Ile Lys Lys Phe Ile Pro Gln Arg Ala Gln Asn Ser Ser His
      305                      310                      315

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<210> 397

<211> 713

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(690)

<223> FRXA00835

<400> 397

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Phe Ala Pro Trp Ala Leu Thr Pro Ile Leu Met Leu Gly Gly Ser Tyr
  1                      5                      10                      15

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ctg tgc ttc gaa ggt gca gaa aag atc tgg cac tcc ctc cac agg cgc 96
 Leu Cys Phe Gly Ala Glu Lys Ile Trp His Ser Leu His Arg Arg
 20 25 30

atc aaa ggt gaa cag cac agc acc gaa ccc aag tgc cag gaa agc cca 144
 Ile Lys Gly Glu Gln His Ser Thr Glu Pro Lys Ser Gln Glu Ser Pro
 35 40 45

aag tca gag gat cag ctg gtc aaa agt gcc atc aca act gac ctc atc 192
 Lys Ser Glu Asp Gln Leu Val Lys Ser Ala Ile Thr Thr Asp Leu Ile
 50 55 60

ctt tcc gca gag atc atg gtt att tca ctc aat cag att gca gat caa 240
 Leu Ser Ala Glu Ile Met Val Ile Ser Leu Asn Gln Ile Ala Asp Gln
 65 70 75 80

act atc tgg atg cag gct gcg gtt ctt ttc gtc gta ggt att ggc atc 288
 Thr Ile Trp Met Ala Ala Val Leu Phe Val Val Gly Ile Gly Ile
 85 90 95

acc gcg ctc gtg tac ggc gta gtc ggt gtt ctt gtg aaa atg gat gac 336
 Thr Ala Leu Val Tyr Gly Val Val Gly Val Leu Val Lys Met Asp Asp
 100 105 110

gtc gga ctt aca ctt tca aag cgt gac tcc gca ggt atc cag aaa ttt 384
 Val Gly Leu Thr Leu Ser Lys Arg Asp Ser Ala Gly Ile Gln Lys Phe
 115 120 125

ggc cgc ggc ttg gtc aaa gcg atg ccc atc gtt ctt caa gtt att tct 432
 Gly Arg Gly Leu Val Lys Ala Met Pro Ile Val Leu Gln Val Ile Ser
 130 135 140

gtt gtc ggc gtt ttt gcc atg ctg tgg gtt ggt ggc cac atc atg gtc 480
 Val Val Gly Val Phe Ala Met Leu Trp Val Gly Gly His Ile Met Val
 145 150 155 160

gtt gga act gaa gag tta gga tgg gaa ctt ccc tac cac ctt gtt cac 528
 Val Gly Thr Glu Glu Leu Leu Gly Trp Glu Leu Pro Tyr His Leu Val His
 165 170 175

gga cta gag tcc tgg gct aac ggt atc gga ggc agt gct ctg gga tgg 576
 Gly Leu Glu Ser Trp Ala Asn Gly Ile Gly Gly Ser Ala Leu Gly Trp
 180 185 190

gtt ggc aat act ttc ggg tca ctt gtg ttc ggc ctc att tgg ggc gcg 624
 Val Gly Asn Thr Phe Gly Ser Leu Val Phe Gly Leu Ile Trp Gly Ala
 195 200 205

att atc acc gtt gtg gtc agt gtg atc aag aag ttc att cca cag cgt 672
 Ile Ile Thr Val Val Val Ser Val Ile Lys Lys Phe Ile Pro Gln Arg
 210 215 220

gcg caa aac tgc tct cat tagtggagag ttgttcgctg taa 713
 Ala Gln Asn Ser Ser His
 225 230

<210> 398

<211> 230

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 398

Phe Ala Pro Trp Ala Leu Thr Pro Ile Leu Met Leu Gly Gly Ser Tyr
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 20 25 30

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 35 40 45

Lys Ser Glu Asp Gln Leu Val Lys Ser Ala Ile Thr Thr Asp Leu Ile
 50 55 60

Leu Ser Ala Glu Ile Met Val Ile Ser Leu Asn Gln Ile Ala Asp Gln
 65 70 75 80

Thr Ile Trp Met Gln Ala Ala Val Leu Phe Val Val Gly Ile Gly Ile
 85 90 95

Thr Ala Leu Val Tyr Gly Val Val Gly Val Leu Val Lys Met Asp Asp
 100 105 110

Val Gly Leu Thr Leu Ser Lys Arg Asp Ser Ala Gly Ile Gln Lys Phe
 115 120 125

Gly Arg Gly Leu Val Lys Ala Met Pro Ile Val Leu Gln Val Ile Ser
 130 135 140

Val Val Gly Val Phe Ala Met Leu Trp Val Gly Gly His Ile Met Val
 145 150 155 160

Val Gly Thr Glu Glu Leu Gly Trp Glu Leu Pro Tyr His Leu Val His
 165 170 175

Gly Leu Glu Ser Trp Ala Asn Gly Ile Gly Gly Ser Ala Leu Gly Trp
 180 185 190

Val Gly Asn Thr Phe Gly Ser Leu Val Phe Gly Leu Ile Trp Gly Ala
 195 200 205

Ile Ile Thr Val Val Val Ser Val Ile Lys Lys Phe Ile Pro Gln Arg
 210 215 220

Ala Gln Asn Ser Ser His
 225 230

<210> 399

<211> 1816

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1816)

<223> RXN00836

<400> 399

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				Met	Tyr	Thr	His	Ser	
				1				5	
aca ggc act cct cag ctt gat ttc gac ggt gac atc tat ccc ctt cac	163								
Thr Gly Thr Pro Gln Leu Asp Phe Asp Gly Asp Ile Tyr Pro Leu His									
	10			15				20	
ctc ttc ttc tct gca cag act gcc caa cat ttc gct ctc gag cgc gtc	211								
Leu Phe Phe Ser Ala Gln Thr Ala Gln His Phe Ala Leu Glu Arg Val									
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aat tgg cat gtc cgc gct att gtg aaa cct gag caa ggc gaa ctc	259								
Asn Trp His Val Leu Arg Ala Ile Val Lys Pro Glu Gln Gly Glu Leu									
	40			45				50	
atc gtc gaa cgc ctt ctc gca cca ata gaa tcc gca aca aaa atc ggt	307								
Ile Val Glu Ala Leu Leu Ala Pro Ile Glu Ser Ala Thr Lys Ile Gly									
	55			60				65	
gtt tgg gtt caa gat gaa ttt ctc ggg gtg att gca gag tcc cag ttc	355								
Val Trp Val Gln Asp Glu Phe Leu Gly Val Ile Ala Glu Ser Gln Phe									
	70			75				80	85
ctg ttg aat tct caa ttg tct cga att ttt gcc tct ggc cac ctg att	403								
Leu Leu Asn Ser Gln Leu Ser Arg Ile Phe Ala Ser Gly His Leu Ile									
	90			95				100	
tcc agc caa cta ctt ctc aca ccg agt aaa gga tct ctc gct tca gtt	451								
Ser Ser Gln Leu Leu Leu Thr Pro Ser Lys Gly Ser Leu Ala Ser Val									
	105			110				115	
ctt ctt cca aac cta aaa ttc ggg ctc atc agc aat gat cct cca cga	499								
Leu Leu Pro Asn Leu Lys Phe Gly Leu Ile Ser Asn Asp Pro Pro Arg									
	120			125				130	
gct gat tcc cac ctc tta ccg cta ggc aga atg tgg cgc gtt gag ccc	547								
Ala Asp Ser His Leu Leu Pro Leu Gly Arg Met Trp Arg Val Glu Pro									
	135			140				145	
acc gtt cat gct ctg ttt gag gat ttc tca ctt ggc tcc acg att ctt	595								
Thr Val His Ala Leu Phe Glu Asp Phe Ser Leu Gly Ser Thr Ile Leu									
	150			155				160	165
ttt ggg ctg agg ctt gat tta gaa gcc cta att gtc tcc tat aac gga	643								
Phe Gly Leu Arg Leu Asp Leu Glu Ala Leu Ile Val Ser Tyr Asn Gly									
	170			175				180	
ata gaa tgt ggc atc tta aac ttt gat gac gcc tca gca cta agc tct	691								
Ile Glu Cys Gly Ile Leu Asn Phe Asp Asp Ala Ser Ala Leu Ser Ser									
	185			190				195	
gct gtg aaa ttc tca aat gca aat ggt ctc acc ccc acg gtg ctc ggc	739								
Ala Val Lys Phe Ser Asn Ala Asn Gly Leu Thr Pro Thr Val Leu Gly									
	200			205				210	
cac gta gtc cgg gag aac ggt gaa aca tcc ttc gag att gac gtt ctc	787								
His Val Val Arg Glu Asn Gly Glu Thr Ser Phe Glu Ile Asp Val Leu									
	215			220				225	

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Pro Leu Glu Leu Trp Ser Lys Lys Gln His Arg Leu Glu Val Leu Lys	
230 235 240 245	
atc cct cgg ttg ata cct aaa gag gca gat tcc caa aat tat gtg aag	883
Ile Pro Arg Leu Ile Pro Lys Glu Ala Asp Ser Gln Asn Tyr Val Lys	
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gcg aca gcg ctc ctt tca gac gag att ctg cga cca caa acg ctg tcc	931
Ala Thr Ala Leu Leu Ser Asp Glu Ile Leu Arg Pro Gln Thr Leu Ser	
265 270 275	
aaa aag gca ctg tct ttg tgg gac acc gca gtt aag tac agc cct cat	979
Lys Lys Ala Leu Ser Leu Ser Asp Thr Ala Val Lys Tyr Ser Pro His	
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gtt gct tgt ggc gtg ggg atg ttt agt ctt ttc gcc gtt att ccc ttt	1027
Val Ala Cys Gly Val Gly Met Phe Ser Leu Phe Ala Val Ile Pro Phe	
295 300 305	
gac aag ttg agt gat cat agt gcg atg ctg ctc gca gtc att agc ttg	1075
Asp Lys Leu Ser Asp His Ser Ala Met Leu Leu Ala Val Ile Ser Leu	
310 315 320 325	
atg ctt ttt gtg ctg gca tta gta att ctt ttc aag aga att cag tca	1123
Met Leu Phe Val Leu Ala Leu Val Ile Leu Phe Lys Arg Ile Gln Ser	
330 335 340	
act aat act cag cgt tgg aac ttg gcc tgg tca gtc gga tta etc gcg	1171
Thr Asn Thr Gln Arg Trp Asn Leu Ala Ser Ser Val Gly Leu Leu Ala	
345 350 355	
aca ctt ccg att atc ata ttc ctg gtt gct gat aca ttg att cct cag	1219
Thr Leu Pro Ile Ile Ile Phe Leu Val Ala Asp Thr Leu Ile Pro Gln	
360 365 370	
ggc agc ctg gaa aac cat gct caa ccc gac gta cag gta aca acg tta	1267
Gly Ser Leu Glu Asn His Ala Gln Pro Asp Val Gln Val Thr Thr Leu	
375 380 385	
gct aac agg cgg cca agt tca cct acc tca ctg gac tca cta ggc gca	1315
Ala Asn Arg Arg Pro Ser Ser Pro Thr Ser Leu Asp Ser Leu Gly Ala	
390 395 400 405	
ctg aat tca cca agt tgg ccg aat tcc ccg agc tca tca atg ctg caa	1363
Leu Asn Ser Pro Ser Ser Pro Asn Ser Pro Ser Ser Ser Met Leu Gln	
410 415 420	
aac tct gaa atg ttc gcc tca cca ccg atc gcc tct ggg cag tca ccg	1411
Asn Ser Glu Met Phe Ala Ser Pro Pro Ile Ala Ser Gly Gln Ser Pro	
425 430 435	
gtt tgg acg ttc cgc tca tgg cta gat cga tcc att ctg cca ctc aca	1459
Val Ser Thr Phe Arg Ser Trp Leu Asp Arg Ser Ile Leu Pro Leu Thr	
440 445 450	
cga gaa aat tcc gct tca gaa agc gca gtg aca gct ctt gga ccg tgg	1507
Arg Glu Asn Ser Ala Ser Glu Ser Ala Val Thr Ala Leu Gly Pro Ser	
455 460 465	
ata gtg cag cct gca tct gaa tgg att aca act cca gct caa acg tgg	1555


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Ile Val Gln Pro Ala Ser Glu Ser Ile Thr Thr Pro Ala Gln Thr Ser
470          475          480          485

caa agt cgc cac gca att gac gat ggt gac gac agt aaa acc tca acg 1603
Gln Ser Arg His Ala Ile Asp Asp Gly Asp Ser Ser Lys Thr Ser Thr
          490          495          500

gga aga cca gct ccc act act aac tcg ccg atc att gct ctt ccc cca 1651
Gly Arg Pro Pro Ala Pro Thr Thr Asn Ser Pro Ile Ile Ala Leu Pro Pro
          505          510          515

acg tgg att atc ggg ccg gaa gat cca gaa tcc acc gac cct aca gca 1699
Thr Trp Ile Ile Gly Pro Glu Asp Pro Glu Ser Thr Asp Pro Thr Ala
          520          525          530

cca acc gag ccc acc gag cca agc gaa cct gtc gca acc gac gaa ccc 1747
Pro Thr Glu Pro Thr Glu Pro Ser Glu Pro Val Ala Thr Asp Glu Pro
          535          540          545

tca gag acc tct gaa caa act tca cct ctc tta gct cgc gac acc ccc 1795
Ser Glu Thr Ser Glu Gln Thr Ser Pro Leu Leu Ala Arg Asp Thr Pro
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gaa ctg aac cgg aaa caa ctg 1816
Glu Leu Asn Arg Lys Gln Leu
          570

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<213> Corynebacterium glutamicum

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Ala Leu Glu Arg Val Asn Trp His Val Leu Arg Ala Ile Val Lys Pro
          35          40          45

Glu Gln Gly Glu Leu Ile Val Glu Ala Leu Leu Ala Pro Ile Glu Ser
          50          55          60

Ala Thr Lys Ile Gly Val Trp Val Gln Asp Glu Phe Leu Gly Val Ile
          65          70          75          80

Ala Glu Ser Gln Phe Leu Leu Asn Ser Gln Leu Ser Arg Ile Phe Ala
          85          90          95

Ser Gly His Leu Ile Ser Ser Gln Leu Leu Leu Thr Pro Ser Lys Gly
          100          105          110

Ser Leu Ala Ser Val Leu Leu Pro Asn Leu Lys Phe Gly Leu Ile Ser
          115          120          125

Asn Asp Pro Pro Arg Ala Asp Ser His Leu Leu Pro Leu Gly Arg Met
          130          135          140

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Trp Arg Val Glu Pro Thr Val His Ala Leu Phe Glu Asp Phe Ser Leu
 145 150 155 160
 Gly Ser Thr Ile Leu Phe Gly Leu Arg Leu Asp Leu Glu Ala Leu Ile
 165 170 175
 Val Ser Tyr Asn Gly Ile Glu Cys Gly Ile Leu Asn Phe Asp Asp Ala
 180 185 190
 Ser Ala Leu Ser Ser Ala Val Lys Phe Ser Asn Ala Asn Gly Leu Thr
 195 200 205
 Pro Thr Val Leu Gly His Val Val Arg Glu Asn Gly Glu Thr Ser Phe
 210 215 220
 Glu Ile Asp Val Leu Pro Leu Glu Leu Trp Ser Lys Lys Gln His Arg
 225 230 235 240
 Leu Glu Val Leu Lys Ile Pro Arg Leu Ile Pro Lys Glu Ala Asp Ser
 245 250 255
 Gln Asn Tyr Val Lys Ala Thr Ala Leu Leu Ser Asp Glu Ile Leu Arg
 260 265 270
 Pro Gln Thr Leu Ser Lys Lys Ala Leu Ser Leu Ser Asp Thr Ala Val
 275 280 285
 Lys Tyr Ser Pro His Val Ala Cys Gly Val Gly Met Phe Ser Leu Phe
 290 295 300
 Ala Val Ile Pro Phe Asp Lys Leu Ser Asp His Ser Ala Met Leu Leu
 305 310 315 320
 Ala Val Ile Ser Leu Met Leu Phe Val Leu Ala Leu Val Ile Leu Phe
 325 330 335
 Lys Arg Ile Gln Ser Thr Asn Thr Gln Arg Trp Asn Leu Ala Ser Ser
 340 345 350
 Val Gly Leu Leu Ala Thr Leu Pro Ile Ile Ile Phe Leu Val Ala Asp
 355 360 365
 Thr Leu Ile Pro Gln Gly Ser Leu Glu Asn His Ala Gln Pro Asp Val
 370 375 380
 Gln Val Thr Thr Leu Ala Asn Arg Arg Pro Ser Ser Pro Thr Ser Leu
 385 390 395 400
 Asp Ser Leu Gly Ala Leu Asn Ser Pro Ser Ser Pro Asn Ser Pro Ser
 405 410 415
 Ser Ser Met Leu Gln Asn Ser Glu Met Phe Ala Ser Pro Pro Ile Ala
 420 425 430
 Ser Gly Gln Ser Pro Val Ser Thr Phe Arg Ser Trp Leu Asp Arg Ser
 435 440 445
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<213>	Corynebacterium glutamicum
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attcacaaagt ttgcacgaaa ttttaaggaaa ggagtgccca atg tat acc cat tca 115	
Met Tyr Thr His Ser 1 5	
aca ggc act cct cag ctt gat ttc gac ggt gac atc tat ccc ctt cac 163	
Thr Gly Thr Pro Gln Leu Asp Phe Asp Gly Asp Ile Tyr Pro Leu His 10 15 20	
ctc ttc ttc tct gca cag act gcc caa cat ttc gct ctc gag cgc gtc 211	
Leu Phe Phe Ser Ala Gln Thr Ala Gln His Phe Ala Leu Glu Arg Val 25 30 35	
aat tgg cat gtc tta cgc gct att gtg aaa cct gag caa ggc gaa ctc 259	
Asn Trp His Val Leu Arg Ala Ile Val Lys Pro Glu Gln Gly Glu Leu 40 45 50	
atc gtc gaa gcg ctt ctc gca cca ata gaa tcc gca aca aaa atc ggt 307	
Ile Val Glu Ala Leu Leu Ala Pro Ile Glu Ser Ala Thr Lys Ile Gly 55 60 65	
gtt tgg gtt caa gat gaa ttt ctc ggg gtg att gca gag tcc cag ttc 355	
Val Trp Val Gln Asp Glu Phe Leu Gly Val Ile Ala Glu Ser Gln Phe 70 75 80 85	
ctg ttg aat tct caa ttg tct cga att ttt gcc tct ggc cac ctg att 403	
Leu Leu Asn Ser Gln Leu Ser Arg Ile Phe Ala Ser Gly His Leu Ile 90 95 100	

tcc agc caa cta ctt ctc aca ccg agt aaa gga tct ctc gct tca gtt	451
Ser Ser Gln Leu Leu Thr Pro Ser Lys Gly Ser Leu Ala Ser Val	
105 110 115	
ctt ctt cca aac cta aaa ttc ggg ctc atc agc aat gat cct cca cga	499
Leu Leu Pro Asn Leu Lys Phe Gly Leu Ile Ser Asn Asp Pro Pro Arg	
120 125 130	
gct gat tcc cac ctc tta ccg cta ggc aga atg tgg cgc gtt gag ccc	547
Ala Asp Ser His Leu Leu Pro Leu Gly Arg Met Trp Arg Val Glu Pro	
135 140 145	
acc gtt cat gct ctg ttt gag gat ttc tca ctt ggc tcc acg att ctt	595
Thr Val His Ala Leu Phe Glu Asp Phe Ser Leu Gly Ser Thr Ile Leu	
150 155 160 165	
ttt ggg ctg agg ctt gat tta gaa gcc cta att gtc tcc tat aac gga	643
Phe Gly Leu Arg Leu Asp Leu Glu Ala Leu Ile Val Ser Tyr Asn Gly	
170 175 180	
ata gaa tgt ggc atc tta aac ttt gat gac gcc tca gca cta agc tct	691
Ile Glu Cys Gly Ile Leu Asn Phe Asp Asp Ala Ser Ala Leu Ser Ser	
185 190 195	
gct gtg aaa ttc tca aat gca aat ggt ctc acc ccc acg gtg ctc ggc	739
Ala Val Lys Phe Ser Asn Ala Asn Gly Leu Thr Pro Thr Val Leu Gly	
200 205 210	
cac gta gtc cgg gag aac ggt gaa aca tcc ttc gag att gac gtt ctc	787
His Val Val Arg Glu Asn Gly Glu Thr Ser Phe Glu Ile Asp Val Leu	
215 220 225	
cca ctg gag ttg tgg tgg aag aag cag cat cgc ctt gag gtt tta aaa	835
Pro Leu Glu Leu Trp Ser Lys Lys Gln His Arg Leu Glu Val Leu Lys	
230 235 240 245	
atc cct cgg ttg ata cct aaa gag gca gat tcc caa aat tat gtg aag	883
Ile Pro Arg Leu Ile Pro Lys Glu Ala Asp Ser Gln Asn Tyr Val Lys	
250 255 260	
gcg aca gcg ctc ctt tca gac gag att ctg cga cca caa acg ctg tcc	931
Ala Thr Ala Leu Leu Ser Asp Glu Ile Leu Arg Pro Gln Thr Leu Ser	
265 270 275	
aaa aag gca ctg tct ttg tgg gac acc gca gtt aag tac agc cct cat	979
Lys Lys Ala Leu Ser Leu Ser Asp Thr Ala Val Lys Tyr Ser Pro His	
280 285 290	
gtt gct tgt ggc gtg ggg atg ttt agt ctt ttc gcc gtt att ccc ttt	1027
Val Ala Cys Gly Val Gly Met Phe Ser Leu Phe Ala Val Ile Pro Phe	
295 300 305	
gac aag ttg agt gat cat agt gcg atg ctg ctc gca gtc att agc ttg	1075
Asp Lys Leu Ser Asp His Ser Ala Met Leu Leu Ala Val Ile Ser Leu	
310 315 320 325	
atg ctt ttt gtg ctg gca tta gta att ctt ttc aag aga att cag tca	1123
Met Leu Phe Val Leu Ala Leu Val Ile Phe Lys Arg Ile Gln Ser	
330 335 340	

act aat act cag cgt tgg aac ttg gcc tgg tca gtc gga tta ctc gcg 1171
 Thr Asn Thr Gln Arg Trp Asn Leu Ala Ser Ser Val Gly Leu Leu Ala
 345 350 355

aca ctt ccg att atc ata ttc ctg gtt gct gat aca ttg att cct cag 1219
 Thr Leu Pro Ile Ile Ile Phe Leu Val Ala Asp Thr Leu Ile Pro Gln
 360 365 370

ggc agc ctg gaa aac cat gct caa ccc gac gta cag gta aca acg tta 1267
 Gly Ser Leu Glu Asn His Ala Gln Pro Asp Val Gln Val Thr Thr Leu
 375 380 385

gct aac agg ccg cca agt tca cct acc tca ctg gac tca cta ggc gca 1315
 Ala Asn Arg Arg Pro Ser Ser Pro Thr Ser Leu Asp Ser Leu Gly Ala
 390 395 400 405

ctg aat tca cca agt tgc ccg aat tcc ccg agc tca tca atg ctg caa 1363
 Leu Asn Ser Pro Ser Ser Pro Asn Ser Pro Ser Ser Ser Met Leu Gln
 410 415 420

aac tct gaa atg ttc gcc tca cca ccg atc gcc tct ggg cag tca ccg 1411
 Asn Ser Glu Met Phe Ala Ser Pro Pro Ile Ala Ser Gly Gln Ser Pro
 425 430 435

gtt tgc acg ttc cgc tca tgg cta gat cga tcc att ctg cca ctc aca 1459
 Val Ser Thr Phe Arg Ser Trp Leu Asp Arg Ser Ile Leu Pro Leu Thr
 440 445 450

cga gaa aat tcc gct tca gaa agc gca gtg aca gct ctt gga ccg tgc 1507
 Arg Glu Asn Ser Ala Ser Glu Ser Ala Val Thr Ala Leu Gly Pro Ser
 455 460 465

ata gtg cag cct gca tct gaa tgc att aca act cca gct caa acg tgc 1555
 Ile Val Gln Pro Ala Ser Glu Ser Ile Thr Thr Pro Ala Gln Thr Ser
 470 475 480 485

caa agt cgc cac gca att gac gat ggt gac gac agt aaa acc tca acg 1603
 Gln Ser Arg His Ala Ile Asp Asp Gly Asp Asp Ser Lys Thr Ser Thr
 490 495 500

gga aga cca gct ccc act act aac tgc ccg atc att gct ctt ccc cca 1651
 Gly Arg Pro Ala Pro Thr Thr Asn Ser Pro Ile Ile Ala Leu Pro Pro
 505 510 515

acg tgg att atc ggg ccg gaa gat cca gaa tcc acc gac cct aca gca 1699
 Thr Trp Ile Ile Gly Pro Glu Asp Pro Glu Ser Thr Asp Pro Thr Ala
 520 525 530

cca acc gag ccc acc gag cca agc gaa cct gtc gca acc gac gaa ccc 1747
 Pro Thr Glu Pro Thr Glu Pro Ser Glu Pro Val Ala Thr Asp Glu Pro
 535 540 545

tca gag acc tct gaa caa act tca 1771
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<212> PRT

<213> Corynebacterium glutamicum

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Ala Leu Glu Arg Val Asn Trp His Val Leu Arg Ala Ile Val Lys Pro
 35 40 45

Glu Gln Gly Glu Leu Ile Val Glu Ala Leu Leu Ala Pro Ile Glu Ser
 50 55 60

Ala Thr Lys Ile Gly Val Trp Val Gln Asp Glu Phe Leu Gly Val Ile
 65 70 75 80

Ala Glu Ser Gln Phe Leu Leu Asn Ser Gln Leu Ser Arg Ile Phe Ala
 85 90 95

Ser Gly His Leu Ile Ser Ser Gln Leu Leu Thr Pro Ser Lys Gly
 100 105 110

Ser Leu Ala Ser Val Leu Leu Pro Asn Leu Lys Phe Gly Leu Ile Ser
 115 120 125

Asn Asp Pro Pro Arg Ala Asp Ser His Leu Leu Pro Leu Gly Arg Met
 130 135 140

Trp Arg Val Glu Pro Thr Val His Ala Leu Phe Glu Asp Phe Ser Leu
 145 150 155 160

Gly Ser Thr Ile Leu Phe Gly Leu Arg Leu Asp Leu Glu Ala Leu Ile
 165 170 175

Val Ser Tyr Asn Gly Ile Glu Cys Gly Ile Leu Asn Phe Asp Asp Ala
 180 185 190

Ser Ala Leu Ser Ser Ala Val Lys Phe Ser Asn Ala Asn Gly Leu Thr
 195 200 205

Pro Thr Val Leu Gly His Val Val Arg Glu Asn Gly Glu Thr Ser Phe
 210 215 220

Glu Ile Asp Val Leu Pro Leu Glu Leu Trp Ser Lys Lys Gln His Arg
 225 230 235 240

Leu Glu Val Leu Lys Ile Pro Arg Leu Ile Pro Lys Glu Ala Asp Ser
 245 250 255

Gln Asn Tyr Val Lys Ala Thr Ala Leu Leu Ser Asp Glu Ile Leu Arg
 260 265 270

Pro Gln Thr Leu Ser Lys Lys Ala Leu Ser Leu Ser Asp Thr Ala Val
 275 280 285

Lys Tyr Ser Pro His Val Ala Cys Gly Val Gly Met Phe Ser Leu Phe
 290 295 300

Ala Val Ile Pro Phe Asp Lys Leu Ser Asp His Ser Ala Met Leu Leu
 305 310 315 320

Ala Val Ile Ser Leu Met Leu Phe Val Leu Ala Leu Val Ile Leu Phe
325 330 335

Lys Arg Ile Gln Ser Thr Asn Thr Gln Arg Trp Asn Leu Ala Ser Ser
340 345 350

Val Gly Leu Leu Ala Thr Leu Pro Ile Ile Ile Phe Leu Val Ala Asp
355 360 365

Thr Leu Ile Pro Gln Gly Ser Leu Glu Asn His Ala Gln Pro Asp Val
370 375 380

Gln Val Thr Thr Leu Ala Asn Arg Arg Pro Ser Ser Pro Thr Ser Leu
385 390 395 400

Asp Ser Leu Gly Ala Leu Asn Ser Pro Ser Ser Pro Asn Ser Pro Ser
405 410 415

Ser Ser Met Leu Gln Asn Ser Glu Met Phe Ala Ser Pro Pro Ile Ala
420 425 430

Ser Gly Gln Ser Pro Val Ser Thr Phe Arg Ser Trp Leu Asp Arg Ser
435 440 445

Ile Leu Pro Leu Thr Arg Glu Asn Ser Ala Ser Glu Ser Ala Val Thr
450 455 460

Ala Leu Gly Pro Ser Ile Val Gln Pro Ala Ser Glu Ser Ile Thr Thr
465 470 475 480

Pro Ala Gln Thr Ser Gln Ser Arg His Ala Ile Asp Asp Gly Asp Asp
485 490 495

Ser Lys Thr Ser Thr Gly Arg Pro Ala Pro Thr Thr Asn Ser Pro Ile
500 505 510

Ile Ala Leu Pro Pro Thr Trp Ile Ile Gly Pro Glu Asp Pro Glu Ser
515 520 525

Thr Asp Pro Thr Ala Pro Thr Glu Pro Thr Glu Pro Ser Glu Pro Val
530 535 540

Ala Thr Asp Glu Pro Ser Glu Thr Ser Glu Gln Thr Ser
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<211> 837

<212> DNA

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<221> CDS

<222> {101}..(814)

<223> RXN00840

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tcctccgcga ttgtctcgtt gaaaggttaag taaactcaa gtg aca aag aca ctc 115

	Val	Thr	Lys	Thr	Leu	
	1				5	
ccc cga ctg ctt aca gtc gct gcc gct cta gcc att gca ctc ccg gca	163					
Pro Arg Leu Leu Thr Val Ala Ala Leu Ala Ile Ala Leu Pro Ala						
	10			15	20	
acc ccg gta gca tcg gct gtc aca cca gtt gaa caa gct ttc aac gcc	211					
Thr Pro Val Ala Ser Ala Val Thr Pro Val Glu Gln Ala Phe Asn Ala						
	25		30	35		
tca tcg aat ctc tcc agc ggt ctc ccc gta gac caa tgg gga cgc ccc	259					
Ser Ser Asn Leu Ser Ser Gly Leu Pro Val Asp Gln Trp Gly Arg Pro				50		
	40		45			
aac gag cag ttc cgc caa caa atc gaa cag gca gta aac caa ccg tgg	307					
Asn Glu Gln Phe Arg Gln Gln Ile Glu Gln Ala Val Asn Gln Pro Trp				65		
	55		60			
gtc ccg cag gaa atc aag aac atc gtt tct cag gcc atg ggt ttt atc	355					
Val Pro Gln Glu Ile Lys Asn Ile Val Ser Gln Ala Met Gly Phe Ile				80		
	70		75		85	
acc ggt gac ggc agc gaa ggt ggg gac att gaa atc ccc gac aac gca	403					
Thr Gly Asp Gly Ser Glu Gly Gly Asp Ile Glu Ile Pro Asp Asn Ala				95		
		90			100	
cca cgc atc gcg cag ttc ttc tgg ccc acc cga tca gaa aac tgc atc	451					
Pro Arg Ile Ala Gln Phe Phe Trp Pro Thr Arg Ser Glu Asn Cys Ile				110	115	
		105				
aac gga aat tct gca gcc gta gga tct gcc ttc gca gtt cca gga cca	499					
Asn Gly Asn Ser Ala Ala Val Gly Ser Ala Phe Ala Val Pro Gly Pro				125	130	
		120				
gca gat ctc ccc ctc ccc gcc gca ggt gtc gcc caa acc tcc ttc gtg	547					
Ala Asp Leu Pro Leu Pro Gly Ala Gly Val Gly Gln Thr Ser Phe Val				140	145	
	135					
ttc acc gca ctg gga act gcc ccc ctc gca gaa cag caa agc acc gca	595					
Phe Thr Ala Leu Gly Thr Gly Pro Leu Ala Glu Gln Gln Ser Thr Ala				155	160	
	150					165
atg act gtt caa tgg gca aac tta agc aac ttc acc cat gcc acc acg	643					
Met Thr Val Gln Trp Ala Asn Leu Ser Asn Phe Thr His Gly Thr Thr				175		
		170			180	
acg ttg agc aac acc gga atc aac ccc gat gcc ccc tca acg att tcc	691					
Thr Leu Ser Asn Thr Gly Ile Asn Pro Asp Gly Pro Ser Thr Ile Ser				190	195	
		185				
ggt gtg gca gac aca gga cgc gcc atc atc gtc gcc tcc atg tca gcc	739					
Gly Val Ala Asp Thr Gly Arg Gly Ile Ile Val Ala Ser Met Ser Gly				205	210	
	200					
ggc ctc acc aca tcc acc gaa aac ggt tca cgc aac tgt aat ttc atc	787					
Gly Leu Thr Thr Ser Thr Glu Asn Gly Ser Ala Asn Cys Asn Phe Ile				220	225	
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ccg act gcc gtc gta ttc gat gtg agg taagaaaaa atgactgac	834					
Pro Thr Ala Val Val Phe Asp Val Arg						

230 235

ttc

837

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<211> 238

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 404

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 20 25 30

Gln Ala Phe Asn Ala Ser Ser Asn Leu Ser Ser Gly Leu Pro Val Asp
 35 40 45

Gln Trp Gly Arg Pro Asn Glu Gln Phe Arg Gln Gln Ile Glu Gln Ala
 50 55 60

Val Asn Gln Pro Trp Val Pro Gln Glu Ile Lys Asn Ile Val Ser Gln
 65 70 75 80

Ala Met Gly Phe Ile Thr Gly Asp Gly Ser Glu Gly Gly Asp Ile Glu
 85 90 95

Ile Pro Asp Asn Ala Pro Arg Ile Ala Gln Phe Phe Trp Pro Thr Arg
 100 105 110

Ser Glu Asn Cys Ile Asn Gly Asn Ser Ala Ala Val Gly Ser Ala Phe
 115 120 125

Ala Val Pro Gly Pro Ala Asp Leu Pro Leu Pro Gly Ala Gly Val Gly
 130 135 140

Gln Thr Ser Phe Val Phe Thr Ala Leu Gly Thr Gly Pro Leu Ala Glu
 145 150 155 160

Gln Gln Ser Thr Ala Met Thr Val Gln Trp Ala Asn Leu Ser Asn Phe
 165 170 175

Thr His Gly Thr Thr Thr Leu Ser Asn Thr Gly Ile Asn Pro Asp Gly
 180 185 190

Pro Ser Thr Ile Ser Gly Val Ala Asp Thr Gly Arg Gly Ile Ile Val
 195 200 205

Ala Ser Met Ser Gly Gly Leu Thr Thr Ser Thr Glu Asn Gly Ser Ala
 210 215 220

Asn Cys Asn Phe Ile Pro Thr Ala Val Val Phe Asp Val Arg
 225 230 235

<210> 405

<211> 837

<212> DNA

<213> *Corynebacterium glutamicum*

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<220>
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<222> (101)..(814)
<223> FRXA00840

<400> 405
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tcctccgcga ttgtctcggt gaaaggtaag taaaactcaa gtg aca aag aca ctc 115
                                     Val Thr Lys Thr Leu
                                     1 5

ccc cga ctg ctt aca gtc gct gcc gct cta gcc att gca ctc ccg gca 163
Pro Arg Leu Leu Thr Val Ala Ala Ala Leu Ala Ile Ala Leu Pro Ala
                10                15                20

acc ccg gta gca tcg gct gtc aca cca gtt gaa caa gct ttc aac gcc 211
Thr Pro Val Ala Ser Ala Val Thr Pro Val Glu Gln Ala Phe Asn Ala
                25                30                35

tca tcg aat ctc tcc agc ggt ctc ccc gta gac caa tgg gga cgc ccc 259
Ser Ser Asn Leu Ser Ser Gly Leu Pro Val Asp Gln Trp Gly Arg Pro
                40                45                50

aac gag cag ttc cgc caa caa atc gaa cag gca gta aac caa ccg tgg 307
Asn Glu Gln Phe Arg Gln Gln Ile Glu Gln Ala Val Asn Gln Pro Trp
                55                60                65

gtc ccg cag gaa atc aag aac atc gtt tct cag gcc atg ggt ttt atc 355
Val Pro Gln Glu Ile Lys Asn Ile Val Ser Gln Ala Met Gly Phe Ile
                70                75                80                85

acc ggt gac ggc agc gaa ggt ggg gac att gaa atc ccc gac aac gca 403
Thr Gly Asp Gly Ser Glu Gly Gly Asp Ile Glu Ile Pro Asp Asn Ala
                90                95                100

cca cgc atc cgc cag ttc ttc tgg ccc acc cga tca gaa aac tgc atc 451
Pro Arg Ile Ala Gln Phe Phe Trp Pro Thr Arg Ser Glu Asn Cys Ile
                105                110                115

aac gga aat tct gca gcc gta gga tct gcc ttc gca gtt cca gga cca 499
Asn Gly Asn Ser Ala Ala Val Gly Ser Ala Phe Ala Val Pro Gly Pro
                120                125                130

gca gat ctc ccc ctc ccc gcc gca ggt gtc gcc caa acc tcc ttc gtg 547
Ala Asp Leu Pro Leu Pro Gly Ala Gly Val Gly Gln Thr Ser Phe Val
                135                140                145

ttc acc gca ctg gga act ggc ccc ctc gca gaa cag caa agc acc gca 595
Phe Thr Ala Leu Gly Thr Gly Pro Leu Ala Glu Gln Gln Ser Thr Ala
                150                155                160                165

atg act gtt caa tgg gca aac tta agc aac ttc acc cat ggc acc acg 643
Met Thr Val Gln Trp Ala Asn Leu Ser Asn Phe Thr His Gly Thr Thr
                170                175                180

acg ttg agc aac acc gga atc aac ccc gat ggc ccc tca acg att tcc 691
Thr Leu Ser Asn Thr Gly Ile Asn Pro Asp Gly Pro Ser Thr Ile Ser
                185                190                195

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ggt gtg gca gac aca gga cgc ggc atc atc gtc gcc tcc atg tca ggc 739
 Gly Val Ala Asp Thr Gly Arg Gly Ile Ile Val Ala Ser Met Ser Gly
 200 205 210

ggc ctc acc aca tcc acc gaa aac ggt tca gcg aac tgt aat ttc atc 787
 Gly Leu Thr Thr Ser Thr Glu Asn Gly Ser Ala Asn Cys Asn Phe Ile
 215 220 225

cgc act gcc gtc gta ttc gat gtg agg taagaaaaca atgactgac 834
 Pro Thr Ala Val Val Phe Asp Val Arg
 230 235

ttc 837

<210> 406

<211> 238

<212> PRT

<213> Corynebacterium glutamicum

<400> 406

Val Thr Lys Thr Leu Pro Arg Leu Leu Thr Val Ala Ala Ala Leu Ala
 1 5 10 15

Ile Ala Leu Pro Ala Thr Pro Val Ala Ser Ala Val Thr Pro Val Glu
 20 25 30

Gln Ala Phe Asn Ala Ser Ser Asn Leu Ser Ser Gly Leu Pro Val Asp
 35 40 45

Gln Trp Gly Arg Pro Asn Glu Gln Phe Arg Gln Gln Ile Glu Gln Ala
 50 55 60

Val Asn Gln Pro Trp Val Pro Gln Glu Ile Lys Asn Ile Val Ser Gln
 65 70 75 80

Ala Met Gly Phe Ile Thr Gly Asp Gly Ser Glu Gly Gly Asp Ile Glu
 85 90 95

Ile Pro Asp Asn Ala Pro Arg Ile Ala Gln Phe Phe Trp Pro Thr Arg
 100 105 110

Ser Glu Asn Cys Ile Asn Gly Asn Ser Ala Ala Val Gly Ser Ala Phe
 115 120 125

Ala Val Pro Gly Pro Ala Asp Leu Pro Leu Pro Gly Ala Gly Val Gly
 130 135 140

Gln Thr Ser Phe Val Phe Thr Ala Leu Gly Thr Gly Pro Leu Ala Glu
 145 150 155 160

Gln Gln Ser Thr Ala Met Thr Val Gln Trp Ala Asn Leu Ser Asn Phe
 165 170 175

Thr His Gly Thr Thr Thr Leu Ser Asn Thr Gly Ile Asn Pro Asp Gly
 180 185 190

Pro Ser Thr Ile Ser Gly Val Ala Asp Thr Gly Arg Gly Ile Ile Val
 195 200 205

Ala Ser Met Ser Gly Gly Leu Thr Thr Ser Thr Glu Asn Gly Ser Ala

210

215

220

Asn Cys Asn Phe Ile Pro Thr Ala Val Val Phe Asp Val Arg
 225 230 235

<210> 407

<211> 660

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(637)

<223> RXN00841

<400> 407

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atccccgactg ccgtcgtatt cgatgtgagg taagaaaaca atg act gat ctt cat 115
 Met Thr Asp Leu His
 1 5

ccc gta aag cag gaa att ttc aac act gct gaa tcc ata aac aca gat 163
 Pro Val Lys Gln Glu Ile Phe Asn Thr Ala Glu Ser Ile Asn Thr Asp
 10 15 20

ccc aag ggg ttt ctc cgc gag gta gac acc ttc aaa gta acc gac ttc 211
 Pro Lys Gly Phe Leu Arg Glu Val Asp Thr Phe Lys Val Thr Asp Phe
 25 30 35

ggc ctg tac atg gct cgt ggt gca aac cac ccc aag ttc gga tac ttg 259
 Gly Leu Tyr Met Ala Arg Gly Ala Asn His Pro Lys Phe Gly Tyr Leu
 40 45 50

gaa agc tgg ctc ctc cca gaa ctt gga ttg cgt gcc aac att ttc cac 307
 Glu Ser Trp Leu Leu Pro Glu Leu Gly Leu Arg Ala Asn Ile Phe His
 55 60 65

ttc cgc aaa ggc gtg gat gaa cgt cag gat tac tac atc gat gtc gct 355
 Phe Arg Lys Gly Val Asp Glu Arg Gln Asp Tyr Thr Ile Asp Val Ala
 70 75 80 85

gaa att cgc gtc gaa gac aac atc tgg acc acc cgc gac ctc tac gtg 403
 Glu Ile Arg Val Glu Asp Asn Ile Trp Thr Thr Arg Asp Leu Tyr Val
 90 95 100

gat ctc atc tct gtc tgc gga gaa cca gta aca gtc atg gac atc gac 451
 Asp Leu Ile Ser Val Cys Gly Glu Pro Val Thr Val Met Asp Ile Asp
 105 110 115

gaa cta gct gca gca acc tca gca ggg ctt atc act gca gat gac gct 499
 Glu Leu Ala Ala Thr Ser Ala Gly Leu Ile Thr Ala Asp Asp Ala
 120 125 130

gag cgc gca att gat gcc acc ttg aat gct gtt gaa gga atc acc cgc 547
 Glu Arg Ala Ile Asp Ala Thr Leu Asn Ala Val Glu Gly Ile Thr Arg
 135 140 145

cac ggc gac gat cct atg cag tgg ctg cgc tcc aag gga atc gaa ctc 595
 His Gly Asp Asp Pro Met Gln Trp Leu Arg Ser Lys Gly Ile Glu Leu

150 155 160 165

acc tgg gct gac gcc agc cag gta gag ctc gtc cct gca gag 637

Thr Trp Ala Asp Ala Ser Gln Val Glu Leu Val Pro Ala Glu

 170 175

taactacttc ctaaccgctg ctt 660

<210> 408
 <211> 179
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 408

Met Thr Asp Leu His Pro Val Lys Gln Glu Ile Phe Asn Thr Ala Glu

1 5 10 15

Ser Ile Asn Thr Asp Pro Lys Gly Phe Leu Arg Glu Val Asp Thr Phe

 20 25 30

Lys Val Thr Asp Phe Gly Leu Tyr Met Ala Arg Gly Ala Asn His Pro

 35 40 45

Lys Phe Gly Tyr Leu Glu Ser Trp Leu Leu Pro Glu Leu Gly Leu Arg

 50 55 60

Ala Asn Ile Phe His Phe Arg Lys Gly Val Asp Glu Arg Gln Asp Tyr

 65 70 75 80

Tyr Ile Asp Val Ala Glu Ile Arg Val Glu Asp Asn Ile Trp Thr Thr

 85 90 95

Arg Asp Leu Tyr Val Asp Leu Ile Ser Val Cys Gly Glu Pro Val Thr

 100 105 110

Val Met Asp Ile Asp Glu Leu Ala Ala Thr Ser Ala Gly Leu Ile

 115 120 125

Thr Ala Asp Asp Ala Glu Arg Ala Ile Asp Ala Thr Leu Asn Ala Val

 130 135 140

Glu Gly Ile Thr Arg His Gly Asp Asp Pro Met Gln Trp Leu Arg Ser

 145 150 155 160

Lys Gly Ile Glu Leu Thr Trp Ala Asp Ala Ser Gln Val Glu Leu Val

 165 170 175

Pro Ala Glu

<210> 409
 <211> 660
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(637)
 <223> FRXA00841

<400> 409															
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atccccgactg cgcgtgtatt cgatgtgagg taagaaaaca						atg	act	gat	ctt	cat	115				
						Met	Thr	Asp	Leu	His					
						1				5					
ccc gta aag cag gaa att ttc aac act gct gaa tcc ata aac aca gat	163														
Pro Val Lys Gln Phe Ile Phe Asn Thr Ala Glu Ser Ile Asn Thr Asp															
						10				20					
ccc aag ggg ttt ctc cgc gag gta gac acc ttc aaa gta acc gac ttc	211														
Pro Lys Gly Phe Leu Arg Glu Val Asp Thr Phe Lys Val Thr Asp Phe															
						25				35					
ggc ctg tac atg gct cgt ggt gca aac cac ccc aag ttc gga tac ttg	259														
Gly Leu Tyr Met Ala Arg Gly Ala Asn His Pro Lys Phe Gly Tyr Leu															
						40				50					
gaa agc tgg ctc ctc cca gaa ctt gga ttg cgt gcc aac att ttc cac	307														
Glu Ser Trp Leu Leu Pro Glu Leu Gly Leu Arg Ala Asn Ile Phe His															
						55				65					
ttc cgc aaa ggc gtg gat gaa cgt cag gat tac tac atc gat gtc gct	355														
Phe Arg Lys Gly Val Asp Glu Arg Gln Asp Tyr Tyr Ile Asp Val Ala															
						70				85					
gaa att cgc gtc gaa gac aac atc tgg acc acc cgc gac ctc tac gtg	403														
Glu Ile Arg Val Glu Asp Asn Ile Trp Thr Thr Asp Leu Tyr Val															
						90				100					
gat ctc atc tot gtc tgc gga gaa cca gta aca gtc atg gac atc gac	451														
Asp Leu Ile Ser Val Cys Gly Glu Pro Val Thr Val Met Asp Ile Asp															
						105				115					
gaa cta gct gca gca acc tca gca ggg ctt atc act gca gat gac gct	499														
Glu Leu Ala Ala Thr Ser Ala Gly Leu Ile Thr Ala Asp Asp Ala															
						120				130					
gag cgc gca att gat gcc acc ttg aat gct gtt gaa gga atc acc cgc	547														
Glu Arg Ala Ile Asp Ala Thr Leu Asn Ala Val Glu Gly Ile Thr Arg															
						135				145					
cac ggc gac gat cct atg cag tgg ctg cgc tcc aag gga atc gaa ctc	595														
His Gly Asp Asp Pro Met Gln Trp Leu Arg Ser Lys Gly Ile Glu Leu															
						150				165					
acc tgg gct gac gcc agc cag gta gag ctc gtc cct gca gag	637														
Thr Trp Ala Asp Ala Ser Gln Val Glu Leu Val Pro Ala Glu															
						170				175					
taactacttc ctaaccgtg ctt											660				
<210> 410															
<211> 179															
<212> PRT															
<213> <i>Corynebacterium glutamicum</i>															
<400> 410															

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Met Thr Asp Leu His Pro Val Lys Gln Glu Ile Phe Asn Thr Ala Glu
 1          5          10          15
Ser Ile Asn Thr Asp Pro Lys Gly Phe Leu Arg Glu Val Asp Thr Phe
          20          25          30
Lys Val Thr Asp Phe Gly Leu Tyr Met Ala Arg Gly Ala Asn His Pro
          35          40          45
Lys Phe Gly Tyr Leu Glu Ser Trp Leu Leu Pro Glu Leu Gly Leu Arg
          50          55          60
Ala Asn Ile Phe His Phe Arg Lys Gly Val Asp Glu Arg Gln Asp Tyr
          65          70          75          80
Tyr Ile Asp Val Ala Glu Ile Arg Val Glu Asp Asn Ile Trp Thr Thr
          85          90          95
Arg Asp Leu Tyr Val Asp Leu Ile Ser Val Cys Gly Glu Pro Val Thr
          100          105          110
Val Met Asp Ile Asp Glu Leu Ala Ala Ala Thr Ser Ala Gly Leu Ile
          115          120          125
Thr Ala Asp Asp Ala Glu Arg Ala Ile Asp Ala Thr Leu Asn Ala Val
          130          135          140
Glu Gly Ile Thr Arg His Gly Asp Asp Pro Met Gln Trp Leu Arg Ser
          145          150          155          160
Lys Gly Ile Glu Leu Thr Trp Ala Asp Ala Ser Gln Val Glu Leu Val
          165          170          175
Pro Ala Glu

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<210> 411
<211> 993
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(970)
<223> RXN00846

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<400> 411
ctgcgggaga ctgcggtaga agcgaaaaat aacggtatcc tcggggctgc ggatggctgg 60
cctgggggaa ttccaagtgc tgcaagttgg agggaaaaacg atg ttg aag aat gat 115
Met Leu Lys Asn Asp
1          5
ctg tct ggt gct cga gtt gta gct gtg cat gcg cac cct gac gat gag 163
Leu Ser Gly Ala Arg Val Val Ala Val His Ala His Pro Asp Asp Glu
          10          15          20
gcg att acc acc ggt ggt gtg ctt gcg gat ctt gct got cgt ggc gcc 211
Ala Ile Thr Thr Gly Gly Val Leu Ala Asp Leu Ala Ala Arg Gly Ala
          25          30          35

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gat gtc acg gta att acc tgc acg ttg ggc gag cag ggt gag gtt atc 259
 Asp Val Thr Val Ile Thr Cys Thr Leu Gly Glu Gln Gly Glu Val Ile
 40 45 50

ggg ttt agg atc cat gag ctt tac gcc tcg ctg gag att ctg ggc gtg 355
 Gly Phe Arg Ile His Glu Leu Tyr Ala Ser Leu Glu Ile Leu Gly Val
 70 75 80 85

cgt ggc att cat ctg ggt ggc gct ggc tgc tgg agg gat tcc ggt atg 403
 Arg Gly Ile His Leu Gly Gly Ala Gly Cys Trp Arg Asp Ser Gly Met
 90 95 100

gtt ggt gat cct gca aat gag cat cgg cgt gcg ttt att cac tct ggt 451
 Val Gly Asp Pro Ala Asn Glu His Pro Arg Ala Phe Ile His Ser Gly
 105 110 115

gac cgt gca gtg gag caa ttg aaa gaa ctt ctt gcg gaa ttg aag cca 499
 Asp Arg Ala Val Glu Gln Leu Lys Glu Leu Leu Ala Glu Leu Lys Pro
 120 125 130

cat ctt ttg atc acc tat ggc cct gac ggc ggc tat ggg cac ccc gat 547
 His Leu Leu Ile Thr Tyr Gly Pro Asp Gly Gly Tyr Gly His Pro Asp
 135 140 145

cac att cgt gcg cat gaa atc acc cac gca gca gcc ggc gag caa cgc 595
 His Ile Arg Ala His Glu Ile Thr His Ala Ala Gly Glu Gln Arg
 150 155 160 165

att ctg tgg gct gtg agc gac cgt gag gag ctc gag gac ggt cta aag 643
 Ile Leu Trp Ala Val Ser Asp Arg Glu Glu Leu Glu Asp Gly Leu Lys
 170 175 180

gca atc act ggg ctt cct gaa ggt tgg ggc agg gga gag ctc tct gcg 691
 Ala Ile Thr Gly Leu Pro Glu Gly Trp Gly Arg Gly Glu Leu Ser Ala
 185 190 195

gtc gat tcc gtg gac ctc tct gtt gag ctg aac gat gaa gtg tat gcc 739
 Val Asp Ser Val Asp Leu Ser Val Glu Leu Asn Asp Glu Val Tyr Ala
 200 205 210

acc aag gtg gaa tcc atg cgc gcg cat gcg aca caa ttg tgg atc gct 787
 Thr Lys Val Glu Ser Met Arg Ala His Ala Thr Gln Leu Trp Ile Ala
 215 220 225

gac ggt tcc gta tct cgc acc aac ccg gtt gcc gca cac gca gtg aca 835
 Asp Gly Ser Val Ser Arg Thr Asn Pro Val Ala Ala His Ala Val Thr
 230 235 240 245

cag cag gac aat gtg aag gtg tgg gcg cta tct aat ttg att gca caa 883
 Gln Gln Asp Asn Val Lys Val Trp Ala Leu Ser Asn Leu Ile Ala Gln
 250 255 260

ccc atc atg cgc cac gag cac tac caa ctc ggc gcc gga aca cca ctg 931
 Pro Ile Met Arg His Glu His Tyr Gln Leu Gly Ala Gly Thr Pro Leu
 265 270 275

cct gaa ggt gca act gga gtg ctt gac gga ctg gag ttc tgacacgggt 980
 Pro Glu Gly Ala Thr Gly Val Leu Asp Gly Leu Glu Phe
 280 285 290

atggcagaat cta 993

<210> 412

<211> 290

<212> PRT

<213> Corynebacterium glutamicum

<400> 412

Met Leu Lys Asn Asp Leu Ser Gly Ala Arg Val Val Ala Val His Ala
 1 5 10 15

His Pro Asp Asp Glu Ala Ile Thr Thr Gly Gly Val Leu Ala Asp Leu
 20 25 30

Ala Ala Arg Gly Ala Asp Val Thr Val Ile Thr Cys Thr Leu Gly Glu
 35 40 45

Gln Gly Glu Val Ile Gly Glu Thr Phe Ala Gln Leu Val Asn Gly Asp
 50 55 60

Ala Asp Gln Leu Gly Gly Phe Arg Ile His Glu Leu Tyr Ala Ser Leu
 65 70 75 80

Glu Ile Leu Gly Val Arg Gly Ile His Leu Gly Gly Ala Gly Cys Trp
 85 90 95

Arg Asp Ser Gly Met Val Gly Asp Pro Ala Asn Glu His Pro Arg Ala
 100 105 110

Phe Ile His Ser Gly Asp Arg Ala Val Glu Gln Leu Lys Glu Leu Leu
 115 120 125

Ala Glu Leu Lys Pro His Leu Leu Ile Thr Tyr Gly Pro Asp Gly Gly
 130 135 140

Tyr Gly His Pro Asp His Ile Arg Ala His Glu Ile Thr His Ala Ala
 145 150 155 160

Ala Gly Glu Gln Arg Ile Leu Trp Ala Val Ser Asp Arg Glu Glu Leu
 165 170 175

Glu Asp Gly Leu Lys Ala Ile Thr Gly Leu Pro Glu Gly Trp Gly Arg
 180 185 190

Gly Glu Leu Ser Ala Val Asp Ser Val Asp Leu Ser Val Glu Leu Asn
 195 200 205

Asp Glu Val Tyr Ala Thr Lys Val Glu Ser Met Arg Ala His Ala Thr
 210 215 220

Gln Leu Trp Ile Ala Asp Gly Ser Val Ser Arg Thr Asn Pro Val Ala
 225 230 235 240

Ala His Ala Val Thr Gln Gln Asp Asn Val Lys Val Trp Ala Leu Ser
 245 250 255

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Asn Leu Ile Ala Gln Pro Ile Met Arg His Glu His Tyr Gln Leu Gly
    260                      265                      270

Ala Gly Thr Pro Leu Pro Glu Gly Ala Thr Gly Val Leu Asp Gly Leu
    275                      280                      285

Glu Phe
    290

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<210> 413
<211> 487
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(487)
<223> FRXA00846

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<400> 413
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cctgggggaa tttcaagtgc tgcaagttgg aggaaaaaacg atg ttg aag aat gat 115
Met Leu Lys Asn Asp
1 5

ctg tct ggt gct cga gtt gta gct gtg cat gcg cac cct gac gat gag 163
Leu Ser Gly Ala Arg Val Val Ala Val His Ala His Pro Asp Asp Glu
10 15 20

gcg att acc acc ggt ggt gtg ctt gcg gat ctt gct gct cgt ggc gcc 211
Ala Ile Thr Thr Gly Gly Val Leu Ala Asp Leu Ala Ala Arg Gly Ala
25 30 35

gat gtc acg gta att acc tgc acg ttg ggc gag cag ggt gag gtt atc 259
Asp Val Thr Val Ile Thr Cys Thr Leu Gly Glu Gln Gly Glu Val Ile
40 45 50

ggt gag aca ttc gcg cag cta gtc aac ggt gat gcg gat cag ctt ggc 307
Gly Glu Thr Phe Ala Gln Leu Val Asn Gly Asp Ala Asp Gln Leu Gly
55 60 65

ggg ttt agg atc cat gag ctt tac gcc tcg ctg gag att ctg ggc gtg 355
Gly Phe Arg Ile His Glu Leu Tyr Ala Ser Leu Glu Ile Leu Gly Val
70 75 80 85

cgt ggc att cat ctg ggt ggc gct ggc tgc tgg agg gat tcc ggt atg 403
Arg Gly Ile His Leu Gly Gly Ala Gly Cys Trp Arg Asp Ser Gly Met
90 95 100

gtt ggt gat cct gca aat gag cat ccg cgt gcg ttt att cac tct ggt 451
Val Gly Asp Pro Ala Asn Glu His Pro Arg Ala Phe Ile His Ser Gly
105 110 115

gac cgt gca gtg gag caa ttg aaa gaa ctt ctt gcg 487
Asp Arg Ala Val Glu Gln Leu Lys Glu Leu Leu Ala
120 125

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<210> 414

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<211> 129

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 414

Met Leu Lys Asn Asp Leu Ser Gly Ala Arg Val Val Ala Val His Ala
 1 5 10 15

His Pro Asp Asp Glu Ala Ile Thr Thr Gly Gly Val Leu Ala Asp Leu
 20 25 30

Ala Ala Arg Gly Ala Asp Val Thr Val Ile Thr Cys Thr Leu Gly Glu
 35 40 45

Gln Gly Glu Val Ile Gly Glu Thr Phe Ala Gln Leu Val Asn Gly Asp
 50 55 60

Ala Asp Gln Leu Gly Gly Phe Arg Ile His Glu Leu Tyr Ala Ser Leu
 65 70 75 80

Glu Ile Leu Gly Val Arg Gly Ile His Leu Gly Gly Ala Gly Cys Trp
 85 90 95

Arg Asp Ser Gly Met Val Gly Asp Pro Ala Asn Glu His Pro Arg Ala
 100 105 110

Phe Ile His Ser Gly Asp Arg Ala Val Glu Gln Leu Lys Glu Leu Leu
 115 120 125

Ala

<210> 415

<211> 951

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(928)

<223> RXN00850

<400> 415

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attacctgtt tcagatatatt aggaaggctc acttttcaac atg gct aat cca ttc 115
 Met Ala Asn Pro Phe
 1 5

tcc aag gca tgg aag tac ctc atg gcg ttg ttc gac tcc aag att gag 163
 Ser Lys Ala Trp Lys Tyr Leu Met Ala Leu Phe Asp Ser Lys Ile Glu
 10 15 20

gag aac gcg gat cct aag gta cag atc cag caa gcc atc gaa gat gct 211
 Glu Asn Ala Asp Pro Lys Val Gln Ile Gln Gln Ala Ile Glu Asp Ala
 25 30 35

cag cgc cag cat cag gag ctc tcc cag cag gca gca gct gtt att ggt 259
 Gln Arg Gln His Gln Glu Leu Ser Gln Gln Ala Ala Val Ile Gly
 40 45 50

aac cag cgt cag ctt gaa atg cag ctg aac cgc cgt ctg gct gaa att	307
Asn Gln Arg Gln Leu Glu Met Gln Leu Asn Arg Arg Leu Ala Glu Ile	
55 60 65	
gag aag ctg cag ggc aac acc cgc cag gct atc cag ctg gct gac aag	355
Glu Lys Leu Gln Gly Asn Thr Arg Gln Ala Ile Gln Leu Ala Asp Lys	
70 75 80 85	
gct cgc gct gac ggt gat gtc aag aag gct act gag tac gaa aac gcc	403
Ala Arg Ala Asp Gly Asp Val Lys Lys Ala Thr Asn Ala	
90 95 100	
gct gag gct ttc gct gca cag ctg gtt act gct gag cag tcc gtt gaa	451
Ala Glu Ala Phe Ala Ala Gln Leu Val Thr Ala Glu Gln Ser Val Glu	
105 110 115	
gat acc aag cag ctc cac gac cag gct ctg cag cag gct gat cag gct	499
Asp Thr Lys Gln Leu His Asp Gln Ala Leu Gln Gln Ala Asp Gln Ala	
120 125 130	
aag aag gct gtg gag cgt aac tcc atg gct ttg cag cag aag gtt gct	547
Lys Lys Ala Val Glu Arg Asn Ser Met Ala Leu Gln Gln Lys Val Ala	
135 140 145	
gag cgc acc aag ctt ctg agc cag ctg gag cag gcg aag atg cag gaa	595
Glu Arg Thr Lys Leu Leu Ser Gln Leu Glu Gln Ala Lys Met Gln Glu	
150 155 160 165	
aag gtt tcc gag tcc ctg aag tcc atg gat tct ttg acc tcc gcc agc	643
Lys Val Ser Glu Ser Leu Lys Ser Met Asp Ser Leu Thr Ser Gly Ser	
170 175 180	
act cct aac ctg gat caa gtt cgt gag aag att gag cgt cgt tac gct	691
Thr Pro Asn Leu Asp Gln Val Arg Glu Lys Ile Glu Arg Arg Tyr Ala	
185 190 195	
aac gcg ctt ggc cag gct gag ctt gcg tcc aac tct gtt gag gcc cgc	739
Asn Ala Leu Gly Gln Ala Glu Leu Ala Ser Asn Ser Val Glu Gly Arg	
200 205 210	
atg gct gag gtt gag cag gct gcc gtt cag atg gct gga cac tcc cgc	787
Met Ala Glu Val Glu Gln Ala Gly Val Gln Met Ala Gly His Ser Arg	
215 220 225	
ctt gag cag atc cgc gct gag atg gct ggt ggt tcc ctg acc gct ggt	835
Leu Glu Gln Ile Arg Ala Glu Met Ala Gly Gly Ser Leu Thr Ala Gly	
230 235 240 245	
aac aag cag gag tcc att gag gct cct gca gcg gcc aac aac gtc act	883
Asn Lys Gln Glu Ser Ile Glu Ala Pro Ala Ala Gly Asn Asn Val Thr	
250 255 260	
gat gac gca gtt gca cag cgc atg cgt gag ctg cgc gcc gag gct	928
Asp Asp Ala Val Ala Gln Arg Met Arg Glu Leu Arg Gly Glu Ala	
265 270 275	
taaacctgcc acagcagact aaa	951

<211> 276

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 416

Met Ala Asn Pro Phe Ser Lys Ala Trp Lys Tyr Leu Met Ala Leu Phe
 1 5 10 15

Asp Ser Lys Ile Glu Glu Asn Ala Asp Pro Lys Val Gln Ile Gln Gln
 20 25 30

Ala Ile Glu Asp Ala Gln Arg Gln His Gln Glu Leu Ser Gln Gln Ala
 35 40 45

Ala Ala Val Ile Gly Asn Gln Arg Gln Leu Glu Met Gln Leu Asn Arg
 50 55 60

Arg Leu Ala Glu Ile Glu Lys Leu Gln Gly Asn Thr Arg Gln Ala Ile
 65 70 75 80

Gln Leu Ala Asp Lys Ala Arg Ala Asp Gly Asp Val Lys Lys Ala Thr
 85 90 95

Glu Tyr Glu Asn Ala Ala Glu Ala Phe Ala Ala Gln Leu Val Thr Ala
 100 105 110

Glu Gln Ser Val Glu Asp Thr Lys Gln Leu His Asp Gln Ala Leu Gln
 115 120 125

Gln Ala Asp Gln Ala Lys Lys Ala Val Glu Arg Asn Ser Met Ala Leu
 130 135 140

Gln Gln Lys Val Ala Glu Arg Thr Lys Leu Leu Ser Gln Leu Glu Gln
 145 150 155 160

Ala Lys Met Gln Glu Lys Val Ser Glu Ser Leu Lys Ser Met Asp Ser
 165 170 175

Leu Thr Ser Gly Ser Thr Pro Asn Leu Asp Gln Val Arg Glu Lys Ile
 180 185 190

Glu Arg Arg Tyr Ala Asn Ala Leu Gly Gln Ala Glu Leu Ala Ser Asn
 195 200 205

Ser Val Glu Gly Arg Met Ala Glu Val Glu Gln Ala Gly Val Gln Met
 210 215 220

Ala Gly His Ser Arg Leu Glu Gln Ile Arg Ala Glu Met Ala Gly Gly
 225 230 235 240

Ser Leu Thr Ala Gly Asn Lys Gln Glu Ser Ile Glu Ala Pro Ala Ala
 245 250 255

Gly Asn Asn Val Thr Asp Asp Ala Val Ala Gln Arg Met Arg Glu Leu
 260 265 270

Arg Gly Glu Ala
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<210> 417

<211> 336
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(313)
 <223> RXN00854

<400> 417
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ggacacgtaa cttctgtgct tgcgctgtat tatcgtcccc atg cgt tta tcg gag 115
 Met Arg Leu Ser Glu
 1 5

ttt cgg caa ctc att gaa gat gaa ttc gga gaa gcc aaa ggg gag tgg 163
 Phe Arg Gln Leu Ile Glu Asp Glu Phe Gly Glu Ala Lys Gly Glu Trp
 10 15 20

att gca cac tcg cat gtg att ggt gcc ctc ggc gtc act gca gat gtt 211
 Ile Ala His Ser His Val Ile Gly Ala Leu Gly Val Thr Ala Asp Val
 25 30 35

gca gta gat acc ggg gtt gat ctg cgc gat gta tgg gaa caa ctg tgc 259
 Ala Val Asp Thr Gly Val Asp Leu Arg Asp Val Trp Glu Gln Leu Cys
 40 45 50

att gat ttc agt gtt ccc gaa gag cga cga ctt ggt aaa gat gaa cca 307
 Ile Asp Phe Ser Val Pro Glu Glu Arg Arg Leu Gly Lys Asp Glu Pro
 55 60 65

ggg ttc tagctgttc gagggggttc gca 336
 Gly Phe
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<210> 418
 <211> 71
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 418
 Met Arg Leu Ser Glu Phe Arg Gln Leu Ile Glu Asp Glu Phe Gly Glu
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Ala Lys Gly Glu Trp Ile Ala His Ser His Val Ile Gly Ala Leu Gly
 20 25 30

Val Thr Ala Asp Val Ala Val Asp Thr Gly Val Asp Leu Arg Asp Val
 35 40 45

Trp Glu Gln Leu Cys Ile Asp Phe Ser Val Pro Glu Glu Arg Arg Leu
 50 55 60

Gly Lys Asp Glu Pro Gly Phe
 65 70

<210> 419
 <211> 336

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}..{313}

<223> FRXA00854

<400> 419

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				Met	Arg	Leu	Ser	Glu	
				1				5	

ttt	cgg	caa	ctc	att	gaa	gat	gaa	ttc	gga	gaa	gcc	aaa	ggg	gag	tgg	163
Phe	Arg	Gln	Leu	Ile	Glu	Asp	Glu	Phe	Gly	Glu	Ala	Lys	Gly	Glu	Trp	
			10					15						20		

att	gca	cac	tgc	cat	gtg	att	ggt	gcc	ctc	ggc	gtc	act	gca	gat	gtt	211
Ile	Ala	His	Ser	His	Val	Ile	Gly	Ala	Leu	Gly	Val	Thr	Ala	Asp	Val	
			25				30						35			

gca	gta	gat	acc	ggg	gtt	gat	ctg	cgc	gat	gta	tgg	gaa	caa	ctg	tgc	259
Ala	Val	Asp	Thr	Gly	Val	Asp	Leu	Arg	Asp	Val	Trp	Glu	Gln	Leu	Cys	
		40					45					50				

att	gat	ttc	agt	gtt	ccc	gaa	gag	cga	cga	ctt	ggt	aaa	gat	gaa	cca	307
Ile	Asp	Phe	Ser	Val	Pro	Glu	Glu	Arg	Arg	Leu	Gly	Lys	Asp	Glu	Pro	
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ggg	ttc	tagcttgttc	gagggggttc	gca		336
Gly	Phe					
70						

<210> 420

<211> 71

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 420

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Ala	Lys	Gly	Glu	Trp	Ile	Ala	His	Ser	His	Val	Ile	Gly	Ala	Leu	Gly
			20					25					30		

Val	Thr	Ala	Asp	Val	Ala	Val	Asp	Thr	Gly	Val	Asp	Leu	Arg	Asp	Val
			35				40					45			

Trp	Glu	Gln	Leu	Cys	Ile	Asp	Phe	Ser	Val	Pro	Glu	Glu	Arg	Arg	Leu
	50					55					60				

Gly	Lys	Asp	Glu	Pro	Gly	Phe
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<210> 421

<211> 408

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(385)

<223> RXN00855

<400> 421

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				Met	Thr	Tyr	Phe	Ala	
				1				5	

gtg	ctt	tac	aca	tac	aac	cca	gac	agc	gag	aaa	gtc	gct	gaa	gtt	cgt	163
Val	Leu	Tyr	Thr	Tyr	Asn	Pro	Asp	Ser	Glu	Lys	Val	Ala	Glu	Val	Arg	
				10				15						20		

acc	gtc	cac	cgc	gag	ttc	att	gcc	aac	ctt	cat	gcg	gag	ggc	aaa	atc	211
Thr	Val	His	Arg	Glu	Phe	Ile	Ala	Asn	Leu	His	Ala	Glu	Gly	Lys	Ile	
			25					30					35			

gtt	ggc	tcc	ggt	cct	ttc	gtg	gac	ggc	gac	ggt	ggc	gcg	ctg	att	gtc	259
Val	Gly	Ser	Gly	Pro	Phe	Val	Asp	Gly	Asp	Gly	Gly	Ala	Leu	Ile	Val	
			40				45					50				

atc	aag	ttg	gaa	gaa	ggc	tcc	aac	ctt	gtt	gat	gct	gaa	acc	ctg	atg	307
Ile	Lys	Leu	Glu	Glu	Gly	Ser	Asn	Leu	Val	Asp	Ala	Glu	Thr	Leu	Met	
			55			60					65					

aac	aat	gat	cca	ttc	cac	gta	gaa	aac	gtg	ctg	gac	aac	cgc	gtc	atc	355
Asn	Asn	Asp	Pro	Phe	His	Val	Glu	Asn	Val	Leu	Asp	Asn	Arg	Val	Ile	
	70				75					80				85		

cgt	agc	tgg	aac	cct	gtg	acc	aaa	gat	ttc	taggcaactt	tttctttaac	405
Arg	Ser	Trp	Asn	Pro	Val	Thr	Lys	Asp	Phe			
			90					95				

aat	408
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<210> 422

<211> 95

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 422

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Val	Ala	Glu	Val	Arg	Thr	Val	His	Arg	Glu	Phe	Ile	Ala	Asn	Leu	His
		20						25					30		

Ala	Glu	Gly	Lys	Ile	Val	Gly	Ser	Gly	Pro	Phe	Val	Asp	Gly	Asp	Gly
		35					40					45			

Gly	Ala	Leu	Ile	Val	Ile	Lys	Leu	Glu	Glu	Gly	Ser	Asn	Leu	Val	Asp
	50					55					60				

Ala	Glu	Thr	Leu	Met	Asn	Asn	Asp	Pro	Phe	His	Val	Glu	Asn	Val	Leu
	65				70					75				80	

<400> 424
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1 5 10 15
Val Ala Glu Val Arg Thr Val His Arg Glu Phe Ile Ala Asn Leu His
20 25 30

400> 425																									
gcc	aac	acc	cg	gg	tgc	gct	tgt	ggc	gtc	cgt	tct	tga	aat	gtc	cc	acc	gc	g	aat	gc	c	act	act	60	
accgatgagg																tggaagcctc	cctcaaccag	aaagtctgat	atg	act	cct	ccg	att		115
																			Met	Thr	Pro	Pro	Ile	5	
atc	tcc	cca	gag	agc	ttt			gaa	gcc	cta	agg	cg	atg	cgt	gcg	gct	gaa		163						
Ile	Ser	Pro	Glu	Ser	Phe	Glu	Ala	Leu	Arg	15	Arg	Met	Arg	Ala	Ala	Ala	Glu	20							
																10									
ccc	acg	atg	gtg	gcg	gaa	cgt	ttc	aag	cag	cgc	cgt	aag	cgt	gaa	ctg		211								
Pro	Thr	Met	Val	Ala	Glu	Arg	Phe	Lys	Gln	Arg	Arg	Lys	Arg	Glu	Leu		35								
																25									
ctc	ggt	gag	gac	ggc	aag	ctg	ttt	atc	gtg	gct	gcc	gac	cac	cca	gcg		259								
Leu	Gly	Glu	Asp	Gly	Lys	Leu	Phe	Ile	Val	Ala	Ala	Asp	His	Pro	Ala		40								
																45									
cgc	ggc	gca	ctt	gct	gtt	ggc	gac	aat	gaa	acc	gcc	atg	gct	aac	cgc		307								
Arg	Gly	Ala	Leu	Ala	Val	Gly	Asp	Asn	Glu	Thr	Ala	Met	Ala	Asn	Arg		55								
																60									
tat	gaa	ctg	ctc	gaa	cgc	atg	gct	atc	gca	ctg	tct	cgc	ccg	ggt	gtg		355								
Tyr	Glu	Leu	Leu	Glu	Arg	Met	Ala	Ile	Ala	Leu	Ser	Arg	Pro	Gly	Val		70								
																75									
gat	ggt	gtg	ctg	gga	act	cca	gac	atc	att	gat	gat	ctg	gcg	gcg	ctc		403								
Asp	Gly	Val	Leu	Gly	Thr	Pro	Asp	Ile	Ile	Asp	Asp	Leu	Ala	Ala	Leu		90								
																95									
gga	ctg	ctc	gat	gac	aag	atc	gtg	gtt	ggc	tcc	atg	aac	cgt	ggt	ggc		451								
Gly	Leu	Leu	Asp	Asp	Lys	Ile	Val	Val	Gly	Ser	Met	Asn	Arg	Gly	Gly		105								
																110									
ctg	cgt	ggc	gct	tcc	ttt	gaa	atg	gat	gat	cgc	tac	acc	ggc	tac	aac		499								
Leu	Arg	Gly	Ala	Ser	Phe	Glu	Met	Asp	Asp	Arg	Tyr	Thr	Gly	Tyr	Asn		120								
																125									

gtg tcc tcc atg gtt gat cgt ggc gtg gat ttc gcg aaa acc cta gtg 547
Val Ser Ser Met Val Asp Arg Gly Val Asp Phe Ala Lys Thr Leu Val
135 140 145

cgc atc aac ttg agc gac gcc gga acc gcc ccg acc ttg gaa gcc acc 595
Arg Ile Asn Leu Ser Asp Ala Gly Thr Ala Pro Thr Leu Glu Ala Thr
150 155 160 165

gcg cat gca gtc aat gag gct gca gca gca cag ctg ccc atc atg ctc 643
Ala His Ala Val Asn Glu Ala Ala Ala Gln Leu Pro Ile Met Leu
170 175 180

gag ccg ttc atg agt aac tgg gta aac ggc aag gtg gtc aat gat ctt 691
Glu Pro Phe Met Ser Asn Trp Val Asn Gly Lys Val Val Asn Asp Leu
185 190 195

tcc acc gat gca gtt atc caa tct gtc gcc att got gct ggt ctg ggc 739
Ser Thr Asp Ala Val Ile Gln Ser Val Ala Ile Ala Gly Leu Gly
200 205 210

aat gat tct tcc tat acc tgg atg aag ctt cca gtg gtg gag gag atg 787
Asn Asp Ser Ser Tyr Thr Trp Met Lys Leu Pro Val Val Glu Glu Met
215 220 225

gag cgc gtc atg gaa tcc acc acc atg cca acc ctg ttg ttg ggc ggc 835
Glu Arg Val Met Glu Ser Thr Thr Met Pro Thr Leu Leu Leu Gly Gly
230 235 240 245

gaa ggc ggc aac gat cca gat gcc acc ttc gca tcc tgg gag cat gca 883
Glu Gly Gly Asn Asp Pro Asp Ala Thr Phe Ala Ser Trp Glu His Ala
250 255 260

ctc acc ctg ccg ggt gtg cgt ggc ctg acc gtg gga cgc act ctg ctg 931
Leu Thr Leu Pro Gly Val Arg Gly Leu Thr Val Gly Arg Thr Leu Leu
265 270 275

tat ccg caa gac ggc gat gtc gcc gcc gct gtt gat acc gca gcg cga 979
Tyr Pro Gln Asp Gly Asp Val Ala Ala Ala Val Asp Thr Ala Ala Arg
280 285 290

ctt gtt cac aca gat att caa caa ttc act tcg cag agc att 1021
Leu Val His Thr Asp Ile Gln Gln Phe Thr Ser Gln Ser Ile
295 300 305

taaggaattt acacacatgt ctg 1044

<210> 426

<211> 307

<212> PRT

<213> Corynebacterium glutamicum

<400> 426

Met Thr Pro Pro Ile Ile Ser Pro Glu Ser Phe Glu Ala Leu Arg Arg
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20 25 30

Arg Lys Arg Glu Leu Leu Gly Glu Asp Gly Lys Leu Phe Ile Val Ala

35					40					45						
Ala	Asp	His	Pro	Ala	Arg	Gly	Ala	Leu	Ala	Val	Gly	Asp	Asn	Glu	Thr	
50										60						
Ala	Met	Ala	Asn	Arg	Tyr	Glu	Leu	Leu	Glu	Arg	Met	Ala	Ile	Ala	Leu	
65					70					75					80	
Ser	Arg	Pro	Gly	Val	Asp	Gly	Val	Leu	Gly	Thr	Pro	Asp	Ile	Ile	Asp	
85										90					95	
Asp	Leu	Ala	Ala	Leu	Gly	Leu	Leu	Asp	Asp	Lys	Ile	Val	Val	Gly	Ser	
100										105					110	
Met	Asn	Arg	Gly	Gly	Leu	Arg	Gly	Ala	Ser	Phe	Glu	Met	Asp	Asp	Arg	
115										120					125	
Tyr	Thr	Gly	Tyr	Asn	Val	Ser	Ser	Met	Val	Asp	Arg	Gly	Val	Asp	Phe	
130					135					140						
Ala	Lys	Thr	Leu	Val	Arg	Ile	Asn	Leu	Ser	Asp	Ala	Gly	Thr	Ala	Pro	
145					150					155					160	
Thr	Leu	Glu	Ala	Thr	Ala	His	Ala	Val	Asn	Glu	Ala	Ala	Ala	Ala	Gln	
165										170					175	
Leu	Pro	Ile	Met	Leu	Glu	Pro	Phe	Met	Ser	Asn	Trp	Val	Asn	Gly	Lys	
180										185					190	
Val	Val	Asn	Asp	Leu	Ser	Thr	Asp	Ala	Val	Ile	Gln	Ser	Val	Ala	Ile	
195					200					205						
Ala	Ala	Gly	Leu	Gly	Asn	Asp	Ser	Ser	Tyr	Thr	Trp	Met	Lys	Leu	Pro	
210					215					220						
Val	Val	Glu	Glu	Met	Glu	Arg	Val	Met	Glu	Ser	Thr	Thr	Met	Pro	Thr	
225					230					235					240	
Leu	Leu	Leu	Gly	Gly	Glu	Gly	Gly	Asn	Asp	Pro	Asp	Ala	Thr	Phe	Ala	
245										250					255	
Ser	Trp	Glu	His	Ala	Leu	Thr	Leu	Pro	Gly	Val	Arg	Gly	Leu	Thr	Val	
260					265					270						
Gly	Arg	Thr	Leu	Leu	Tyr	Pro	Gln	Asp	Gly	Asp	Val	Ala	Ala	Ala	Val	
275					280					285						
Asp	Thr	Ala	Ala	Arg	Leu	Val	His	Thr	Asp	Ile	Gln	Gln	Phe	Thr	Ser	
290					295					300						
Gln	Ser	Ile														
305																

<222> (1)..(792)

<223> FRXA00869

<400> 427

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ggc gac aat gaa ccc gcc atg gct aac cgc tat gaa ctg ctc gaa cgc	96
Gly Asp Asn Glu Pro Ala Met Ala Asn Arg Tyr Glu Leu Leu Glu Arg	
20 25 30	
atg gct atc gca ctg tct cgc ccg ggt gtg gat ggt gtg ctg gga act	144
Met Ala Ile Ala Leu Ser Arg Pro Gly Val Asp Gly Val Leu Gly Thr	
35 40 45	
cca gac atc att gat gat ctg gcg cgc ctc gga ctg ctc gat gac aag	192
Pro Asp Ile Ile Asp Asp Leu Ala Ala Leu Gly Leu Asp Asp Lys	
50 55 60	
atc gtg gtt ggc tcc atg aac cgt ggt ggc ctg cgt ggc gct tcc ttt	240
Ile Val Val Gly Ser Met Asn Arg Gly Gly Leu Arg Gly Ala Ser Phe	
65 70 75 80	
gaa atg gat gat cgc tac acc ggc tac aac gtg tcc tcc atg gtt gat	288
Glu Met Asp Asp Arg Tyr Thr Gly Tyr Asn Val Ser Ser Met Val Asp	
85 90 95	
cgt ggc gtg gat ttc gcg aaa acc cta gtg cgc atc aac ttg agc gac	336
Arg Gly Val Asp Phe Ala Lys Thr Leu Val Arg Ile Asn Leu Ser Asp	
100 105 110	
gcc gga acc gcc ccg acc ttg gaa gcc acc gcg cat gca gtc aat gag	384
Ala Gly Thr Ala Pro Thr Leu Glu Ala Thr Ala His Ala Val Asn Glu	
115 120 125	
gct gca gca gca cag ctg ccc atc atg ctc gag ccg ttc atg agt aac	432
Ala Ala Ala Ala Gln Leu Pro Ile Met Leu Glu Pro Phe Met Ser Asn	
130 135 140	
tgg gta aac ggc aag gtg gtc aat gat ctt tcc acc gat gca gtt atc	480
Trp Val Asn Gly Lys Val Val Asn Asp Leu Ser Thr Asp Ala Val Ile	
145 150 155 160	
caa tct gtc gcc att gct gct ggt ctg ggc aat gat tct tcc tat acc	528
Gln Ser Val Ala Ile Ala Ala Gly Leu Gly Asn Asp Ser Ser Tyr Thr	
165 170 175	
tgg atg aag ctt cca gtg gtg gag gag atg gag cgc gtc atg gaa tcc	576
Trp Met Lys Leu Pro Val Val Glu Glu Met Glu Arg Val Met Glu Ser	
180 185 190	
acc acc atg cca acc ctg ttg ttg ggc ggc gaa ggc ggc aac gat cca	624
Thr Thr Met Pro Thr Leu Leu Leu Gly Gly Glu Gly Gly Asn Asp Pro	
195 200 205	
gat gcc acc ttc gca tcc tgg gag cat gca ctc acc ctg ccg ggt gtg	672
Asp Ala Thr Phe Ala Ser Trp Glu His Ala Leu Thr Leu Pro Gly Val	
210 215 220	
cgt ggc ctg acc gtg gga cgc act ctg ctg tat ccg caa gac ggc gat	720

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Arg Gly Leu Thr Val Gly Arg Thr Leu Leu Tyr Pro Gln Asp Gly Asp
225                230                235                240

gtc gcc gcc gct gtt gat acc gca gcg cga ctt gtt cac aca gat att    768
Val Ala Ala Ala Val Asp Thr Ala Ala Arg Leu Val His Thr Asp Ile
                245                250                255

caa caa ttc act tcg cag agc att taaggaattt acacacatgt ctg    815
Gln Gln Phe Thr Ser Gln Ser Ile
                260

<210> 428
<211> 264
<212> PRT
<213> Corynebacterium glutamicum

<400> 428
Leu Phe Ile Val Ala Ala Asp His Pro Ala Arg Gly Ala Leu Ala Val
 1                5                10                15

Gly Asp Asn Glu Pro Ala Met Ala Asn Arg Tyr Glu Leu Leu Glu Arg
                20                25                30

Met Ala Ile Ala Leu Ser Arg Pro Gly Val Asp Gly Val Leu Gly Thr
                35                40                45

Pro Asp Ile Ile Asp Asp Leu Ala Ala Leu Gly Leu Leu Asp Asp Lys
 50                55                60

Ile Val Val Gly Ser Met Asn Arg Gly Gly Leu Arg Gly Ala Ser Phe
 65                70                75                80

Glu Met Asp Asp Arg Tyr Thr Gly Tyr Asn Val Ser Ser Met Val Asp
                85                90                95

Arg Gly Val Asp Phe Ala Lys Thr Leu Val Arg Ile Asn Leu Ser Asp
 100                105                110

Ala Gly Thr Ala Pro Thr Leu Glu Ala Thr Ala His Ala Val Asn Glu
 115                120                125

Ala Ala Ala Ala Gln Leu Pro Ile Met Leu Glu Pro Phe Met Ser Asn
 130                135                140

Trp Val Asn Gly Lys Val Val Asn Asp Leu Ser Thr Asp Ala Val Ile
 145                150                155                160

Gln Ser Val Ala Ile Ala Ala Gly Leu Gly Asn Asp Ser Ser Tyr Thr
 165                170                175

Trp Met Lys Leu Pro Val Val Glu Glu Met Glu Arg Val Met Glu Ser
 180                185                190

Thr Thr Met Pro Thr Leu Leu Leu Gly Gly Glu Gly Gly Asn Asp Pro
 195                200                205

Asp Ala Thr Phe Ala Ser Trp Glu His Ala Leu Thr Leu Pro Gly Val
 210                215                220

Arg Gly Leu Thr Val Gly Arg Thr Leu Leu Tyr Pro Gln Asp Gly Asp

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225                230                235                240
Val Ala Ala Ala Val Asp Thr Ala Ala Arg Leu Val His Thr Asp Ile
                245                255

Gln Gln Phe Thr Ser Gln Ser Ile
                260

<210> 429
<211> 753
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(730)
<223> RXN00915

<400> 429
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                Met Ser Ala Ala Tyr
                1                5

tgg cag gac acc att ttg acg gtg ttt ctg ggg agg ggt ctg acc gct 163
Ser Gln Asp Thr Ile Leu Thr Val Phe Leu Gly Arg Gly Leu Thr Ala
                10                15                20

gaa ggg atc cga cag acc cta gaa gac ttc gca gaa acc ggc cta gtc 211
Glu Gly Ile Arg Gln Thr Leu Glu Asp Phe Ala Glu Thr Gly Leu Val
                25                30                35

cgc aac ctg gtg tgg att gat gcc gat agt ttc cac gag tct tca tct 259
Arg Asn Leu Val Trp Ile Asp Ala Asp Ser Phe His Glu Ser Ser Ser
                40                45                50

gaa gtc acc cac ttg gca acc aac caa gac ggt ctt cgg gag ctt cag 307
Glu Val Thr His Leu Ala Thr Asn Gln Asp Gly Leu Pro Glu Leu Gln
                55                60                65

cga cga cct ttc aat gag ttg gtg tcc cgg tca cga acc acc aag ctt 355
Arg Arg Pro Phe Asn Glu Leu Val Ser Arg Arg Thr Thr Lys Leu
                70                75                80                85

cac atc ggt gtc atc aac gtc att gat ggc agc gaa ggc atg ctt cat 403
His Ile Gly Val Ile Asn Val Ile Asp Gly Ser Glu Gly Met Leu His
                90                95                100

gca gaa gaa ctc aac cca ttg gtt ggg atc atc gac agt gtc tgt tca 451
Ala Glu Glu Leu Asn Pro Leu Val Gly Ile Ile Asp Ser Val Cys Ser
                105                110                115

cac cac caa att cac cga tcc aac gtg atg atc ggt cgg gtg gct gcc 499
His His Gln Ile His Arg Ser Asn Val Met Ile Gly Ala Val Ala Ala
                120                125                130

aca ctt gat gag gaa ctt cca att ctt cgt ggt tat gtg aac ctg atg 547
Thr Leu Asp Glu Glu Leu Pro Ile Leu Arg Gly Tyr Val Asn Leu Met
                135                140                145

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ctg gca cct gaa gat agc cac agc cca ggc acc gca aca gtg acc tac 595
 Leu Ala Pro Glu Asp Ser His Ser Pro Gly Thr Ala Thr Val Thr Tyr
 150 155 160 165

cgt cat ggt ttc agc gat cac cgt tta ccc tgc act gcg tgg cta ata 643
 Arg His Gly Phe Ser Asp His Arg Leu Pro Cys Thr Ala Trp Leu Ile
 170 175 180

tgc cca gct tgt acg gac tgt ggg aag gca gca cat cca cac caa tgc 691
 Ser Pro Ala Cys Thr Asp Cys Gly Lys Ala Ala His Pro His Gln Ser
 185 190 195

aac agc tgc tac ctg cga aag gtt cca gct ttc gtt tgg tgaggtcttt 740
 Asn Ser Ser Tyr Leu Arg Lys Val Pro Ala Phe Val Trp
 200 205 210

ttacaggcga att 753

<210> 430

<211> 210

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 430

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Arg Gly Leu Thr Ala Glu Gly Ile Arg Gln Thr Leu Glu Asp Phe Ala
 20 25 30

Glu Thr Gly Leu Val Arg Asn Leu Val Trp Ile Asp Ala Asp Ser Phe
 35 40 45

His Glu Ser Ser Ser Glu Val Thr His Leu Ala Thr Asn Gln Asp Gly
 50 55 60

Leu Pro Glu Leu Gln Arg Arg Pro Phe Asn Glu Leu Val Ser Arg Ser
 65 70 75 80

Arg Thr Thr Lys Leu His Ile Gly Val Ile Asn Val Ile Asp Gly Ser
 85 90 95

Glu Gly Met Leu His Ala Glu Glu Leu Asn Pro Leu Val Gly Ile Ile
 100 105 110

Asp Ser Val Cys Ser His His Gln Ile His Arg Ser Asn Val Met Ile
 115 120 125

Gly Ala Val Ala Ala Thr Leu Asp Glu Glu Leu Pro Ile Leu Arg Gly
 130 135 140

Tyr Val Asn Leu Met Leu Ala Pro Glu Asp Ser His Ser Pro Gly Thr
 145 150 155 160

Ala Thr Val Thr Tyr Arg His Gly Phe Ser Asp His Arg Leu Pro Cys
 165 170 175

Thr Ala Trp Leu Ile Ser Pro Ala Cys Thr Asp Cys Gly Lys Ala Ala
 180 185 190

His Pro His Gln Ser Asn Ser Ser Tyr Leu Arg Lys Val Pro Ala Phe
 195 200 205

Val Trp
 210

<210> 431
 <211> 610
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(610)
 <223> FRXA00915

<400> 431
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 ttcttcagga ccttctctac ctgggtgaggg tgagttctaa atg tcc gcc gcc tat 115
 Met Ser Ala Ala Tyr
 1 5
 tcg cag gac acc att ttg acg gtg ttt ctg ggg agg ggt ctg acc gct 163
 Ser Gln Asp Thr Ile Leu Thr Val Phe Leu Gly Arg Gly Leu Thr Ala
 10 15 20
 gaa ggg atc cga cag acc cta gaa gac ttc gca gaa acc ggc cta gtc 211
 Glu Gly Ile Arg Gln Thr Leu Glu Asp Phe Ala Glu Thr Gly Leu Val
 25 30 35
 cgc aac ctg gtg tgg att gat gcc gat agt ttc cac gag tct tca tct 259
 Arg Asn Leu Val Trp Ile Asp Ala Asp Ser Phe His Glu Ser Ser Ser
 40 45 50
 gaa gtc acc cac ttg gca acc aac caa gac ggt ctt cgg gag ctt cag 307
 Glu Val Thr His Leu Ala Thr Asn Gln Asp Gly Leu Pro Glu Leu Gln
 55 60 65
 cga cga cct ttc aat gag ttg gtg tcc cgg tca cga acc acc aag ctt 355
 Arg Arg Pro Phe Asn Glu Leu Val Ser Arg Ser Arg Thr Thr Lys Leu
 70 75 80 85
 cac atc ggt gtc atc aac gtc att gat ggc agc gaa ggc atg ctt cat 403
 His Ile Gly Val Ile Asn Val Ile Asp Gly Ser Glu Gly Met Leu His
 90 95 100
 gca gaa gaa ctc aac cca ttg gtt ggg atc atc gac agt gtc tgt tca 451
 Ala Glu Glu Leu Asn Pro Leu Val Gly Ile Ile Asp Ser Val Cys Ser
 105 110 115
 cac cac caa att cac cga tcc aac gtg atg atc ggt cgc gtg gct gcc 499
 His His Gln Ile His Arg Ser Asn Val Met Ile Gly Ala Val Ala Ala
 120 125 130
 aca ctt gat gag gaa ctt cca att ctt cgt ggt tat gtg aac ctg atg 547
 Thr Leu Asp Glu Glu Leu Pro Ile Leu Arg Gly Tyr Val Asn Leu Met
 135 140 145

ctg gca cct gaa gat agc cac agc cca ggc acc gca aca gtg acc tac 595
 Leu Ala Pro Glu Asp Ser His Ser Pro Gly Thr Ala Thr Val Thr Tyr
 150 155 160 165

cgt cat ggt ttc agc 610
 Arg His Gly Phe Ser
 170

<210> 432

<211> 170

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 432

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 20 25 30

Glu Thr Gly Leu Val Arg Asn Leu Val Trp Ile Asp Ala Asp Ser Phe
 35 40 45

His Glu Ser Ser Ser Glu Val Thr His Leu Ala Thr Asn Gln Asp Gly
 50 55 60

Leu Pro Glu Leu Gln Arg Arg Pro Phe Asn Glu Leu Val Ser Arg Ser
 65 70 75 80

Arg Thr Thr Lys Leu His Ile Gly Val Ile Asn Val Ile Asp Gly Ser
 85 90 95

Glu Gly Met Leu His Ala Glu Glu Leu Asn Pro Leu Val Gly Ile Ile
 100 105 110

Asp Ser Val Cys Ser His His Gln Ile His Arg Ser Asn Val Met Ile
 115 120 125

Gly Ala Val Ala Ala Thr Leu Asp Glu Glu Leu Pro Ile Leu Arg Gly
 130 135 140

Tyr Val Asn Leu Met Leu Ala Pro Glu Asp Ser His Ser Pro Gly Thr
 145 150 155 160

Ala Thr Val Thr Tyr Arg His Gly Phe Ser
 165 170

<210> 433

<211> 2802

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(2779)

<223> RXN00917

<400> 433

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ggtcggcctt ggatattgcc ctgtgggtag gaaagcagtc atg gtg aac acg ttg 115
 Met Val Asn Thr Leu
 1 5

aac tct aaa acc gtg aat gta ccc cgt ttt gcc aga ggc gtt gtt got 163
 Asn Ser Lys Thr Val Asn Val Pro Arg Phe Ala Arg Gly Val Val Ala
 10 15 20

gca gcc aca gcg cta ttt ttt ggc gct ttg gta agc ctc gcg cct agt 211
 Ala Ala Thr Ala Leu Phe Phe Gly Ala Leu Val Ser Leu Ala Pro Ser
 25 30 35

gcg ttg gcg cag gaa cca cct gca gtt gag gcc gga gcg tca ggt tct 259
 Ala Leu Ala Ala Gln Glu Pro Pro Ala Val Glu Ala Gly Ala Ser Gly Ser
 40 45 50

ttg agc aac ctg ggt gcc tgc atc gct gat aaa ggc act ctt gat gtc 307
 Leu Ser Asn Leu Gly Ala Cys Ile Ala Asp Lys Gly Thr Leu Asp Val
 55 60 65

atc atc atg atc gat gag aca gaa tcc ttg atc cat gaa gct cgt gac 355
 Ile Ile Met Ile Asp Glu Thr Glu Ser Leu Ile His Glu Ala Arg Asp
 70 75 80 85

ggc gtg gtc aac gcc aat gaa cca ggc gcg gac gca cag cac cac cgt 403
 Gly Val Val Asn Ala Asn Glu Pro Gly Ala Asp Ala Gln His His Arg
 90 95 100

gtt cct gca gca cag agc ttt gtg gat gag ctt cta gcc aag caa agc 451
 Val Pro Ala Ala Gln Ser Phe Val Asp Glu Leu Leu Ala Lys Gln Ser
 105 110 115

gat ggt gat ctg aac acc cgc atc cgt gtt gct ggt ttc ggc cag acg 499
 Asp Gly Asp Leu Asn Thr Arg Ile Arg Val Ala Gly Phe Gly Gln Thr
 120 125 130

tac aaa tct ggt gcc act gat cca gac aat tac gga gca tgg acg caa 547
 Tyr Lys Ser Gly Ala Thr Asp Pro Asp Asn Tyr Gly Ala Trp Thr Gln
 135 140 145

cta gat gcc tcc acc gtt ggc gga gta caa gat gaa atc tcc cgc ttc 595
 Leu Asp Ala Ser Thr Val Gly Gly Val Gln Asp Glu Ile Ser Arg Phe
 150 155 160 165

gct gac cgc acc cag gag cag tac acc aac tac gcc tcc gcg att gag 643
 Ala Asp Arg Thr Gln Glu Gln Tyr Thr Asn Tyr Ala Ser Ala Ile Glu
 170 175 180

ggc gct tac cag gac ttc act agg tcc ggc tct gag gac gcc tgc cgc 691
 Gly Ala Tyr Gln Asp Phe Thr Arg Ser Gly Ser Glu Asp Ala Cys Arg
 185 190 195

atg ctg gtg acc ttc acc gac ggc gca ctg acc gct caa gaa ggc gcc 739
 Met Leu Val Thr Phe Thr Asp Gly Ala Leu Thr Ala Gln Glu Gly Ala
 200 205 210

gat gtt gca gaa gca gca ctg tgc gcg cgg ggt ggc gtc acc gat cga 787
 Asp Val Val Ala Glu Ala Ala Leu Cys Ala Pro Gly Gly Val Thr Asp Arg
 215 220 225

ctg cgc agt gct ggc atc acc cac atc ggc atc ggt tta tcg gca cct	835
Leu Arg Ser Ala Gly Ile Thr His Ile Gly Ile Gly Leu Ser Ala Pro	
230 235 240 245	
acc aac cca tct gat ttc agc ctg ctg cgc gga acc acc gca ggt ggc	883
Thr Asn Pro Ser Asp Phe Ser Leu Leu Arg Gly Thr Thr Ala Gly Gly	
250 255 260	
gga aca tgt ggt gtc gaa cca gct aac ggt gca ttc ttc cca gca gat	931
Gly Thr Cys Gly Val Glu Pro Ala Asn Gly Ala Phe Phe Pro Ala Asp	
265 270 275	
aac gtg ggc gga ctt ttc gca gca ttc cgt gaa gcc ctt gcg att ggt	979
Asn Val Gly Gly Leu Phe Ala Ala Phe Arg Glu Ala Leu Ala Ile Gly	
280 285 290	
ggt gaa aca att ggt gaa acc cga gct ggt gat cct ttc agc ttc acc	1027
Gly Glu Thr Ile Gly Glu Thr Arg Ala Gly Asp Pro Phe Ser Phe Thr	
295 300 305	
ctg gac aac tcg gtg aac tct gtg cgt ttc acc gcg atc gcc aag gat	1075
Leu Asp Asn Ser Val Asn Ser Val Arg Phe Thr Ala Ile Ala Lys Asp	
310 315 320 325	
gat ctc ggc ccg aac gcc cac ttg gtg ctc acc gca ccc aac ggc gaa	1123
Asp Leu Gly Pro Asn Ala His Leu Val Leu Thr Ala Pro Asn Gly Glu	
330 335 340	
acg gtt gag ctc aaa gat tct gga agc agc gtc gcc aac agc act gac	1171
Thr Val Glu Leu Lys Asp Ser Gly Ser Ser Val Ala Asn Ser Thr Asp	
345 350 355	
gtg agt tgg gaa gcc gaa agc agc cca gta aaa atg gct gat ggt tcc	1219
Val Ser Trp Glu Ala Glu Ser Ser Pro Val Lys Met Ala Asp Gly Ser	
360 365 370	
ctc aac ctg cag caa ggt ggg gat tgg aag ggt gtc tgg cag att cag	1267
Leu Asn Leu Gln Gln Gly Gly Asp Trp Lys Gly Val Trp Gln Ile Gln	
375 380 385	
ttc caa gga att gat cct gca gcg gtt gat gga cgc gta ttc aac tca	1315
Phe Gln Gly Ile Asp Pro Ala Ala Val Asp Gly Arg Val Phe Asn Ser	
390 395 400 405	
gtg gag atc cag cct gac ctc cag ctt gtg ttc agt ggc ggt gat tcg	1363
Val Glu Ile Gln Pro Asp Leu Gln Leu Val Phe Ser Gly Gly Asp Ser	
410 415 420	
acg tca ggt gca ctt aac ctt cgc gat gat cag cag ctg aat atg cag	1411
Thr Ser Gly Ala Leu Asn Leu Arg Asp Asp Gln Gln Leu Asn Met Gln	
425 430 435	
ctg gtg ggc cgt gat ggt cag cca cgc atc ctt gag ggg tcc gcg ctg	1459
Leu Val Gly Arg Asp Gly Gln Pro Arg Ile Leu Glu Gly Ser Ala Leu	
440 445 450	
gtc gat ctt ggt ttc acc cgc gca gat acc ggc gag ttc gcc cct ttg	1507
Val Asp Leu Gly Phe Thr Arg Ala Asp Thr Gly Glu Phe Ala Pro Leu	
455 460 465	
gct caa gga att gat att tct ggc ggc gaa tta agc ttc ccg ctg gat	1555

Ala Gln Gly Ile Asp Ile Ser Gly Gly Glu Leu Ser Phe Pro Leu Asp	
470 475 480 485	
acg att tcg cag ctc cca gcc atc ggc acg gtg gaa gcg cgt acc acg	1603
Thr Ile Ser Gln Leu Pro Ala Ile Gly Thr Val Glu Ala Arg Thr Thr	
490 495 500	
atc acc acc gca ggc gtc gat gat ctc ccc ggc acc acg ttg agc cca	1651
Ile Thr Thr Ala Gly Val Asp Asp Leu Pro Gly Thr Thr Leu Ser Pro	
505 510 515	
att ctc aac acc acg cgc atc acc atc act cag cgc gat atg cct cag	1699
Ile Leu Asn Thr Thr Arg Ile Thr Ile Thr Gln Arg Asp Met Pro Gln	
520 525 530	
ctg cca gcg tcg gtt cgc ttc aca gcg gat gag gac gtt gtt acc gta	1747
Leu Pro Ala Ser Val Arg Phe Thr Ala Asp Glu Asp Val Val Thr Val	
535 540 545	
gac atc ccc atc acc ggc ccc ggc aag gta tgg att gca ccg gga acc	1795
Asp Ile Pro Ile Thr Gly Pro Gly Lys Val Trp Ile Ala Pro Gly Thr	
550 555 560 565	
cag ctc agc gga gtg ctt cca gac ggc gtg gac ggc att gca gca tca	1843
Gln Leu Ser Gly Val Leu Pro Asp Gly Val Asp Gly Ile Ala Ala Ser	
570 575 580	
agt act ttc gac agc cca gat aat gct ttg gtg ctc gga ctg gat gag	1891
Ser Thr Phe Asp Ser Pro Asp Asn Ala Leu Val Leu Gly Leu Asp Glu	
585 590 595	
cag ggc acg att cct gtt gaa cta acc gtg agc gat ctt cgt gac gga	1939
Gln Gly Thr Ile Pro Val Glu Leu Thr Val Ser Asp Leu Arg Asp Gly	
600 605 610	
ctg gtc aac ggc tcg att cca ctc cag atc tcc aac gct gag ggc gcc	1987
Leu Val Asn Gly Ser Ile Pro Leu Gln Ile Ser Asn Ala Glu Gly Ala	
615 620 625	
aat gaa acc agc gtg gat ctg ccg aca gaa ggc acg ttg agc gtt ccc	2035
Asn Glu Thr Ser Val Asp Leu Pro Thr Glu Gly Thr Leu Ser Val Pro	
630 635 640 645	
att aac gcc tcc act ttc gca ttg gca ttc att ttg gcc ctt gtg ctt	2083
Ile Asn Ala Ser Thr Phe Ala Leu Ala Phe Ile Leu Ala Leu Val Leu	
650 655 660	
tcc ctc ctg att ccg ctg ctc att ttg tat att gtg cgt ttc ctc tcc	2131
Ser Leu Leu Ile Pro Leu Leu Ile Leu Tyr Ile Val Arg Phe Leu Ser	
665 670 675	
gca aag gtt ccg tcc tct gcg atg agt ggc gtg cgc att cca gtg gaa	2179
Ala Lys Val Pro Ser Ser Ala Met Ser Gly Val Arg Ile Pro Val Glu	
680 685 690	
ttc tcc ggt gaa gct ctg cgc tat gcg ggc agc act atg cct gat ctc	2227
Phe Ser Gly Glu Ala Leu Arg Tyr Ala Gly Ser Thr Met Pro Asp Leu	
695 700 705	
gca tcg caa acc acc gcc acc aag cag gtc gtt gtt cat gga gac acc	2275
Ala Ser Gln Thr Thr Ala Thr Lys Gln Val Val Val His Gly Asp Thr	

710	715	720	725
ttc aat gtg gaa ggc cac aaa ctt aaa gtc cag cgc ttc cag ctg aac	2323		
Phe Asn Val Glu Ser Pro Ala Val Ile Val Gln Thr Asp Pro Ser Ile Ser	730	735	740
ccg att ggc tct cct gca gtg atc gtg cag acc gac ccg tgg atc agc	2371		
Pro Ile Ala Ser Pro Ala Val Ile Val Gln Thr Asp Pro Ser Ile Ser	745	750	755
ttc gac ggc aaa caa aag ggc aca caa gct aaa ctc ccg ctg gcg gtc	2419		
Phe Asp Gly Lys Gln Lys Gly Thr Gln Ala Lys Leu Pro Leu Ala Val	760	765	770
caa ggc agt tgg ttc ctc act gca agc ggc gct gac cct tcc aag atg	2467		
Gln Gly Ser Trp Phe Leu Thr Ala Ser Gly Ala Asp Pro Ser Lys Met	775	780	785
gaa ctc atc gcc ctg aca aac ctg ccg ctc gag cag ggc caa atc gac	2515		
Glu Leu Ile Ala Leu Thr Asn Leu Pro Leu Glu Gln Gly Gln Ile Asp	790	795	800
cgc atg atc gca ggt atc acc agc aaa gcc cct gat agg gca cgc gaa	2563		
Arg Met Ile Ala Gly Ile Thr Ser Lys Ala Pro Asp Arg Ala Arg Glu	810	815	820
cta caa aaa ttg ctt gac gac gcc gcg acc tcc cag ccc gca aag gtt	2611		
Leu Gln Lys Leu Leu Asp Asp Ala Ala Thr Ser Gln Pro Ala Lys Val	825	830	835
cca ccg cgc gcc cca gcc gcg cag ggc cac gtc gaa aag caa gct cct	2659		
Pro Pro Arg Ala Pro Ala Ala Gln Gly His Val Glu Lys Gln Ala Pro	840	845	850
agt ttt ggc act ggt tcc ggt ggt ggt ttc ggc tcc agc aat ggt gga	2707		
Ser Phe Gly Thr Gly Ser Gly Gly Gly Phe Gly Ser Ser Asn Gly Gly	855	860	865
ggc ttt ggc tcc ggt agc gga tcc aac gac aca aat ggt gga ttt ggt	2755		
Gly Phe Gly Ser Gly Ser Gly Ser Asn Asp Thr Asn Gly Gly Phe Gly	870	875	880
tcc agc ggc ggc ttc ggc gcg cga taacctgtaa cttgcgatta aaa	2802		
Ser Ser Gly Gly Phe Gly Ala Arg	890		

<210> 434

<211> 893

<212> PRT

<213> Corynebacterium glutamicum

<400> 434

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Arg Gly Val Val Ala Ala Ala Thr Ala Leu Phe Phe Gly Ala Leu Val	20	25	30	
Ser Leu Ala Pro Ser Ala Leu Ala Gln Glu Pro Pro Ala Val Glu Ala	35	40	45	

Gly Ala Ser Gly Ser Leu Ser Asn Leu Gly Ala Cys Ile Ala Asp Lys
 50 55 60
 Gly Thr Leu Asp Val Ile Ile Met Ile Asp Glu Thr Glu Ser Leu Ile
 65 70 75 80
 His Glu Ala Arg Asp Gly Val Val Asn Ala Asn Glu Pro Gly Ala Asp
 85 90 95
 Ala Gln His His Arg Val Pro Ala Ala Gln Ser Phe Val Asp Glu Leu
 100 105 110
 Leu Ala Lys Gln Ser Asp Gly Asp Leu Asn Thr Arg Ile Arg Val Ala
 115 120 125
 Gly Phe Gly Gln Thr Tyr Lys Ser Gly Ala Thr Asp Pro Asp Asn Tyr
 130 135 140
 Gly Ala Trp Thr Gln Leu Asp Ala Ser Thr Val Gly Gly Val Gln Asp
 145 150 155 160
 Glu Ile Ser Arg Phe Ala Asp Arg Thr Gln Glu Gln Tyr Thr Asn Tyr
 165 170 175
 Ala Ser Ala Ile Glu Gly Ala Tyr Gln Asp Phe Thr Arg Ser Gly Ser
 180 185 190
 Glu Asp Ala Cys Arg Met Leu Val Thr Phe Thr Asp Gly Ala Leu Thr
 195 200 205
 Ala Gln Glu Gly Ala Asp Val Ala Glu Ala Ala Leu Cys Ala Pro Gly
 210 215 220
 Gly Val Thr Asp Arg Leu Arg Ser Ala Gly Ile Thr His Ile Gly Ile
 225 230 235 240
 Gly Leu Ser Ala Pro Thr Asn Pro Ser Asp Phe Ser Leu Leu Arg Gly
 245 250 255
 Thr Thr Ala Gly Gly Thr Cys Gly Val Glu Pro Ala Asn Gly Ala
 260 265 270
 Phe Phe Pro Ala Asp Asn Val Gly Gly Leu Phe Ala Ala Phe Arg Glu
 275 280 285
 Ala Leu Ala Ile Gly Gly Glu Thr Ile Gly Glu Thr Arg Ala Gly Asp
 290 295 300
 Pro Phe Ser Phe Thr Leu Asp Asn Ser Val Asn Ser Val Arg Phe Thr
 305 310 315 320
 Ala Ile Ala Lys Asp Asp Leu Gly Pro Asn Ala His Leu Val Leu Thr
 325 330 335
 Ala Pro Asn Gly Glu Thr Val Glu Leu Lys Asp Ser Gly Ser Ser Val
 340 345 350
 Ala Asn Ser Thr Asp Val Ser Trp Glu Ala Glu Ser Ser Pro Val Lys
 355 360 365

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Met Ala Asp Gly Ser Leu Asn Leu Gln Gln Gly Asp Trp Lys Gly
  370                      375                      380

Val Trp Gln Ile Gln Phe Gln Gly Ile Asp Pro Ala Ala Val Asp Gly
  385                      390                      395                      400

Arg Val Phe Asn Ser Val Glu Ile Gln Pro Asp Leu Gln Leu Val Phe
                      405                      410                      415

Ser Gly Gly Asp Ser Thr Ser Gly Ala Leu Asn Leu Arg Asp Asp Gln
                      420                      425                      430

Gln Leu Asn Met Gln Leu Val Gly Arg Asp Gly Gln Pro Arg Ile Leu
                      435                      440                      445

Glu Gly Ser Ala Leu Val Asp Leu Gly Phe Thr Arg Ala Asp Thr Gly
                      450                      455                      460

Glu Phe Ala Pro Leu Ala Gln Gly Ile Asp Ile Ser Gly Gly Glu Leu
                      465                      470                      475                      480

Ser Phe Pro Leu Asp Thr Ile Ser Gln Leu Pro Ala Ile Gly Thr Val
                      485                      490                      495

Glu Ala Arg Thr Thr Ile Thr Thr Ala Gly Val Asp Asp Leu Pro Gly
                      500                      505                      510

Thr Thr Leu Ser Pro Ile Leu Asn Thr Thr Arg Ile Thr Ile Thr Gln
                      515                      520                      525

Arg Asp Met Pro Gln Leu Pro Ala Ser Val Arg Phe Thr Ala Asp Glu
                      530                      535                      540

Asp Val Val Thr Val Asp Ile Pro Ile Thr Gly Pro Gly Lys Val Trp
                      545                      550                      555                      560

Ile Ala Pro Gly Thr Gln Leu Ser Gly Val Leu Pro Asp Gly Val Asp
                      565                      570                      575

Gly Ile Ala Ala Ser Ser Thr Phe Asp Ser Pro Asp Asn Ala Leu Val
                      580                      585                      590

Leu Gly Leu Asp Glu Gln Gly Thr Ile Pro Val Glu Leu Thr Val Ser
                      595                      600                      605

Asp Leu Arg Asp Gly Leu Val Asn Gly Ser Ile Pro Leu Gln Ile Ser
                      610                      615                      620

Asn Ala Glu Gly Ala Asn Glu Thr Ser Val Asp Leu Pro Thr Glu Gly
                      625                      630                      635                      640

Thr Leu Ser Val Pro Ile Asn Ala Ser Thr Phe Ala Leu Ala Phe Ile
                      645                      650                      655

Leu Ala Leu Val Leu Ser Leu Leu Ile Pro Leu Leu Ile Leu Tyr Ile
                      660                      665                      670

Val Arg Phe Leu Ser Ala Lys Val Pro Ser Ser Ala Met Ser Gly Val
                      675                      680                      685

Arg Ile Pro Val Glu Phe Ser Gly Glu Ala Leu Arg Tyr Ala Gly Ser

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690

695

700

Thr Met Pro Asp Leu Ala Ser Gln Thr Thr Ala Thr Lys Gln Val Val
705 710 715 720

Val His Gly Asp Thr Phe Asn Val Glu Gly His Lys Leu Lys Val Gln
725 730 735

Arg Phe Gln Leu Asn Pro Ile Ala Ser Pro Ala Val Ile Val Gln Thr
740 745 750

Asp Pro Ser Ile Ser Phe Asp Gly Lys Gln Lys Gly Thr Gln Ala Lys
755 760 765

Leu Pro Leu Ala Val Gln Gly Ser Trp Phe Leu Thr Ala Ser Gly Ala
770 775 780

Asp Pro Ser Lys Met Glu Leu Ile Ala Leu Thr Asn Leu Pro Leu Glu
785 790 795 800

Gln Gly Gln Ile Asp Arg Met Ile Ala Gly Ile Thr Ser Lys Ala Pro
805 810 815

Asp Arg Ala Arg Glu Leu Gln Lys Leu Leu Asp Asp Ala Ala Thr Ser
820 825 830

Gln Pro Ala Lys Val Pro Pro Arg Ala Pro Ala Ala Gln Gly His Val
835 840 845

Glu Lys Gln Ala Pro Ser Phe Gly Thr Gly Ser Gly Gly Gly Phe Gly
850 855 860

Ser Ser Asn Gly Gly Gly Phe Gly Ser Gly Ser Gly Ser Asn Asp Thr
865 870 875 880

Asn Gly Gly Phe Gly Ser Ser Gly Gly Phe Gly Ala Arg
885 890

<210> 435

<211> 1406

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1383)

<223> FRXA00917

<400> 435

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Gln Leu Asn Met Gln Leu Val Gly Arg Asp Gly Gln Pro Arg Ile Leu
1 5 10 15

gag ggg tcc gcg ctg gtc gat ctt ggt ttc acc cgc gca gat acc ggc 96
Glu Gly Ser Ala Leu Val Asp Leu Gly Phe Thr Arg Ala Asp Thr Gly
20 25 30

gag ttc gcc cct ttg gct caa gga att gat att tct ggc ggc gaa tta 144
Glu Phe Ala Pro Leu Ala Gln Gly Ile Asp Ile Ser Gly Gly Glu Leu
35 40 45

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agc ttc ccg ctg gat acg att tcg cag ctc cca gcc atc ggc acg gtg 192
Ser Phe Pro Leu Asp Thr Ile Ser Gln Leu Pro Ala Ile Gly Thr Val
      50              55              60

gaa gcg cgt acc acg atc acc acc gca ggc gtc gat gat ctc ccc ggc 240
Glu Ala Arg Thr Thr Ile Thr Thr Ala Gly Val Asp Asp Leu Pro Gly
      65              70              75              80

acc acg ttg agc cca att ctc aac acc acg cgc atc acc atc act cag 288
Thr Thr Leu Ser Pro Ile Leu Asn Thr Thr Thr Ile Thr Gln
      85              90              95

cgc gat atg cct cag ctg cca gcg tcg gtt cgc ttc aca gcg gat gag 336
Arg Asp Met Pro Gln Leu Pro Ala Ser Val Arg Phe Thr Ala Asp Glu
      100             105             110

gac gtt gtt acc gta gac atc ccc atc acc ggc ccc ggc aag gta tgg 384
Asp Val Val Thr Val Asp Ile Pro Ile Thr Gly Pro Gly Lys Val Trp
      115             120             125

att gca ccg gga acc cag ctc agc gga gtg ctt cca gac ggc gtg gac 432
Ile Ala Pro Gly Thr Gln Leu Ser Gly Val Leu Pro Asp Gly Val Asp
      130             135             140

ggc att gca gca tca agt act ttc gac agc cca gat aat gct ttg gtg 480
Gly Ile Ala Ala Ser Thr Phe Asp Ser Pro Asp Asn Ala Leu Val
      145             150             155             160

ctc gga ctg gat gag cag ggc acg att cct gtt gaa cta acc gtg agc 528
Leu Gly Leu Asp Glu Gln Gly Thr Ile Pro Val Glu Leu Thr Val Ser
      165             170             175

gat ctt cgt gac gga ctg gtc aac ggc tcg att cca ctc cag atc tcc 576
Asp Leu Arg Asp Gly Leu Val Asn Gly Ser Ile Pro Leu Gln Ile Ser
      180             185             190

aac gct gag ggc gcc aat gaa acc agc gtg gat ctg ccg aca gaa ggc 624
Asn Ala Glu Gly Ala Asn Glu Thr Ser Val Asp Leu Pro Thr Glu Gly
      195             200             205

acg ttg agc gtt ccc att aac gcc tcc act ttc gca ttg gca ttc att 672
Thr Leu Ser Val Pro Ile Asn Ala Ser Thr Phe Ala Leu Ala Phe Ile
      210             215             220

ttg gcc ctt gtg ctt tcc ctc ctg att ccg ctg ctc att ttg tat att 720
Leu Ala Leu Val Leu Ser Leu Leu Ile Pro Leu Leu Ile Leu Tyr Ile
      225             230             235             240

gtg cgt ttc ctc tcc gca aag gtt ccg tcc tct gcg atg agt ggc gtg 768
Val Arg Phe Leu Ser Ala Lys Val Pro Ser Ser Ala Met Ser Gly Val
      245             250             255

cgc att cca gtg gaa ttc tcc ggt gaa gct ctg cgc tat gcg ggc agc 816
Arg Ile Pro Val Glu Phe Ser Gly Glu Ala Leu Arg Tyr Ala Gly Ser
      260             265             270

act atg cct gat ctc gca tcg caa acc acc gcc acc aag cag gtc gtt 864
Thr Met Pro Asp Leu Ala Ser Gln Thr Thr Ala Thr Lys Gln Val Val
      275             280             285

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gtt cat gga gac acc ttc aat gtg gaa ggc cac aaa ctt aaa gtc cag 912
 Val His Gly Asp Thr Phe Asn Val Glu Gly His Lys Leu Lys Val Gln
 290 295 300

cgc ttc cag ctg aac ccg att gcg tct cct gca gtg atc gtg cag acc 960
 Arg Phe Gln Leu Asn Pro Ile Ala Ser Pro Ala Val Ile Val Gln Thr
 305 310 315 320

gac ccg tcg atc agc ttc gac ggc aaa caa aag ggc aca caa gct aaa 1008
 Asp Pro Ser Ile Ser Phe Asp Gly Lys Gln Lys Gly Thr Gln Ala Lys
 325 330 335

ctc ccg ctg gcg gtc caa ggc agt tgg ttc ctc act gca agc ggc gct 1056
 Leu Pro Leu Ala Val Gln Gly Ser Trp Phe Leu Thr Ala Ser Gly Ala
 340 345 350

gac cct tcc aag atg gaa ctc atc gcc ctg aca aac ctg ccg ctc gag 1104
 Asp Pro Ser Lys Met Glu Leu Ile Ala Leu Thr Asn Leu Pro Leu Glu
 355 360 365

cag ggc caa atc gac cgc atg atc gca ggt atc acc agc aaa gcc cct 1152
 Gln Gly Gln Ile Asp Arg Met Ile Ala Gly Ile Thr Ser Lys Ala Pro
 370 375 380

gat agg gca cgc gaa cta caa aaa ttg ctt gac gac gcc gcg acc tcc 1200
 Asp Arg Ala Arg Glu Leu Gln Lys Leu Leu Asp Asp Ala Ala Thr Ser
 385 390 395 400

cag ccc gca aag gtt cca ccg cgc gcc cca gcc gcg cag ggc cac gtc 1248
 Gln Pro Ala Lys Val Pro Pro Arg Ala Pro Ala Ala Gln Gly His Val
 405 410 415

gaa aag caa gct cct agt ttt ggc act ggt tcc ggt ggt ggt ttc ggc 1296
 Glu Lys Gln Ala Pro Ser Phe Gly Thr Gly Ser Gly Gly Gly Phe Gly
 420 425 430

tcc agc aat ggt gga ggc ttt ggc tcc ggt agc gga tcc aac gac aca 1344
 Ser Ser Asn Gly Gly Gly Phe Gly Ser Gly Ser Gly Ser Asn Asp Thr
 435 440 445

aat ggt gga ttt ggt tcc agc ggc ggc ttc ggc gcg cga taacctgtaa 1393
 Asn Gly Gly Phe Gly Ser Ser Gly Gly Phe Gly Ala Arg
 450 455 460

cttgcgatta aaa 1406

<210> 436
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 436
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Glu Gly Ser Ala Leu Val Asp Leu Gly Phe Thr Arg Ala Asp Thr Gly
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Glu Phe Ala Pro Leu Ala Gln Gly Ile Asp Ile Ser Gly Gly Glu Leu
 35 40 45

Ser Phe Pro Leu Asp Thr Ile Ser Gln Leu Pro Ala Ile Gly Thr Val
 50 55 60
 Glu Ala Arg Thr Thr Ile Thr Thr Ala Gly Val Asp Asp Leu Pro Gly
 65 70 75 80
 Thr Thr Leu Ser Pro Ile Leu Asn Thr Thr Arg Ile Thr Ile Thr Gln
 85 90 95
 Arg Asp Met Pro Gln Leu Pro Ala Ser Val Arg Phe Thr Ala Asp Glu
 100 105 110
 Asp Val Val Thr Val Asp Ile Pro Ile Thr Gly Pro Gly Lys Val Trp
 115 120 125
 Ile Ala Pro Gly Thr Gln Leu Ser Gly Val Leu Pro Asp Gly Val Asp
 130 135 140
 Gly Ile Ala Ala Ser Ser Thr Phe Asp Ser Pro Asp Asn Ala Leu Val
 145 150 155 160
 Leu Gly Leu Asp Glu Gln Gly Thr Ile Pro Val Glu Leu Thr Val Ser
 165 170 175
 Asp Leu Arg Asp Gly Leu Val Asn Gly Ser Ile Pro Leu Gln Ile Ser
 180 185 190
 Asn Ala Glu Gly Ala Asn Glu Thr Ser Val Asp Leu Pro Thr Glu Gly
 195 200 205
 Thr Leu Ser Val Pro Ile Asn Ala Ser Thr Phe Ala Leu Ala Phe Ile
 210 215 220
 Leu Ala Leu Val Leu Ser Leu Leu Ile Pro Leu Leu Ile Leu Tyr Ile
 225 230 235 240
 Val Arg Phe Leu Ser Ala Lys Val Pro Ser Ser Ala Met Ser Gly Val
 245 250 255
 Arg Ile Pro Val Glu Phe Ser Gly Glu Ala Leu Arg Tyr Ala Gly Ser
 260 265 270
 Thr Met Pro Asp Leu Ala Ser Gln Thr Thr Ala Thr Lys Gln Val Val
 275 280 285
 Val His Gly Asp Thr Phe Asn Val Glu Gly His Lys Leu Lys Val Gln
 290 295 300
 Arg Phe Gln Leu Asn Pro Ile Ala Ser Pro Ala Val Ile Val Gln Thr
 305 310 315 320
 Asp Pro Ser Ile Ser Phe Asp Gly Lys Gln Lys Gly Thr Gln Ala Lys
 325 330 335
 Leu Pro Leu Ala Val Gln Gly Ser Trp Phe Leu Thr Ala Ser Gly Ala
 340 345 350
 Asp Pro Ser Lys Met Glu Leu Ile Ala Leu Thr Asn Leu Pro Leu Glu
 355 360 365

Gln Gly Gln Ile Asp Arg Met Ile Ala Gly Ile Thr Ser Lys Ala Pro
 370 375 380

Asp Arg Ala Arg Glu Leu Gln Lys Leu Leu Asp Asp Ala Ala Thr Ser
 385 390 395 400

Gln Pro Ala Lys Val Pro Pro Arg Ala Pro Ala Ala Gln Gly His Val
 405 410 415

Glu Lys Gln Ala Pro Ser Phe Gly Thr Gly Ser Gly Gly Gly Phe Gly
 420 425 430

Ser Ser Asn Gly Gly Gly Phe Gly Ser Gly Ser Gly Ser Asn Asp Thr
 435 440 445

Asn Gly Gly Phe Gly Ser Ser Gly Gly Phe Gly Ala Arg
 450 455 460

<210> 437
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 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
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 <222> (1)..(513)
 <223> RXN00921

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 Pro Ala Ala Ile Leu Leu Asp His Ile Val Pro Asn Phe Ser Arg Asp
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cgg tct ttg cca gac atc gaa gac tgg acg aga agc gat gaa gct cag 96
 Arg Ser Leu Pro Asp Ile Glu Asp Trp Thr Arg Ser Asp Glu Ala Gln
 20 25 30

cag atc ttt gca gga atc att gcg ggt gcg tct gtt caa act ggt aga 144
 Gln Ile Phe Ala Gly Ile Ile Ala Gly Ala Ser Val Gln Thr Gly Arg
 35 40 45

agc cac ttc atg tgg gat ctt ttg cgg gcg tat ttt gga gtc gct ttg 192
 Ser His Phe Met Trp Asp Leu Leu Arg Ala Tyr Phe Gly Val Ala Leu
 50 55 60

atc ggc gac gaa gat acc tac agg gct ttt act act ctc acg gtc gat 240
 Ile Gly Asp Glu Asp Thr Tyr Arg Ala Phe Thr Thr Leu Thr Val Asp
 65 70 75 80

tct gtt ctt agt ttc gtg cag tta act ctt caa gag ggc aga acg gaa 288
 Ser Val Leu Ser Phe Val Gln Leu Thr Leu Gln Glu Gly Arg Thr Glu
 85 90 95

gac att aga cga ttc gag aaa tat ggt gag cag att gcc cga gag gat 336
 Asp Ile Arg Arg Phe Glu Lys Tyr Gly Glu Gln Ile Ala Arg Glu Asp
 100 105 110

ttg ccg tcg att ctc acc aat gct cga gca gta cag caa tat ctc ggc 384
 Leu Pro Ser Ile Leu Thr Asn Ala Arg Ala Val Gln Gln Tyr Leu Gly
 115 120 125

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tat atc gac caa gat atc atc aat aag aaa gtg tcc cgg tct agg gat 432
Tyr Ile Asp Gln Asp Ile Ile Asn Lys Lys Val Ser Arg Ser Arg Asp
130 135 140

gtt aac cag att ttt act gag atg gcg cgc gct atc atc aga gca att 480
Val Asn Gln Ile Phe Thr Glu Met Ala Arg Ala Ile Ile Arg Ala Ile
145 150 155 160

agc cgg aat aat att gga aag gac atg cgg tca tgaacgtgat tcgactggat 533
Ser Arg Asn Asn Ile Gly Lys Asp Met Arg Ser
165 170

tcc 536

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<210> 438
<211> 171
<212> PRT
<213> Corynebacterium glutamicum

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20 25 30

Gln Ile Phe Ala Gly Ile Ile Ala Gly Ala Ser Val Gln Thr Gly Arg
35 40 45

Ser His Phe Met Trp Asp Leu Arg Ala Tyr Phe Gly Val Ala Leu
50 55 60

Ile Gly Asp Glu Asp Thr Tyr Arg Ala Phe Thr Thr Leu Thr Val Asp
65 70 75 80

Ser Val Leu Ser Phe Val Gln Leu Thr Leu Gln Glu Gly Arg Thr Glu
85 90 95

Asp Ile Arg Arg Phe Glu Lys Tyr Gly Glu Gln Ile Ala Arg Glu Asp
100 105 110

Leu Pro Ser Ile Leu Thr Asn Ala Arg Ala Val Gln Gln Tyr Leu Gly
115 120 125

Tyr Ile Asp Gln Asp Ile Ile Asn Lys Lys Val Ser Arg Ser Arg Asp
130 135 140

Val Asn Gln Ile Phe Thr Glu Met Ala Arg Ala Ile Ile Arg Ala Ile
145 150 155 160

Ser Arg Asn Asn Ile Gly Lys Asp Met Arg Ser
165 170

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<210> 439
<211> 2022
<212> DNA
<213> Corynebacterium glutamicum

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<220>

<221> CDS

<222> (101)..(1999)

<223> FRXA00921

<400> 439

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 tcacctacgc gtcctttaga ggaactgcag gtaggggtgg gtg gaa ggt gga act 115
 Val Glu Gly Gly Thr 5
 1
 tgg tct gct cag gcc act aaa gaa gac ctc caa ttt atc gcg gag gtt 163
 Trp Ser Ala Gln Ala Thr Lys Glu Asp Leu Gln Phe Ile Ala Glu Val 20
 10 15
 gcg ccc act cat att gaa acg gtg acc cct ttt gat gat ttc atc tca 211
 Ala Pro Thr His Ile Glu Thr Val Thr Pro Phe Asp Asp Phe Ile Ser 35
 25 30
 tca gaa gat atc gat gcg ttg ccg agg agg ttt gag tac cgt cct ttg 259
 Ser Glu Asp Ile Asp Ala Leu Pro Arg Arg Phe Glu Tyr Arg Pro Leu 50
 40 45
 gca ggc cga tcg ttg atc atg cag tct gtt cct gca ggt aaa gat gcc 307
 Ala Gly Arg Ser Leu Ile Met Gln Ser Val Pro Ala Gly Lys Asp Ala 65
 55 60
 act gga cgt cca ggg aat gtg ttc acc cat gca gta ttt gat ggg gat 355
 Thr Gly Arg Pro Gly Asn Val Phe Thr His Ala Val Phe Asp Gly Asp 85
 70 75
 cta gaa agc cca ctg gag tct gtt tat ccc att tcc ctg tac cgt tca 403
 Leu Glu Ser Pro Leu Glu Ser Val Tyr Pro Ile Ser Leu Tyr Arg Ser 100
 90 95
 cct gat ttg ctg acc cct ttt cgt gca gcc gcg gtc aac gct gcc gag 451
 Pro Asp Leu Leu Thr Pro Phe Arg Ala Ala Ala Val Asn Ala Ala Glu 115
 105 110
 ctc cct ttg gat gca ggc gag ccg aga att gcc ccc atc act gat ctg 499
 Leu Pro Leu Asp Ala Gly Glu Pro Arg Ile Gly Pro Ile Thr Asp Leu 130
 120 125
 tcc ttg tcg tgg atg atg atc gac agc atg ttt gcc gat cgc aga cag 547
 Ser Leu Ser Trp Met Met Ile Asp Ser Met Phe Gly Asp Arg Arg Gln 145
 135 140
 cag ttc tac cag ctt caa gat gct ctc caa gct gga gat aaa gct act 595
 Gln Phe Tyr Gln Leu Gln Asp Ala Leu Gln Ala Gly Asp Lys Ala Thr 165
 150 155
 gtt ttg gtt ctg aac agc act aac gag gca gca tat tgg ctt caa gcg 643
 Val Leu Val Leu Asn Ser Thr Asn Glu Ala Ala Tyr Trp Leu Gln Ala 180
 170 175
 ttg tct tct aca ttg act ccg aat gaa gcc cgg cgt ctg ttg cac ttc 691
 Leu Ser Ser Thr Leu Thr Pro Asn Glu Ala Arg Arg Leu Leu His Phe 195
 185 190
 tca acc ttt gag cgt gct gct acc ttg cca gct cca gat aaa tca atg 739

Ser	Thr	Phe	Glu	Arg	Ala	Ala	Thr	Leu	Pro	Ala	Pro	Asp	Lys	Ser	Met	
	200						205					210				
gag	gct	cgt	tct	ctg	ttt	gtg	gtc	cca	gga	att	gat	cgt	gaa	ttg	ttg	787
Glu	Ala	Arg	Ser	Leu	Phe	Val	Val	Pro	Gly	Ile	Asp	Arg	Glu	Leu	Leu	
	215					220					225					
gcg	gag	cat	tca	ggg	att	gtg	att	atc	gat	ccg	gag	att	cca	cag	agc	835
Ala	Glu	His	Ser	Gly	Ile	Val	Ile	Ile	Asp	Pro	Glu	Ile	Pro	Gln	Ser	
	230				235					240					245	
caa	cct	ttc	ggc	ccg	cag	gga	tcc	tgg	tcc	cga	atg	aca	gaa	ggg	ctc	883
Gln	Pro	Phe	Gly	Pro	Gln	Gly	Ser	Trp	Ser	Arg	Met	Thr	Glu	Gly	Leu	
			250						255					260		
ttc	tcc	gac	ggg	ttt	gat	gct	gat	gaa	ctt	gtc	gca	ggg	ctg	att	cgt	931
Phe	Ser	Asp	Gly	Phe	Asp	Ala	Asp	Glu	Leu	Val	Ala	Gly	Leu	Ile	Arg	
			265					270					275			
gcc	aac	gag	aac	ctg	gat	aat	agc	caa	aag	gaa	ctc	gct	caa	ttt	gga	979
Ala	Asn	Glu	Asn	Leu	Asp	Asn	Ser	Gln	Lys	Glu	Leu	Ala	Gln	Phe	Gly	
		280					285					290				
gac	ggg	tta	gcg	cga	ttt	atc	cgg	aat	ggc	cgt	ttt	tcc	ggc	acg	cac	1027
Asp	Gly	Leu	Ala	Arg	Phe	Ile	Arg	Asn	Gly	Arg	Phe	Ser	Gly	Thr	His	
	295					300					305					
ccg	ctt	cgc	gta	ctt	gct	gat	cag	cat	atg	ttt	gga	aag	gtg	cca	gac	1075
Pro	Leu	Arg	Val	Leu	Ala	Asp	Gln	His	Met	Phe	Gly	Lys	Val	Pro	Asp	
	310				315					320				325		
aag	cca	gca	cct	aag	gtg	gag	cct	gtc	gct	ccg	gca	cca	aac	ccc	aat	1123
Lys	Pro	Ala	Pro	Lys	Val	Glu	Pro	Val	Ala	Pro	Ala	Pro	Asn	Pro	Asn	
			330					335						340		
gca	att	tgg	gcg	cgt	gca	tct	gag	gta	gtt	cac	aat	cct	cgg	aga	gca	1171
Ala	Ile	Trp	Ala	Arg	Ala	Ser	Glu	Val	Val	His	Asn	Pro	Arg	Arg	Ala	
			345					350					355			
tca	gaa	tca	caa	gat	tgg	cca	agt	ctg	agg	cga	ttg	ccg	gat	agt	cgg	1219
Ser	Glu	Ser	Gln	Asp	Trp	Pro	Ser	Leu	Arg	Arg	Leu	Pro	Asp	Ser	Arg	
		360					365					370				
cgc	agg	atc	atc	aat	atg	tca	gag	cag	gcg	atc	aac	agc	att	gag	aag	1267
Arg	Arg	Ile	Ile	Asn	Met	Ser	Glu	Gln	Ala	Ile	Asn	Ser	Ile	Glu	Lys	
		375				380				385						
ctt	cat	gat	tcg	ccg	gca	cag	gat	ctt	gtt	gcc	tat	ttg	gat	ttc	ctt	1315
Leu	His	Asp	Ser	Pro	Ala	Gln	Asp	Leu	Val	Ala	Tyr	Leu	Asp	Phe	Leu	
		390			395					400				405		
ttg	aaa	act	gag	ctt	gcg	aca	agc	att	aat	gct	tcg	gat	ccc	ttt	ttt	1363
Leu	Lys	Thr	Glu	Leu	Ala	Thr	Ser	Ile	Asn	Ala	Ser	Asp	Pro	Phe	Phe	
				410					415					420		
cgg	agt	agt	ttt	tca	gac	ttt	cca	gcg	atg	gac	aac	tgg	cga	cac	att	1411
Arg	Ser	Ser	Phe	Ser	Asp	Phe	Pro	Ala	Met	Asp	Asn	Trp	Arg	His	Ile	
			425					430					435			
aag	ttc	acc	gag	gat	gcg	cac	cct	cgc	ttg	agg	gaa	cta	ctc	gtg	gac	1459
Lys	Phe	Thr	Glu	Asp	Ala	His	Pro	Arg	Leu	Arg	Glu	Leu	Leu	Val	Asp	

440	445	450	
gca gaa cgc gat gct agg aac aga gca cct gcg gca atc gtc ttg gac			1507
Ala Glu Arg Asp Ala Arg Asn Arg Ala Pro Ala Ala Ile Val Leu Asp			
455	460	465	
cat atc gtt ccg aac ttc agc aga gat cgg tct ttg cca gac atc gaa			1555
His Ile Val Pro Asn Phe Ser Arg Asp Arg Ser Leu Pro Asp Ile Glu			
470	475	480	485
gac tgg acg aga agc gat gaa gct cag cag atc ttt gca gga atc att			1603
Asp Trp Thr Arg Ser Asp Glu Ala Gln Gln Ile Phe Ala Gly Ile Ile			
	490	495	500
gcg ggt gcg tct gtt caa act ggt aga agc cac ttc atg tgg gat ctt			1651
Ala Gly Ala Ser Val Gln Thr Gly Arg Ser His Phe Met Trp Asp Leu			
	505	510	515
ttg cgg gcg tat ttt gga gtc gct ttg atc ggc gac gaa gat acc tac			1699
Leu Arg Ala Tyr Phe Gly Val Ala Leu Ile Gly Asp Glu Asp Thr Tyr			
	520	525	530
agg gct ttt act act ctc acg gtc gat tct gtt ctt agt ttc gtg cag			1747
Arg Ala Phe Thr Thr Leu Thr Val Asp Ser Val Leu Ser Phe Val Gln			
	535	540	545
tta act ctt caa gag gcc aga acg gaa gac att aga cga ttc gag aaa			1795
Leu Thr Leu Gln Glu Gly Arg Thr Glu Asp Ile Arg Arg Phe Glu Lys			
	550	555	560
tat ggt gag cag att gcc cga gag gat ttg cgg tcg att ctc acc aat			1843
Tyr Gly Glu Gln Ile Ala Arg Glu Asp Leu Pro Ser Ile Leu Thr Asn			
	570	575	580
gct cga gca gta cag caa tat ctc gcc tat atc gac caa gat atc atc			1891
Ala Arg Ala Val Gln Gln Tyr Leu Gly Tyr Ile Asp Gln Asp Ile Ile			
	585	590	595
aat aag aaa gtg tcc cgg tct agg gat gtt aac cag att ttt act gag			1939
Asn Lys Lys Val Ser Arg Ser Arg Asp Val Asn Gln Ile Phe Thr Glu			
	600	605	610
atg gcg cgc gct atc atc aga gca att agc cgg aat aat att gga aag			1987
Met Ala Arg Ala Ile Ile Arg Ala Ile Ser Arg Asn Asn Ile Gly Lys			
	615	620	625
gac atg cgg tca tgaacgtgat tcgactggat tcc			2022
Asp Met Arg Ser			
630			

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<211> 633

<212> PRT

<213> Corynebacterium glutamicum

<400> 440

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Phe Ile Ala Glu Val Ala Pro Thr His Ile Glu Thr Val Thr Pro Phe

					20					25					30				
Asp	Asp	Phe	Ile	Ser	Ser	Glu	Asp	Ile	Asp	Ala	Leu	Pro	Arg	Arg	Phe				
		35					40					45							
Glu	Tyr	Arg	Pro	Leu	Ala	Gly	Arg	Ser	Leu	Ile	Met	Gln	Ser	Val	Pro				
	50					55					60								
Ala	Gly	Lys	Asp	Ala	Thr	Gly	Arg	Pro	Gly	Asn	Val	Phe	Thr	His	Ala				
	65				70					75					80				
Val	Phe	Asp	Gly	Asp	Leu	Glu	Ser	Pro	Leu	Glu	Ser	Val	Tyr	Pro	Ile				
				85					90					95					
Ser	Leu	Tyr	Arg	Ser	Pro	Asp	Leu	Leu	Thr	Pro	Phe	Arg	Ala	Ala	Ala				
			100					105					110						
Val	Asn	Ala	Ala	Glu	Leu	Pro	Leu	Asp	Ala	Gly	Glu	Pro	Arg	Ile	Gly				
		115					120					125							
Pro	Ile	Thr	Asp	Leu	Ser	Leu	Ser	Trp	Met	Met	Ile	Asp	Ser	Met	Phe				
	130					135					140								
Gly	Asp	Arg	Arg	Gln	Gln	Phe	Tyr	Gln	Leu	Gln	Asp	Ala	Leu	Gln	Ala				
	145				150					155					160				
Gly	Asp	Lys	Ala	Thr	Val	Leu	Val	Leu	Asn	Ser	Thr	Asn	Glu	Ala	Ala				
			165					170					175						
Tyr	Trp	Leu	Gln	Ala	Leu	Ser	Ser	Thr	Leu	Thr	Pro	Asn	Glu	Ala	Arg				
		180						185					190						
Arg	Leu	Leu	His	Phe	Ser	Thr	Phe	Glu	Arg	Ala	Ala	Thr	Leu	Pro	Ala				
		195					200					205							
Pro	Asp	Lys	Ser	Met	Glu	Ala	Arg	Ser	Leu	Phe	Val	Val	Pro	Gly	Ile				
	210					215					220								
Asp	Arg	Glu	Leu	Leu	Ala	Glu	His	Ser	Gly	Ile	Val	Ile	Ile	Asp	Pro				
	225				230					235				240					
Glu	Ile	Pro	Gln	Ser	Gln	Pro	Phe	Gly	Pro	Gln	Gly	Ser	Trp	Ser	Arg				
			245					250						255					
Met	Thr	Glu	Gly	Leu	Phe	Ser	Asp	Gly	Phe	Asp	Ala	Asp	Glu	Leu	Val				
		260						265					270						
Ala	Gly	Leu	Ile	Arg	Ala	Asn	Glu	Asn	Leu	Asp	Asn	Ser	Gln	Lys	Glu				
		275					280					285							
Leu	Ala	Gln	Phe	Gly	Asp	Gly	Leu	Ala	Arg	Phe	Ile	Arg	Asn	Gly	Arg				
		290				295					300								
Phe	Ser	Gly	Thr	His	Pro	Leu	Arg	Val	Leu	Ala	Asp	Gln	His	Met	Phe				
	305				310				315						320				
Gly	Lys	Val	Pro	Asp	Lys	Pro	Ala	Pro	Lys	Val	Glu	Pro	Val	Ala	Pro				
				325					330					335					
Ala	Pro	Asn	Pro	Asn	Ala	Ile	Trp	Ala	Arg	Ala	Ser	Glu	Val	Val	His				
		340						345					350						

Asn Pro Arg Arg Ala Ser Glu Ser Gln Asp Trp Pro Ser Leu Arg Arg
 355 360 365
 Leu Pro Asp Ser Arg Arg Arg Ile Ile Asn Met Ser Glu Gln Ala Ile
 370 375 380
 Asn Ser Ile Glu Lys Leu His Asp Ser Pro Ala Gln Asp Leu Val Ala
 385 390 395 400
 Tyr Leu Asp Phe Leu Leu Lys Thr Glu Leu Ala Thr Ser Ile Asn Ala
 405 410 415
 Ser Asp Pro Phe Phe Arg Ser Ser Phe Ser Asp Phe Pro Ala Met Asp
 420 425 430
 Asn Trp Arg His Ile Lys Phe Thr Glu Asp Ala His Pro Arg Leu Arg
 435 440 445
 Glu Leu Leu Val Asp Ala Glu Arg Asp Ala Arg Asn Arg Ala Pro Ala
 450 455 460
 Ala Ile Val Leu Asp His Ile Val Pro Asn Phe Ser Arg Asp Arg Ser
 465 470 475 480
 Leu Pro Asp Ile Glu Asp Trp Thr Arg Ser Asp Glu Ala Gln Gln Ile
 485 490 495
 Phe Ala Gly Ile Ile Ala Gly Ala Ser Val Gln Thr Gly Arg Ser His
 500 505 510
 Phe Met Trp Asp Leu Leu Arg Ala Tyr Phe Gly Val Ala Leu Ile Gly
 515 520 525
 Asp Glu Asp Thr Tyr Arg Ala Phe Thr Thr Leu Thr Val Asp Ser Val
 530 535 540
 Leu Ser Phe Val Gln Leu Thr Leu Gln Glu Gly Arg Thr Glu Asp Ile
 545 550 555 560
 Arg Arg Phe Glu Lys Tyr Gly Glu Gln Ile Ala Arg Glu Asp Leu Pro
 565 570 575
 Ser Ile Leu Thr Asn Ala Arg Ala Val Gln Gln Tyr Leu Gly Tyr Ile
 580 585 590
 Asp Gln Asp Ile Ile Asn Lys Lys Val Ser Arg Ser Arg Asp Val Asn
 595 600 605
 Gln Ile Phe Thr Glu Met Ala Arg Ala Ile Ile Arg Ala Ile Ser Arg
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 Asn Asn Ile Gly Lys Asp Met Arg Ser
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<210> 441

<211> 1035

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101) .. (1012)

<223> RXN00943

<400> 441

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Met Ile Arg Lys Leu
1 5

gct cga cca atg ctt gca tgc gtc tac gtc gca gat ggc gca gaa aca 163
Ala Arg Pro Met Leu Ala Ser Val Tyr Val Ala Asp Gly Ala Glu Thr
10 15 20

gta ttg aac acc agc gca cac gtc gaa ggc act cag gta gtt ctg gat 211
Val Leu Asn Thr Ser Ala His Val Glu Gly Thr Gln Val Val Leu Asp
25 30 35

cgt atc cgt tat gtg ctg ccc cgt aag tac gca aag cgc att tcc aga 259
Arg Ile Arg Tyr Val Leu Pro Arg Lys Tyr Ala Lys Arg Ile Ser Arg
40 45 50

gat cca gaa ttg gtc acc cgc gtc att ggc ggc acc aaa gtc ggt gcg 307
Asp Pro Glu Leu Val Thr Arg Val Ile Gly Gly Thr Lys Val Gly Ala
55 60 65

ggt tct ttg cta gct att ggt cgt gca cca cgc acc tct gca gct acc 355
Gly Ser Leu Leu Ala Ile Gly Arg Ala Pro Arg Thr Ser Ala Ala Thr
70 75 80 85

ctc gca atc ctg act atc cct aac atc ctg gct cgc aat gcg ttc tgg 403
Leu Ala Ile Leu Thr Ile Pro Asn Ile Leu Ala Arg Asn Ala Phe Trp
90 95 100

gaa acc cag gat gcg gat gaa aag cgt aac cgc cgc aac ggt ttc ctc 451
Glu Thr Gln Asp Ala Asp Glu Lys Arg Asn Arg Arg Asn Gly Phe Leu
105 110 115

acc aac att gcc ctg ctt ggt ggc ctg ttt atc act tct gtt gat act 499
Thr Asn Ile Ala Leu Leu Gly Gly Leu Phe Ile Thr Ser Val Asp Thr
120 125 130

gag ggc aag cct ggc gtg aag tgg cgt gca acc aat gct aca aag cgt 547
Glu Gly Lys Pro Gly Val Lys Trp Arg Ala Thr Asn Ala Thr Lys Arg
135 140 145

ggc aag aag cag ctg cag cag gca ctt cca acc aaa tot gag act gaa 595
Gly Lys Lys Gln Leu Gln Gln Ala Leu Pro Thr Lys Ser Glu Thr Glu
150 155 160 165

aag ttc ggt gag aag gcc tct gat tgg ttc aac gat act tct gac aag 643
Lys Phe Gly Glu Lys Ala Ser Asp Trp Phe Asn Asp Thr Ser Asp Lys
170 175 180

gtc acc gag tac gcg tac acc gct cag gat ttt gtc ggt gag aac aag 691
Val Thr Glu Tyr Ala Tyr Thr Ala Gln Asp Phe Val Gly Glu Asn Lys
185 190 195

gat gac tgg atc aag tcc gca acc gag act gct cac aag gtc gct gat 739

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Asp Asp Trp Ile Lys Ser Ala Thr Glu Thr Ala His Lys Val Ala Asp
200 205 210

act gtg agc gat tac gct cac aag gct acc tct tac ctt gag gag aac 787
Thr Val Ser Asp Tyr Ala His Lys Ala Thr Ser Tyr Leu Glu Glu Asn
215 220 225

agc ggt gac tgg ctt gag gct gcg cag gct aac gcc aag act gct cgt 835
Ser Gly Asp Trp Leu Glu Ala Ala Gln Ala Asn Ala Lys Thr Ala Arg
230 235 240 245

aag tct gca gtg aag gct gcc gcc aag gct cag gaa aag gct aac ttt 883
Lys Ser Ala Val Lys Ala Ala Gly Lys Ala Gln Glu Lys Ala Asn Phe
250 255 260

gct ctt cag gtc gca gag gaa acc tct ggt cgc gcc aac aag aag gca 931
Ala Leu Gln Val Ala Glu Glu Thr Ser Gly Arg Ala Asn Lys Lys Ala
265 270 275

act aag agc tac gac aag ctt cag aag cag gct gat aag gcc atc gat 979
Thr Lys Ser Tyr Asp Lys Leu Gln Lys Gln Ala Asp Lys Ala Ile Asp
280 285 290

cgt gca cag aag aag ctg aag gcc atc gaa ctt taagtaactt cttcctgatt 1032
Arg Ala Gln Lys Lys Leu Lys Gly Ile Glu Leu
295 300

gag 1035

<210> 442
<211> 304
<212> PRT
<213> Corynebacterium glutamicum

<400> 442
Met Ile Arg Lys Leu Ala Arg Pro Met Leu Ala Ser Val Tyr Val Ala
1 5 10 15

Asp Gly Ala Glu Thr Val Leu Asn Thr Ser Ala His Val Glu Gly Thr
20 25 30

Gln Val Val Leu Asp Arg Ile Arg Tyr Val Leu Pro Arg Lys Tyr Ala
35 40 45

Lys Arg Ile Ser Arg Asp Pro Glu Leu Val Thr Arg Val Ile Gly Gly
50 55 60

Thr Lys Val Gly Ala Gly Ser Leu Leu Ala Ile Gly Arg Ala Pro Arg
65 70 75 80

Thr Ser Ala Ala Thr Leu Ala Ile Leu Thr Ile Pro Asn Ile Leu Ala
85 90 95

Arg Asn Ala Phe Trp Glu Thr Gln Asp Ala Asp Glu Lys Arg Asn Arg
100 105 110

Arg Asn Gly Phe Leu Thr Asn Ile Ala Leu Leu Gly Gly Leu Phe Ile
115 120 125

Thr Ser Val Asp Thr Glu Gly Lys Pro Gly Val Lys Trp Arg Ala Thr

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130					135					140				
Asn	Ala	Thr	Lys	Arg	Gly	Lys	Lys	Gln	Leu	Gln	Ala	Leu	Pro	Thr
145					150					155				160
Lys	Ser	Glu	Thr	Glu	Lys	Phe	Gly	Glu	Lys	Ala	Ser	Asp	Trp	Phe
				165					170					175
Asp	Thr	Ser	Asp	Lys	Val	Thr	Glu	Tyr	Ala	Tyr	Thr	Ala	Gln	Asp
			180					185					190	Phe
Val	Gly	Glu	Asn	Lys	Asp	Asp	Trp	Ile	Lys	Ser	Ala	Thr	Glu	Thr
			195				200						205	Ala
His	Lys	Val	Ala	Asp	Thr	Val	Ser	Asp	Tyr	Ala	His	Lys	Ala	Thr
			210				215						220	Ser
Tyr	Leu	Glu	Glu	Asn	Ser	Gly	Asp	Trp	Leu	Glu	Ala	Ala	Gln	Ala
			225				230						235	Asn
Ala	Lys	Thr	Ala	Arg	Lys	Ser	Ala	Val	Lys	Ala	Ala	Gly	Lys	Ala
				245					250					255
Glu	Lys	Ala	Asn	Phe	Ala	Leu	Gln	Val	Ala	Glu	Glu	Thr	Ser	Gly
			260					265						270
Ala	Asn	Lys	Lys	Ala	Thr	Lys	Ser	Tyr	Asp	Lys	Leu	Gln	Lys	Gln
			275					280						285
Asp	Lys	Ala	Ile	Asp	Arg	Ala	Gln	Lys	Lys	Leu	Lys	Gly	Ile	Glu
			290				295						300	Leu

<210> 443

<211> 530

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(507)

<223> FRXA00943

<400> 443

aag	cct	ggc	gtg	aag	tgg	cgt	gca	acc	aat	gct	aca	aag	cgt	ggc	aag	48
Lys	Pro	Gly	Val	Lys	Trp	Arg	Ala	Thr	Asn	Ala	Thr	Lys	Arg	Gly	Lys	
1				5					10					15		

aag	cag	ctg	cag	cag	gca	ctt	tca	acc	aaa	tct	gag	act	gaa	aag	ttc	96
Lys	Gln	Leu	Gln	Gln	Ala	Leu	Ser	Thr	Lys	Ser	Glu	Thr	Glu	Lys	Phe	
			20					25					30			

ggt	gag	aag	gcc	tct	gat	tgg	ttc	aac	gat	act	tct	gac	aag	gtc	acc	144
Gly	Glu	Lys	Ala	Ser	Asp	Trp	Phe	Asn	Asp	Thr	Ser	Asp	Lys	Val	Thr	
			35				40						45			

gag	tac	gcg	tac	acc	gct	cag	gat	ttt	gtc	ggt	gag	aac	aag	gat	gac	192
Glu	Tyr	Ala	Tyr	Thr	Ala	Gln	Asp	Phe	Val	Gly	Glu	Asn	Lys	Asp	Asp	

50	55	60	
tgg atc aag tcc gca acc gag act gct cac aag gtc gct gat act gtg			240
Trp Ile Lys Ser Ala Thr Glu Thr Ala His Lys Val Ala Asp Thr Val			
65	70	75	80
agc gat tac gct cac aag gct acc tct tac ctt gag gag aac agc ggt			288
Ser Asp Tyr Ala His Lys Ala Thr Ser Tyr Leu Glu Glu Asn Ser Gly			
	85	90	95
gac tgg ctt gag gct gcg cag gct aac gcc aag act gct cgt aag tct			336
Asp Trp Leu Glu Ala Ala Gln Ala Asn Ala Lys Thr Ala Arg Lys Ser			
	100	105	110
gca gtg aag gct gcc gcc aag gct cac gaa aag gct aac ttt gct ctt			384
Ala Val Lys Ala Ala Gly Lys Ala His Glu Lys Ala Asn Phe Ala Leu			
	115	120	125
cag gtc gca gag gaa acc tct ggt cgc gcc aac aag aag gca act aag			432
Gln Val Ala Glu Glu Thr Ser Gly Arg Ala Asn Lys Lys Ala Thr Lys			
	130	135	140
agc tac gac aag ctt cag aag cag gct gat aag gcc atc gat cgt gca			480
Ser Tyr Asp Lys Leu Gln Lys Gln Ala Asp Lys Ala Ile Asp Arg Ala			
	145	150	155
cag aag aag ctg aag gcc atc gaa ctt taagtaactt cttcctgatt			527
Gln Lys Lys Leu Lys Gly Ile Glu Leu			
	165		
gag			530
<210> 444			
<211> 169			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 444			
Lys Pro Gly Val Lys Trp Arg Ala Thr Asn Ala Thr Lys Arg Gly Lys			
1	5	10	15
Lys Gln Leu Gln Gln Ala Leu Ser Thr Lys Ser Glu Thr Glu Lys Phe			
	20	25	30
Gly Glu Lys Ala Ser Asp Trp Phe Asn Asp Thr Ser Asp Lys Val Thr			
	35	40	45
Glu Tyr Ala Tyr Thr Ala Gln Asp Phe Val Gly Glu Asn Lys Asp Asp			
	50	55	60
Trp Ile Lys Ser Ala Thr Glu Thr Ala His Lys Val Ala Asp Thr Val			
	65	70	75
Ser Asp Tyr Ala His Lys Ala Thr Ser Tyr Leu Glu Glu Asn Ser Gly			
	85	90	95
Asp Trp Leu Glu Ala Ala Gln Ala Asn Ala Lys Thr Ala Arg Lys Ser			
	100	105	110
Ala Val Lys Ala Ala Gly Lys Ala His Glu Lys Ala Asn Phe Ala Leu			

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      115              120              125
Gln Val Ala Glu Glu Thr Ser Gly Arg Ala Asn Lys Lys Ala Thr Lys
 130              135              140

Ser Tyr Asp Lys Leu Gln Lys Gln Ala Asp Lys Ala Ile Asp Arg Ala
 145              150              155              160

Gln Lys Lys Leu Lys Gly Ile Glu Leu
      165

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<210> 445
<211> 316
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(316)
<223> FRXA02423

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<400> 445
taggtacgat cggacgagga gaaaaaatct gaaaacaatc cagtggccca cctcggctta 60
taaaactgga caacagtatt ttgattggag catcaccata atg atc cgc aaa ctt 115
                                         Met Ile Arg Lys Leu
                                         1               5

gct cga cca atg ctt gca tcg gtc tac gtc gca gat ggc gca gaa aca 163
Ala Arg Pro Met Leu Ala Ser Val Tyr Val Ala Asp Gly Ala Glu Thr
              10              15              20

gta ttg aac acc agc gca cac gtc gaa ggc act cag gta gtt ctg gat 211
Val Leu Asn Thr Ser Ala His Val Glu Gly Thr Gln Val Val Leu Asp
              25              30              35

cgt atc cgt tat gtg ctg ccc cgt aag tac gca aag cgc att tcc aga 259
Arg Ile Arg Tyr Val Leu Pro Arg Lys Tyr Ala Lys Arg Ile Ser Arg
      40              45              50

gat cca gaa ttg gtc acc cgc gtc att ggc ggc acc aaa gtc tgt gcg 307
Asp Pro Glu Leu Val Thr Arg Val Ile Gly Gly Thr Lys Val Cys Ala
      55              60              65

ggt tct tgt
Gly Ser Cys
 70

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<210> 446
<211> 72
<212> PRT
<213> Corynebacterium glutamicum

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<400> 446
Met Ile Arg Lys Leu Ala Arg Pro Met Leu Ala Ser Val Tyr Val Ala
 1               5              10              15

Asp Gly Ala Glu Thr Val Leu Asn Thr Ser Ala His Val Glu Gly Thr
      20              25              30

```


Gln Val Val Leu Asp Arg Ile Arg Tyr Val Leu Pro Arg Lys Tyr Ala
 35 40 45

Lys Arg Ile Ser Arg Asp Pro Glu Leu Val Thr Arg Val Ile Gly Gly
 50 55 60

Thr Lys Val Cys Ala Gly Ser Cys
 65 70

<210> 447

<211> 1095

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1072)

<223> RKN00945

<400> 447

tcacagtacc acccacaagc cacaaggagg gtatggagggt gggcgtctaa agccaaattt 60

ttcccgtgtg ttgaggcgat tgcaccgtac actaatgtgc atg ctt gaa cgc ctc 115
 Met Leu Glu Arg Leu
 1 5

aaa cgc cta gat ccg ctc att gtc ctc att gtg ctg gct gtc att gtg 163
 Lys Arg Leu Asp Pro Leu Ile Val Leu Ile Val Leu Ala Val Ile Val
 10 15 20

gcg atc atc att cca gtt cgc ggg gtt gct gcg gat tgg ttt gat gtc 211
 Ala Ile Ile Ile Pro Val Arg Gly Val Ala Ala Asp Trp Phe Asp Val
 25 30 35

gcc gtc aag att gcc att gcg ctg ctg ttt ttt ctt tat ggt gcc cgc 259
 Ala Val Lys Ile Ala Ile Ala Leu Leu Phe Phe Leu Tyr Gly Ala Arg
 40 45 50

cta tcc acc caa gag gcg ctg aat ggt ctg aag cac tgg agg ctt cac 307
 Leu Ser Thr Gln Glu Ala Leu Asn Gly Leu Lys His Trp Arg Leu His
 55 60 65

ctg act att ttg gcg atc act ttc gga ata ttc cca ctt atc ggc att 355
 Leu Thr Ile Leu Ala Ile Thr Phe Gly Ile Phe Pro Leu Ile Gly Ile
 70 75 80 85

ggg ctc gag ccg atg act gca ttt gtg tgg gaa gat att tat cgg gga 403
 Gly Leu Glu Pro Met Thr Ala Phe Val Ser Glu Asp Ile Tyr Arg Gly
 90 95 100

att ttg ttc ctc acg ctc gtt ccg tcc acc gtg cag tca tgg gtg gcg 451
 Ile Leu Phe Leu Thr Leu Val Pro Ser Thr Val Gln Ser Ser Val Ala
 105 110 115

ttt acc tgg atc gct aaa ggc aac gta gct ggt gcg att gtg tgg gca 499
 Phe Thr Ser Ile Ala Lys Gly Asn Val Ala Gly Ala Ile Val Ser Ala
 120 125 130

tgg ctc tcc aac ctt gcg ggt gtt ttc ctc act ccg ctg ctg gtc atg 547

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Ser Leu Ser Asn Leu Ala Gly Val Phe Leu Thr Pro Leu Leu Val Met
135                               140                               145

ctc atc atg tct gcg ggc ggg gga gtt cac gtg gat tcc cag gtc ttc 595
Leu Ile Met Ser Ala Gly Gly Gly Val His Val Asp Ser Gln Val Phe
150                               155                               160

ctc gac att gcg att cag ctt ctg ctg ccg ttc atc ctc ggc cag gta 643
Leu Asp Ile Ala Ile Gln Leu Leu Leu Pro Phe Ile Leu Gly Gln Val
170                               175                               180

tgt agg cgt tgg gtg aag aat ttt gcg gcc aac aaa gca aca aaa atc 691
Cys Arg Arg Trp Val Lys Asn Phe Ala Ala Asn Lys Ala Thr Lys Ile
185                               190                               195

gtg gac cgc ggc tgc atc gcg atg gtc gtg tac tcc gcg ttt tct gcc 739
Val Asp Arg Gly Ser Ile Ala Met Val Val Tyr Ser Val Leu Phe Ser Ala
200                               205                               210

ggc atg gtg gct ggc att tgg tcc act gtg agc gtt cta gag att atc 787
Gly Met Val Ala Gly Ile Trp Ser Thr Val Ser Val Leu Glu Ile Ile
215                               220                               225

tac ctc att gtt ttc gct att ctg ctg gtg atg gcc atg ctg tgg ttc 835
Tyr Leu Ile Val Phe Ala Ile Leu Leu Val Met Ala Met Leu Trp Phe
230                               235                               240

acg ctg ttc atg gct aca cgc ctt gga ttt aac cgg gca gat tcc atc 883
Thr Leu Phe Met Ala Thr Arg Leu Gly Phe Asn Arg Ala Asp Ser Ile
250                               255                               260

gct att cag ttc tgc gga acc aag aaa tcc ctg gcc aca ggc ctc cca 931
Ala Ile Gln Phe Cys Gly Thr Lys Lys Ser Leu Ala Thr Gly Leu Pro
265                               270                               275

atg gcg gca gtc atc ttc ggt ggc gcc aat atc ggc ctg ctc atc ttg 979
Met Ala Ala Val Ile Phe Gly Gly Ala Asn Ile Gly Leu Leu Ile Leu
280                               285                               290

cgg ttg atg atc ttc cac caa gtc cag ctg atg att tgt gca tgg ctt 1027
Pro Leu Met Ile Phe His Gln Val Gln Leu Met Ile Cys Ala Trp Leu
295                               300                               305

gca gct cgt tat ggt cgt gat gcg cag gaa cag aaa gcc aac gcc 1072
Ala Ala Arg Tyr Gly Arg Asp Ala Gln Glu Gln Lys Ala Asn Ala
310                               315                               320

taaaagtcct cagtagctag cca 1095

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<210> 448

<211> 324

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 448

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Met Leu Glu Arg Leu Lys Arg Leu Asp Pro Leu Ile Val Leu Ile Val
1 5 10 15

```

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Leu Ala Val Ile Val Ala Ile Ile Ile Pro Val Arg Gly Val Ala Ala
20 25 30

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Asp Trp Phe Asp Val Ala Val Lys Ile Ala Ile Ala Leu Leu Phe Phe
 35 40 45
 Leu Tyr Gly Ala Arg Leu Ser Thr Gln Glu Ala Leu Asn Gly Leu Lys
 50 55 60
 His Trp Arg Leu His Leu Thr Ile Leu Ala Ile Thr Phe Gly Ile Phe
 65 70 75 80
 Pro Leu Ile Gly Ile Gly Leu Glu Pro Met Thr Ala Phe Val Ser Glu
 85 90 95
 Asp Ile Tyr Arg Gly Ile Leu Phe Leu Thr Leu Val Pro Ser Thr Val
 100 105 110
 Gln Ser Ser Val Ala Phe Thr Ser Ile Ala Lys Gly Asn Val Ala Gly
 115 120 125
 Ala Ile Val Ser Ala Ser Leu Ser Asn Leu Ala Gly Val Phe Leu Thr
 130 135 140
 Pro Leu Leu Val Met Leu Ile Met Ser Ala Gly Gly Val His Val
 145 150 155 160
 Asp Ser Gln Val Phe Leu Asp Ile Ala Ile Gln Leu Leu Leu Pro Phe
 165 170 175
 Ile Leu Gly Gln Val Cys Arg Arg Trp Val Lys Asn Phe Ala Ala Asn
 180 185 190
 Lys Ala Thr Lys Ile Val Asp Arg Gly Ser Ile Ala Met Val Val Tyr
 195 200 205
 Ser Ala Phe Ser Ala Gly Met Val Ala Gly Ile Trp Ser Thr Val Ser
 210 215 220
 Val Leu Glu Ile Ile Tyr Leu Ile Val Phe Ala Ile Leu Leu Val Met
 225 230 235 240
 Ala Met Leu Trp Phe Thr Leu Phe Met Ala Thr Arg Leu Gly Phe Asn
 245 250 255
 Arg Ala Asp Ser Ile Ala Ile Gln Phe Cys Gly Thr Lys Lys Ser Leu
 260 265 270
 Ala Thr Gly Leu Pro Met Ala Ala Val Ile Phe Gly Gly Ala Asn Ile
 275 280 285
 Gly Leu Leu Ile Leu Pro Leu Met Ile Phe His Gln Val Gln Leu Met
 290 295 300
 Ile Cys Ala Trp Leu Ala Ala Arg Tyr Gly Arg Asp Ala Gln Glu Gln
 305 310 315 320
 Lys Ala Asn Ala

<210> 449

<211> 897

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(874)

<223> RXN00946

<400> 449

gggcccgtgt gaataaaaa ccttccccc atagacagca tggcttagat tagcttgaaa 60

cgaaagcgta	cattcgcagc	aactaacgga	aagcacactc	atg	act	cac	act	ctg	115
				Met	Thr	His	Thr	Leu	
				1				5	

cag	gca	act	aat	ccc	ctt	gat	caa	acc	gct	tgg	cac	gct	tgg	cat	ttc	163
Gln	Ala	Thr	Asn		Pro	Leu	Asp	Gln	Thr	Ala	Trp	His	Ala	Trp	His	Phe
				10						15				20		

tcc	cga	aac	aaa	gag	gcc	atc	agc	cgc	acc	ggc	gcc	acc	agc	ctg	agt	211
Ser	Arg	Asn	Lys	Glu	Ala	Ile	Ser	Arg	Thr	Gly	Ala	Thr	Ser	Leu	Ser	
			25					30					35			

gcc	aca	gag	tgg	att	agc	gcc	acc	aca	ctc	aag	gac	gcg	cac	act	ttt	259
Ala	Thr	Glu	Trp	Ile	Ser	Ala	Thr	Thr	Leu	Lys	Asp	Ala	His	Thr	Phe	
			40				45				50					

cct	tca	ctt	ccc	ggg	cga	tgg	tat	aaa	cga	ggc	ggc	ggg	gta	gtg	gga	307
Pro	Ser	Leu	Pro	Gly	Arg	Trp	Tyr	Lys	Arg	Gly	Gly	Val	Val	Gly		
			55			60					65					

gca	cat	tta	cca	cca	gct	ttc	gca	aca	act	gga	acg	gtg	caa	ctg	cgc	355
Ala	His	Leu	Pro	Pro	Ala	Phe	Ala	Thr	Thr	Gly	Thr	Val	Gln	Leu	Arg	
			70			75				80					85	

ccc	ggt	gag	ctc	ttg	ata	gcg	gaa	gat	ttc	acc	ctc	acc	gtc	att	gaa	403
Pro	Gly	Glu	Leu	Leu	Ile	Ala	Glu	Asp	Phe	Thr	Leu	Thr	Val	Ile	Glu	
				90					95					100		

cgg	ctt	gga	cag	ttt	gca	ctt	cag	gtt	ttt	gat	gca	cgc	aat	ccg	aag	451
Arg	Leu	Gly	Gln	Phe	Ala	Leu	Gln	Val	Phe	Asp	Ala	Arg	Asn	Pro	Lys	
			105					110					115			

cgt	ttt	gaa	ttc	cac	tcc	atc	gca	gct	ttc	cca	ccg	tcc	gag	gaa	tgg	499
Arg	Phe	Glu	Phe	His	Ser	Ile	Ala	Ala	Phe	Pro	Pro	Ser	Glu	Glu	Trp	
			120				125					130				

cgg	att	gag	gct	cgc	ttc	ttc	ccg	gaa	cct	gac	act	gtt	aac	acc	gct	547
Arg	Ile	Glu	Ala	Arg	Phe	Phe	Pro	Glu	Pro	Asp	Thr	Val	Asn	Thr	Ala	
			135			140					145					

gca	gct	gat	gga	gtt	atc	gtt	gcc	acg	cct	act	gcg	ggt	tgg	gtg	cac	595
Ala	Ala	Asp	Gly	Val	Ile	Val	Ala	Thr	Pro	Thr	Ala	Gly	Trp	Val	His	
			150			155				160				165		

ttt	ttg	aag	ggc	cgt	ctg	gat	tac	cgt	ctt	cgt	gta	acc	gtt	cag	aaa	643
Phe	Leu	Lys	Gly	Arg	Leu	Asp	Tyr	Arg	Leu	Arg	Val	Thr	Val	Gln	Lys	
				170					175					180		

aat	aat	cta	cgg	gca	cta	ttt	agc	gac	aat	tcc	tcg	acg	ttg	ggc	gtt	691
Asn	Asn	Leu	Arg	Ala	Leu	Phe	Ser	Asp	Asn	Ser	Ser	Thr	Leu	Gly	Val	

185	190	195	
tat cag cat cgt ttt gtc gac atc cca cgc cct gat gcc gag gga aac			739
Tyr Gln His Arg Phe Val Asp Ile Pro Arg Pro Asp Ala Glu Gly Asn			
200	205	210	
acc atc att gat ttc aac cgc gct tat ctt ccc cca aag gca ttg aac			787
Thr Ile Ile Asp Phe Asn Arg Ala Tyr Leu Pro Pro Lys Ala Leu Asn			
215	220	225	
cga aag ttc ctg tgc cca tgc ccc agc ctg aac aac cac ctc aat ctc			835
Arg Lys Phe Leu Cys Pro Ser Pro Ser Leu Asn Asn His Leu Asn Leu			
230	235	240	245
acc gtg gag gca ggg gag aag tgg gtg gtt gct gga gga taataacttgc			884
Thr Val Glu Ala Gly Glu Lys Trp Val Val Ala Gly Gly			
250	255		
taaccgtcct aaa			897

<210> 450

<211> 258

<212> FRT

<213> Corynebacterium glutamicum

<400> 450

Met Thr His Thr Leu Gln Ala Thr Asn Pro Leu Asp Gln Thr Ala Trp	
1	5
10	15

His Ala Trp His Phe Ser Arg Asn Lys Glu Ala Ile Ser Arg Thr Gly	
20	25
30	

Ala Thr Ser Leu Ser Ala Thr Glu Trp Ile Ser Ala Thr Thr Leu Lys	
35	40
45	

Asp Ala His Thr Phe Pro Ser Leu Pro Gly Arg Trp Tyr Lys Arg Gly	
50	55
60	

Gly Gly Val Val Gly Ala His Leu Pro Pro Ala Phe Ala Thr Thr Gly	
65	70
75	80

Thr Val Gln Leu Arg Pro Gly Glu Leu Leu Ile Ala Glu Asp Phe Thr	
85	90
95	

Leu Thr Val Ile Glu Arg Leu Gly Gln Phe Ala Leu Gln Val Phe Asp	
100	105
110	

Ala Arg Asn Pro Lys Arg Phe Glu Phe His Ser Ile Ala Ala Phe Pro	
115	120
125	

Pro Ser Glu Glu Trp Arg Ile Glu Ala Arg Phe Phe Pro Glu Pro Asp	
130	135
140	

Thr Val Asn Thr Ala Ala Ala Asp Gly Val Ile Val Ala Thr Pro Thr	
145	150
155	160

Ala Gly Trp Val His Phe Leu Lys Gly Arg Leu Asp Tyr Arg Leu Arg	
165	170
175	

Val Thr Val Gln Lys Asn Asn Leu Arg Ala Leu Phe Ser Asp Asn Ser

180 185 190

Ser Thr Leu Gly Val Tyr Gln His Arg Phe Val Asp Ile Pro Arg Pro
195 200 205

Asp Ala Glu Gly Asn Thr Ile Ile Asp Phe Asn Arg Ala Tyr Leu Pro
210 215 220

Pro Lys Ala Leu Asn Arg Lys Phe Leu Cys Pro Ser Pro Ser Leu Asn
225 230 235 240

Asn His Leu Asn Leu Thr Val Glu Ala Gly Glu Lys Trp Val Val Ala
245 250 255

Gly Gly

<210> 451
<211> 897
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(874)
<223> FRXA00946

<400> 451
gggccggtgt gaataaaaca ccttccccaa atagacagca tggcttagat tagcttgaaa 60

cgaaagcgta cattcgcagc aactaacgga aagcacactc atg act cac act ctg 115
Met Thr His Thr Leu
1 5

cag gca act aat ccc ctt gat caa acc gct tgg cac gct tgg cat ttc 163
Gln Ala Thr Asn Pro Leu Asp Gln Thr Ala Trp His Ala Trp His Phe
10 15 20

tcc cga aac aaa gag gcc atc agc cgc acc ggc gcc acc agc ctg agt 211
Ser Arg Asn Lys Glu Ala Ile Ser Arg Thr Gly Ala Thr Ser Leu Ser
25 30 35

gcc aca gag tgg att agc gcc acc aca ctc aag gac gcg cac act ttt 259
Ala Thr Glu Trp Ile Ser Ala Thr Thr Leu Lys Asp Ala His Thr Phe
40 45 50

cct tca ctt ccc ggg cga tgg tat aaa cga ggc ggc ggc gta gtg gga 307
Pro Ser Leu Pro Gly Arg Trp Tyr Lys Arg Gly Gly Val Val Gly
55 60 65

gca cat tta cca cca gct ttc gca aca act gga acg gtg caa ctg cgc 355
Ala His Leu Pro Pro Ala Phe Ala Thr Thr Gly Thr Val Gln Leu Arg
70 75 80 85

ccc ggt gag ctc ttg ata gcg gaa gat ttc acc ctc acc gtc att gaa 403
Pro Gly Glu Leu Leu Ile Ala Glu Asp Phe Thr Leu Thr Val Ile Glu
90 95 100

cgg ctt gga cag ttt gca ctt cag gtt ttt gat gca cgc aat ccg aag 451
Arg Leu Gly Gln Phe Ala Leu Gln Val Phe Asp Ala Arg Asn Pro Lys

	105	110	115	
	cgt ttt gaa ttc cac tcc atc gca gct ttc cca ccg tcc gag gaa tgg			499
	Arg Phe Glu Phe His Ser Ile Ala Ala Phe Pro Pro Ser Glu Glu Trp			
	120	125	130	
	cgg att gag gct cgc ttc ttc ccg gaa cct gac act gtt aac acc gct			547
	Arg Ile Glu Ala Arg Phe Phe Pro Glu Pro Asp Thr Val Asn Thr Ala			
	135	140	145	
	gca gct gat gga gtt atc gtt gcc acg cct act gcg ggt tgg gtg cac			595
	Ala Ala Asp Gly Val Ile Val Ala Thr Pro Thr Ala Gly Trp Val His			
	150	155	160	165
	ttt ttg aag ggc cgt ctg gat tac cgt ctt cgt gta acc gtt cag aaa			643
	Phe Leu Lys Gly Arg Leu Asp Tyr Arg Leu Arg Val Thr Val Gln Lys			
	170	175	180	
	aat aat cta cgg gca cta ttt agc gac aat tcc tcg acg ttg ggc gtt			691
	Asn Asn Leu Arg Ala Leu Phe Ser Asp Asn Ser Ser Thr Leu Gly Val			
	185	190	195	
	tat cag cat cgt ttt gtc gac atc cca cgc cct gat gcc gag gga aac			739
	Tyr Gln His Arg Phe Val Asp Ile Pro Arg Pro Asp Ala Glu Gly Asn			
	200	205	210	
	acc atc att gat ttc aac cgc gct tat ctt ccc cca aag gca ttg aac			787
	Thr Ile Ile Asp Phe Asn Arg Ala Tyr Leu Pro Pro Lys Ala Leu Asn			
	215	220	225	
	cga aag ttc ctg tgc cca tcg ccc agc ctg aac aac cac ctc aat ctc			835
	Arg Lys Phe Leu Cys Pro Ser Pro Ser Leu Asn Asn His Leu Asn Leu			
	230	235	240	245
	acc gtg gag gca ggg gag aag tgg gtg gtt gct gga gga taataactg			884
	Thr Val Glu Ala Gly Glu Lys Trp Val Val Ala Gly Gly			
	250	255		
	taacogtcc			897
	aaa			
	<210> 452			
	<211> 258			
	<212> PRT			
	<213> Corynebacterium glutamicum			
	<400> 452			
	Met Thr His Thr Leu Gln Ala Thr Asn Pro Leu Asp Gln Thr Ala Trp			
	1	5	10	15
	His Ala Trp His Phe Ser Arg Asn Lys Glu Ala Ile Ser Arg Thr Gly			
	20	25	30	
	Ala Thr Ser Leu Ser Ala Thr Glu Trp Ile Ser Ala Thr Thr Leu Lys			
	35	40	45	
	Asp Ala His Thr Phe Pro Ser Leu Pro Gly Arg Trp Tyr Lys Arg Gly			
	50	55	60	
	Gly Gly Val Val Gly Ala His Leu Pro Pro Ala Phe Ala Thr Thr Gly			
	65	70	75	80

Thr Val Gln Leu Arg Pro Gly Glu Leu Leu Ile Ala Glu Asp Phe Thr
85 90 95

Leu Thr Val Ile Glu Arg Leu Gly Gln Phe Ala Leu Gln Val Phe Asp
100 105 110

Ala Arg Asn Pro Lys Arg Phe Glu Phe His Ser Ile Ala Ala Phe Pro
115 120 125

Pro Ser Glu Glu Trp Arg Ile Glu Ala Arg Phe Phe Pro Glu Pro Asp
130 135 140

Thr Val Asn Thr Ala Ala Ala Asp Gly Val Ile Val Ala Thr Pro Thr
145 150 155 160

Ala Gly Trp Val His Phe Leu Lys Gly Arg Leu Asp Tyr Arg Leu Arg
165 170 175

Val Thr Val Gln Lys Asn Asn Leu Arg Ala Leu Phe Ser Asp Asn Ser
180 185 190

Ser Thr Leu Gly Val Tyr Gln His Arg Phe Val Asp Ile Pro Arg Pro
195 200 205

Asp Ala Glu Gly Asn Thr Ile Ile Asp Phe Asn Arg Ala Tyr Leu Pro
210 215 220

Pro Lys Ala Leu Asn Arg Lys Phe Leu Cys Pro Ser Pro Ser Leu Asn
225 230 235 240

Asn His Leu Asn Leu Thr Val Glu Ala Gly Glu Lys Trp Val Val Ala
245 250 255

Gly Gly

<210> 453

<211> 789

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (14)..(766)

<223> RXN00953

<400> 453

cttgcatctcc ccaatg gcg cca cca acg gta ggc aac tac atc atg cag tcc 52
Met Ala Pro Pro Thr Val Gly Asn Tyr Ile Met Gln Ser
1 5 10

ttc act caa ggt ctg cag ttc ggc gtt gca gtt gcc gtg att ctc ttt 100
Phe Thr Gln Gly Leu Gln Phe Gly Val Ala Val Ala Val Ile Leu Phe
15 20 25

ggc gtc cgc acc att ctt ggt gaa ctg gtc ccc gca ttc caa ggt att 148
Gly Val Arg Thr Ile Leu Gly Glu Leu Val Pro Ala Phe Gln Gly Ile
30 35 40 45


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gct gcg aag gtt gtt ccc gga gct atc ccc gca ttg gat gca ccg atc 196
Ala Ala Lys Val Val Pro Gly Ala Ile Pro Ala Leu Asp Ala Pro Ile
                    50                    55                    60

gtg ttc ccc tac gcg cag aac gcc gtt ctc att ggt ttc ttg tct tcc 244
Val Phe Pro Tyr Ala Gln Asn Ala Val Leu Ile Gly Phe Leu Ser Ser
                    65                    70                    75

ttc gtc ggt ggc ttg gtt ggc ctg act gtt ctt gca tcg tgg ctg aac 292
Phe Val Gly Gly Leu Val Gly Leu Thr Val Leu Ala Ser Trp Leu Asn
                    80                    85                    90

cca gct ttt ggt gtc gcg ttg att ctg cct ggt ttg gtc ccc cac ttc 340
Pro Ala Phe Gly Val Ala Leu Ile Leu Pro Gly Leu Val Pro His Phe
                    95                    100                    105

ttc act ggt ggc gcg gcc ggc gtt tac ggt aat gcc acg ggt ggt cgt 388
Phe Thr Gly Gly Ala Ala Gly Val Tyr Gly Asn Ala Thr Gly Gly Arg
110                    115                    120                    125

cga gga gca gta ttt ggc gcc ttt gcc aac ggt ctt ctg att acc ttc 436
Arg Gly Ala Val Phe Gly Ala Phe Ala Asn Gly Leu Leu Ile Thr Phe
                    130                    135                    140

ctc cct gct ttc ctg ctt ggt gtg ctt ggt tcc ttc ggg tca gag aac 484
Leu Pro Ala Phe Leu Leu Gly Val Leu Gly Ser Phe Gly Ser Glu Asn
                    145                    150                    155

acc act ttc ggt gat gcg gac ttt ggt tgg ttc gga atc gtt gtt ggt 532
Thr Thr Phe Gly Asp Ala Asp Phe Gly Trp Phe Gly Ile Val Val Gly
160                    165                    170

tct gca gcc aag gtg gaa ggt gct ggc ggg ctc atc ttg ttg ctc atc 580
Ser Ala Ala Lys Val Glu Gly Ala Gly Gly Leu Ile Leu Leu Leu Ile
175                    180                    185

atc gca gcg gtt ctt ctg ggt ggc gcg atg gtc ttc cag aag cgc gtc 628
Ile Ala Ala Val Leu Leu Gly Gly Ala Met Val Phe Gln Lys Arg Val
190                    195                    200                    205

gtg aat ggg cac tgg gat cca gct ccc aac cgt gag cgc gtg gag aag 676
Val Asn Gly His Trp Asp Pro Ala Pro Asn Arg Glu Arg Val Glu Lys
210                    215                    220                    225

gcg gaa gct gat gcc act cca acg gct ggg gct cgg acc tac cct aag 724
Ala Glu Ala Asp Ala Thr Pro Thr Ala Gly Ala Arg Thr Tyr Pro Lys
225                    230                    235

att gct cct cgg gcg ggc gct cct acc cca cgg gct cga agc 766
Ile Ala Pro Pro Ala Gly Ala Pro Thr Pro Pro Ala Arg Ser
240                    245                    250

taagatctcc aaaacctga gat 789

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<210> 454

<211> 251

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 454

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Met Ala Pro Pro Thr Val Gly Asn Tyr Ile Met Gln Ser Phe Thr Gln
  1              5              10              15

Gly Leu Gln Phe Gly Val Ala Val Ala Val Ile Leu Phe Gly Val Arg
              20              25              30

Thr Ile Leu Gly Glu Leu Val Pro Ala Phe Gln Gly Ile Ala Ala Lys
      35              40              45

Val Val Pro Gly Ala Ile Pro Ala Leu Asp Ala Pro Ile Val Phe Pro
      50              55              60

Tyr Ala Gln Asn Ala Val Leu Ile Gly Phe Leu Ser Ser Phe Val Gly
      65              70              75              80

Gly Leu Val Gly Leu Thr Val Leu Ala Ser Trp Leu Asn Pro Ala Phe
      85              90              95

Gly Val Ala Leu Ile Leu Pro Gly Leu Val Pro His Phe Phe Thr Gly
      100             105             110

Gly Ala Ala Gly Val Tyr Gly Asn Ala Thr Gly Gly Arg Arg Gly Ala
      115             120             125

Val Phe Gly Ala Phe Ala Asn Gly Leu Leu Ile Thr Phe Leu Pro Ala
      130             135             140

Phe Leu Leu Gly Val Leu Gly Ser Phe Gly Ser Glu Asn Thr Thr Phe
      145             150             155             160

Gly Asp Ala Asp Phe Gly Trp Phe Gly Ile Val Val Gly Ser Ala Ala
      165             170             175

Lys Val Glu Gly Ala Gly Gly Leu Ile Leu Leu Leu Ile Ile Ala Ala
      180             185             190

Val Leu Leu Gly Gly Ala Met Val Phe Gln Lys Arg Val Val Asn Gly
      195             200             205

His Trp Asp Pro Ala Pro Asn Arg Glu Arg Val Glu Lys Ala Glu Ala
      210             215             220

Asp Ala Thr Pro Thr Ala Gly Ala Arg Thr Tyr Pro Lys Ile Ala Pro
      225             230             235             240

Pro Ala Gly Ala Pro Thr Pro Pro Ala Arg Ser
      245             250

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<210> 455

<211> 579

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(556)

<223> RXN00959

<400> 455

tttggaggcg gagcatcata ccttttaatg tcaggatcgt gcagtgaaga attcaggatg 60

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aattactcgc tggaatatgt gtggggatag agttgttgtt atg acg gtg atc gga 115
Met Thr Val Ile Gly
1 5

att att ctt ggc agc ctt ttt ggc gtt ctt gca gtc ctt ctc atc gtg 163
Ile Ile Leu Gly Ser Leu Phe Gly Val Leu Ala Val Leu Leu Ile Val
10 15 20

gtt ggt gct ttg ggg tgg gcg gct aag ctc cct ggc aac ccg gtt gtg 211
Val Gly Ala Leu Gly Trp Ala Ala Lys Leu Pro Gly Asn Pro Val Val
25 30 35

ggc att cgt gtc cct gag gtg cgt aaa tcc caa gaa ttg tgg gat atg 259
Gly Ile Arg Val Pro Glu Val Arg Lys Ser Gln Glu Leu Trp Asp Met
40 45 50

gcg cac cgt gtc gct ggc ccg ttg tgg gtg ctg tcg gga gtt tcc ttt 307
Ala His Arg Val Ala Gly Pro Leu Trp Val Leu Ser Gly Val Ser Phe
55 60 65

gtt att gca tgc cta gtt gcg ttt gtt gct tct ggt tgg atg tgg ctt 355
Val Ile Ala Ser Leu Val Ala Phe Val Ala Ser Gly Trp Met Trp Leu
70 75 80 85

gtt gtg gcg ttg ggt gtt gag gct gcc atc gcg ttc att ggt atg ggt 403
Val Val Ala Leu Gly Val Glu Ala Ala Ile Ala Phe Ile Gly Met Gly
90 95 100

gcg ggt atg gct gca cat act gtt gcg atg gtt gac gcg aag cgc att 451
Ala Gly Met Ala Ala His Thr Val Ala Met Val Asp Ala Lys Arg Ile
105 110 115

cgc gaa acc ccg cag gcg cct gtt tcc gct gaa att gaa gag gcc ggt 499
Arg Glu Thr Pro Gln Ala Pro Val Ser Ala Glu Ile Glu Glu Ala Gly
120 125 130

ggt gtg act att acc tct gcc gat tat caa caa gac tcc gct gaa tgc 547
Gly Val Thr Ile Thr Ser Ala Asp Tyr Gln Gln Asp Ser Ala Glu Cys
135 140 145

ccc caa gat tgacttggat gcagtcgta gag 579
Pro Gln Asp
150

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<210> 456

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 456

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Met Thr Val Ile Gly Ile Ile Leu Gly Ser Leu Phe Gly Val Leu Ala
1 5 10 15

Val Leu Leu Ile Val Val Gly Ala Leu Gly Trp Ala Ala Lys Leu Pro
20 25 30

Gly Asn Pro Val Val Gly Ile Arg Val Pro Glu Val Arg Lys Ser Gln
35 40 45

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Glu Leu Trp Asp Met Ala His Arg Val Ala Gly Pro Leu Trp Val Leu
 50 55 60
 Ser Gly Val Ser Phe Val Ile Ala Ser Leu Val Ala Phe Val Ala Ser
 65 70 75 80
 Gly Trp Met Trp Leu Val Val Ala Leu Gly Val Glu Ala Ala Ile Ala
 85 90 95
 Phe Ile Gly Met Gly Ala Gly Met Ala Ala His Thr Val Ala Met Val
 100 105 110
 Asp Ala Lys Arg Ile Arg Glu Thr Pro Gln Ala Pro Val Ser Ala Glu
 115 120 125
 Ile Glu Glu Ala Gly Gly Val Thr Ile Thr Ser Ala Asp Tyr Gln Gln
 130 135 140
 Asp Ser Ala Glu Cys Pro Gln Asp
 145 150

<210> 457
 <211> 427
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>
 <221> CDS
 <222> (101)..(427)
 <223> FRXA00959

<400> 457
 ttggaggcgc gagcatcata ccttttaaatg tcaggatcgt gcagtggaaga attcaggatg 60
 aataactcgc tggaatattg gtggggatag agttgttgtt atg acg gtg atc gga 115
 Met Thr Val Ile Gly
 1 5
 att att ctt ggc agc ctt ttt ggc gtt ctt gca gtc ctt ctc atc gtg 163
 Ile Ile Leu Gly Ser Leu Phe Gly Val Leu Ala Val Leu Leu Ile Val
 10 15 20
 gtt ggt gct ttg ggg tgg gcg gct aag ctc cct ggc aac ccg gtt gtg 211
 Val Gly Ala Leu Gly Trp Ala Ala Lys Leu Pro Gly Asn Pro Val Val
 25 30 35
 ggc att cgt gtc cct gag gtg cgt aaa tcc caa gaa ttg tgg gat atg 259
 Gly Ile Arg Val Pro Glu Val Arg Lys Ser Gln Glu Leu Trp Asp Met
 40 45 50
 gcg cac cgt gtc gct ggc ccg ttg tgg gtg ctg tgc gga gtt tcc ttt 307
 Ala His Arg Val Ala Gly Pro Leu Trp Val Leu Ser Gly Val Ser Phe
 55 60 65
 gtt att gca tcg cta gtt gcg ttt gtt gct tct ggt tgg atg tgg ctt 355
 Val Ile Ala Ser Leu Val Ala Phe Val Ala Ser Gly Trp Met Trp Leu
 70 75 80 85
 gtt gtg gcg ttg ggt gtt gag gct gcc atc gcg ttc att ggt atg ggt 403
 Val Val Ala Leu Gly Val Glu Ala Ala Ile Ala Phe Ile Gly Met Gly

90

95

100

gcg ggt atg gct gcg cat act ggt
 Ala Gly Met Ala Ala His Thr Gly
 105

427

<210> 458

<211> 109

<212> PRT

<213> Corynebacterium glutamicum

<400> 458

Met Thr Val Ile Gly Ile Ile Leu Gly Ser Leu Phe Gly Val Leu Ala
 1 5 10 15

Val Leu Leu Ile Val Val Gly Ala Leu Gly Trp Ala Ala Lys Leu Pro
 20 25 30

Gly Asn Pro Val Val Gly Ile Arg Val Pro Glu Val Arg Lys Ser Gln
 35 40 45

Glu Leu Trp Asp Met Ala His Arg Val Ala Gly Pro Leu Trp Val Leu
 50 55 60

Ser Gly Val Ser Phe Val Ile Ala Ser Leu Val Ala Phe Val Ala Ser
 65 70 75 80

Gly Trp Met Trp Leu Val Val Ala Leu Gly Val Glu Ala Ala Ile Ala
 85 90 95

Phe Ile Gly Met Gly Ala Gly Met Ala Ala His Thr Gly
 100 105

<210> 459

<211> 960

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(937)

<223> RXN00963

<400> 459

ctggctctga cggcgtcgac ttgttctgct tctctgatac accaattttc gaggccctta 60

acctgcacg tacttttact cgggaaggaa tctagaactt atg cgt ctt gca aca 115
 Met Arg Leu Ala Thr
 1 5

atc cgc acc aac ggc acc acc att gct gct cgt gtt gaa tct gaa aac 163
 Ile Arg Thr Asn Gly Thr Thr Ile Ala Ala Arg Val Glu Ser Glu Asn
 10 15 20

acc gct acc acc atc gag ggc ttt gcc aac gtc ggt gaa tta ctc cag 211
 Thr Ala Thr Thr Ile Glu Gly Phe Ala Asn Val Gly Glu Leu Gln
 25 30 35

gaa tcc aac tgg cgc gag ctg gca gaa aac gct gct ggt gag gct gtg 259

Glu Ser Asn Trp Arg Glu Leu Ala Glu Asn Ala Ala Gly Glu Ala Val
 40 45 50
 acc ttt gaa aac aag gag cta gat gca gta gtt cca gca cct aag aag 307
 Thr Phe Glu Asn Lys Glu Leu Asp Ala Val Val Pro Ala Pro Lys Lys
 55 60 65
 att gtg tgc gtc ggc ctt aac tac gcc aac cac att aaa gaa atg ggc 355
 Ile Val Cys Val Gly Leu Asn Tyr Ala Asn His Ile Lys Glu Met Gly
 70 75 80 85
 cgc gac ctc cct gat acc cca acc ctt ttt gtt aag ttc cct gac gcg 403
 Arg Asp Leu Pro Asp Thr Pro Thr Leu Phe Val Lys Phe Pro Asp Ala
 90 95 100
 ctc atc gga cct ttc gat gat gtt gtc gtt cca gag tgg gct aac aag 451
 Leu Ile Gly Asp Phe Asp Asp Val Val Val Pro Glu Trp Ala Asn Lys
 105 110 115
 gct ctc gac tgg gaa ggc gag atg gca gtt atc att ggc aag cgc gca 499
 Ala Leu Asp Trp Glu Gly Glu Met Ala Val Ile Ile Gly Lys Arg Ala
 120 125 130
 cgc cgt gtc aag cag gcc gat gct gct gag tac atc gct ggc tac gca 547
 Arg Arg Val Lys Gln Ala Asp Ala Ala Glu Tyr Ile Ala Gly Tyr Ala
 135 140 145
 gtg atg aac gat tac acc cgc gat ttc cag tac gca gca cct gca 595
 Val Met Asn Asp Tyr Thr Thr Arg Asp Phe Gln Tyr Ala Ala Pro Ala
 150 155 160 165
 aag act cca cag tgg cac cag ggc aag tct ttg gaa aag tcc gct ggc 643
 Lys Thr Pro Gln Trp His Gln Gly Lys Ser Leu Glu Lys Ser Ala Gly
 170 175 180
 ttc ggg cct tgg atg act acc cca gat tct ttt gag ttc ggc ggc gag 691
 Phe Gly Pro Trp Met Thr Thr Pro Asp Ser Phe Glu Phe Gly Gly Glu
 185 190 195
 ctg gca acc tac ctc gag ggc gag aag gta cag tcc acc cct acc aat 739
 Leu Ala Thr Tyr Leu Glu Gly Glu Lys Val Gln Ser Thr Pro Thr Asn
 200 205 210
 gac ctg gtc ttt agc cca gaa aag ctc atc gaa tac atc acc cac atc 787
 Asp Leu Val Phe Ser Pro Glu Lys Leu Ile Glu Tyr Ile Thr His Ile
 215 220 225
 tac cca ttg gat gct ggc gac gtc att gtc acc ggt acc cca ggc ggc 835
 Tyr Pro Leu Asp Ala Gly Asp Val Ile Val Thr Gly Thr Pro Gly Gly
 230 235 240 245
 gtt ggc cac gca cgt aac cca cag cgc tac atc ggt gac ggc gaa acc 883
 Val Gly His Ala Arg Asn Pro Gln Arg Tyr Ile Gly Asp Gly Glu Thr
 250 255 260
 gta aag gtt gag att gcg ggc ctc ggc ttc att gaa aac aag acg gtg 931
 Val Lys Val Glu Ile Ala Gly Leu Gly Phe Ile Glu Asn Lys Thr Val
 265 270 275
 ttt gaa taaatgacaa ctttccacga tct 960
 Phe Glu

<210> 460

<211> 279

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 460

Met Arg Leu Ala Thr Ile Arg Thr Asn Gly Thr Thr Ile Ala Ala Arg
 1 5 10 15

Val Glu Ser Glu Asn Thr Ala Thr Thr Ile Glu Gly Phe Ala Asn Val
 20 25 30

Gly Glu Leu Leu Gln Glu Ser Asn Trp Arg Glu Leu Ala Glu Asn Ala
 35 40 45

Ala Gly Glu Ala Val Thr Phe Glu Asn Lys Glu Leu Asp Ala Val Val
 50 55 60

Pro Ala Pro Lys Lys Ile Val Cys Val Gly Leu Asn Tyr Ala Asn His
 65 70 75 80

Ile Lys Glu Met Gly Arg Asp Leu Pro Asp Thr Pro Thr Leu Phe Val
 85 90 95

Lys Phe Pro Asp Ala Leu Ile Gly Pro Phe Asp Asp Val Val Val Pro
 100 105 110

Glu Trp Ala Asn Lys Ala Leu Asp Trp Glu Gly Glu Met Ala Val Ile
 115 120 125

Ile Gly Lys Arg Ala Arg Arg Val Lys Gln Ala Asp Ala Ala Glu Tyr
 130 135 140

Ile Ala Gly Tyr Ala Val Met Asn Asp Tyr Thr Arg Asp Phe Gln
 145 150 155 160

Tyr Ala Ala Pro Ala Lys Thr Pro Gln Trp His Gln Gly Lys Ser Leu
 165 170 175

Glu Lys Ser Ala Gly Phe Gly Pro Trp Met Thr Thr Pro Asp Ser Phe
 180 185 190

Glu Phe Gly Gly Glu Leu Ala Thr Tyr Leu Glu Gly Glu Lys Val Gln
 195 200 205

Ser Thr Pro Thr Asn Asp Leu Val Phe Ser Pro Glu Lys Leu Ile Glu
 210 215 220

Tyr Ile Thr His Ile Tyr Pro Leu Asp Ala Gly Asp Val Ile Val Thr
 225 230 235 240

Gly Thr Pro Gly Gly Val Gly His Ala Arg Asn Pro Gln Arg Tyr Ile
 245 250 255

Gly Asp Gly Glu Thr Val Lys Val Glu Ile Ala Gly Leu Gly Phe Ile
 260 265 270

Glu Asn Lys Thr Val Phe Glu

<210> 461
<211> 538
<212> DNA
<213> *Cornebacterium glutamicum*

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<220>
<221> CDS
<222> (101)..(538)
<223> FRXA00963
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400> 461															
ctggctctga	cggcgtcgac	tgtttctgct	tctctgatac	accaaatttc	gaggccctta	60									
acctcgcaag						tacttttact	cggaagaa	tctagaact	atg	cgt	ctt	gca	aca	115	
									Met	Arg	Leu	Ala	Thr		
									1				5		
atc	cgc	acc	aac	ggc	acc	acc	att	gct	gct	gaa	tct	gaa	aac	163	
Ile	Arg	Thr	Asn	Gly	Thr	Thr	Ile	Ala	Arg	Val	Glu	Ser	Glu		
				10					15					20	
acc	gct	acc	acc	atc	gag	ggc	ttt	gcc	aac	gtc	ggt	gaa	tta	211	
Thr	Ala	Thr		Ile	Glu	Gly	Phe	Ala	Asn	Val	Gly	Glu	Leu		
				25					30					35	
gaa	tcc	aac	tgg	cgc	gag	ctg	gca	gaa	aac	gct	gct	ggt	gag	259	
Glu	Ser	Asn	Trp	Arg	Glu	Leu	Ala	Glu	Asn	Ala	Ala	Gly	Glu		
				40					45					50	
acc	ttt	gaa	aac	aag	gag	cta	gat	gca	gta	gtt	cca	gca	cct	307	
Thr	Phe	Glu	Asn	Lys	Glu	Leu	Asp	Ala	Val	Val	Pro	Ala	Pro		
				55					60					65	
att	gtg	tgc	gtc	ggc	ctt	aac	tac	gcc	aac	cac	att	aaa	gaa	355	
Ile	Val	Cys	Val	Gly	Leu	Asn	Tyr	Ala	Asn	His	Ile	Lys	Glu		
				70					75					80	
cgc	gac	ctc	cct	gat	acc	cca	acc	ctt	ttt	ggt	aag	ttc	cct	403	
Arg	Asp	Leu	Pro	Asp	Thr	Pro	Thr	Leu	Phe	Val	Lys	Phe	Pro		
				90					95					100	
ctc	atc	gga	cct	ttc	gat	gat	ggt	gtc	ggt	cca	gag	tgg	gct	451	
Leu	Ile	Gly	Pro	Phe	Asp	Asp	Val	Val	Val	Pro	Glu	Trp	Ala		
				105					110					115	
gct	ctc	gac	tgg	gaa	ggc	gag	atg	gca	ggt	atc	att	ggc	aag	499	
Ala	Leu	Asp	Trp	Glu	Gly	Glu	Met	Ala	Val	Ile	Ile	Gly	Lys		
				120					125					130	
cgc	cgt	gtc	aag	cag	gcc	gat	gct	gct	gag	tac	atc	gct		538	
Arg	Arg	Val	Lys	Gln	Ala	Asp	Ala	Ala	Glu	Tyr	Ile	Ala			
				135					140					145	

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<210> 462
<211> 146
<212> PRT
<213> Corvnebacterium glutamicum
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<400> 462

Met Arg Leu Ala Thr Ile Arg Thr Asn Gly Thr Thr Ile Ala Ala Arg
 1 5 10 15

Val Glu Ser Glu Asn Thr Ala Thr Thr Ile Glu Gly Phe Ala Asn Val
 20 25 30

Gly Glu Leu Leu Gln Glu Ser Asn Trp Arg Glu Leu Ala Glu Asn Ala
 35 40 45

Ala Gly Glu Ala Val Thr Phe Glu Asn Lys Glu Leu Asp Ala Val Val
 50 55 60

Pro Ala Pro Lys Lys Ile Val Cys Val Gly Leu Asn Tyr Ala Asn His
 65 70 75 80

Ile Lys Glu Met Gly Arg Asp Leu Pro Asp Thr Pro Thr Leu Phe Val
 85 90 95

Lys Phe Pro Asp Ala Leu Ile Gly Pro Phe Asp Asp Val Val Pro
 100 105 110

Glu Trp Ala Asn Lys Ala Leu Asp Trp Glu Gly Glu Met Ala Val Ile
 115 120 125

Ile Gly Lys Arg Ala Arg Arg Val Lys Gln Ala Asp Ala Ala Glu Tyr
 130 135 140

Ile Ala
 145

<210> 463

<211> 341

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(318)

<223> RXN00971

<400> 463

aaa gca ctt tcc atc gga acc cag tgg gca caa gtc atg ggc att aac 48
 Lys Ala Leu Ser Ile Gly Thr Gln Trp Ala Gln Val Met Gly Ile Asn
 1 5 10 15

cac gcc gaa gcc gaa gaa ctc gac gaa gcc ctc tcc ccg ctc att aac 96
 His Ala Glu Ala Glu Glu Leu Asp Glu Ala Leu Ser Pro Leu Ile Asn
 20 25 30

cgc ctc cgc gaa atg ggc ttt gac ccc acc gaa acc gaa gaa gca aac 144
 Arg Leu Arg Glu Met Gly Phe Asp Pro Thr Glu Thr Glu Glu Ala Asn
 35 40 45

tcc ctc gct cta cac agc tgc cca ttt gtg gtc aac gac aaa cgc cca 192
 Ser Leu Ala Leu His Ser Cys Pro Phe Val Val Asn Asp Lys Arg Pro
 50 55 60

tca gcc ttc gtc tgc gcc atc cac gcc gga ttc atc caa gaa agc ctc 240

```

Ser Ala Phe Val Cys Ala Ile His Ala Gly Phe Ile Gln Glu Ser Leu
65                      70                      75                      80

ggt gaa aac aac cgc atc cag ctg gaa ctc aaa cca ctc aac gcg cgg 288
Gly Glu Asn Asn Arg Ile Gln Leu Glu Leu Lys Pro Leu Asn Ala Pro
                        85                      90                      95

ggc acc tgt aag gtt cac gtg ttc agc gaa taattgctgc actaataagg 338
Gly Thr Cys Lys Val His Val Phe Ser Glu
                        100                     105

ccc 341

```

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<210> 464
<211> 106
<212> PRT
<213> Corynebacterium glutamicum

```

```

<400> 464
Lys Ala Leu Ser Ile Gly Thr Gln Trp Ala Gln Val Met Gly Ile Asn
1                      5                      10                      15

His Ala Glu Ala Glu Glu Leu Asp Glu Ala Leu Ser Pro Leu Ile Asn
                        20                      25                      30

Arg Leu Arg Glu Met Gly Phe Asp Pro Thr Glu Thr Glu Glu Ala Asn
                        35                      40                      45

Ser Leu Ala Leu His Ser Cys Pro Phe Val Val Asn Asp Lys Arg Pro
50                      55                      60

Ser Ala Phe Val Cys Ala Ile His Ala Gly Phe Ile Gln Glu Ser Leu
65                      70                      75                      80

Gly Glu Asn Asn Arg Ile Gln Leu Glu Leu Lys Pro Leu Asn Ala Pro
                        85                      90                      95

Gly Thr Cys Lys Val His Val Phe Ser Glu
100                     105

```

```

<210> 465
<211> 296
<212> DNA
<213> Corynebacterium glutamicum

```

```

<220>
<221> CDS
<222> (1)..(273)
<223> FRXA00971

```

```

<400> 465
aac cac gcc gaa gcc gaa gaa ctc gac gaa gcc ctc tcc cgg ctc att 48
Asn His Ala Glu Ala Glu Glu Leu Asp Glu Ala Leu Ser Pro Leu Ile
1                      5                      10                      15

aac cgc ctc cgc gaa atg ggc ttt gac ccc acc gaa acc gaa gaa gca 96
Asn Arg Leu Arg Glu Met Gly Phe Asp Pro Thr Glu Thr Glu Glu Ala
                        20                      25                      30

```

```

aac tcc ctc gct cta cac agc tgc cca ttt gtg gtc aac gac aaa cgc 144
Asn Ser Leu Ala Leu His Ser Cys Pro Phe Val Val Asn Asp Lys Arg
      35              40              45

cca tca gcc ttc gtc tgc gcc atc cac gcc gga ttc atc caa gaa agc 192
Pro Ser Ala Phe Val Cys Ala Ile His Ala Gly Phe Ile Gln Glu Ser
      50              55              60

ctc ggt gaa aac aac cgc atc cag ctg gaa ctc aaa cca ctc aac gcg 240
Leu Gly Glu Asn Asn Arg Ile Gln Leu Glu Lys Pro Leu Asn Ala
      65              70              75              80

ccg gcc acc tgt aag gtt cac gtg ttc agc gaa taattgctgc actaataagg 293
Pro Gly Thr Cys Lys Val His Val Phe Ser Glu
      85              90

ccc 296

```

```

<210> 466
<211> 91
<212> PRT
<213> Corynebacterium glutamicum

```

```

<400> 466
Asn His Ala Glu Ala Glu Glu Leu Asp Glu Ala Leu Ser Pro Leu Ile
 1              5              10              15

Asn Arg Leu Arg Glu Met Gly Phe Asp Pro Thr Glu Thr Glu Glu Ala
      20              25              30

Asn Ser Leu Ala Leu His Ser Cys Pro Phe Val Val Asn Asp Lys Arg
      35              40              45

Pro Ser Ala Phe Val Cys Ala Ile His Ala Gly Phe Ile Gln Glu Ser
      50              55              60

Leu Gly Glu Asn Asn Arg Ile Gln Leu Glu Leu Lys Pro Leu Asn Ala
      65              70              75              80

Pro Gly Thr Cys Lys Val His Val Phe Ser Glu
      85              90

```

```

<210> 467
<211> 1503
<212> DNA
<213> Corynebacterium glutamicum

```

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<220>
<221> CDS
<222> (101)..(1480)
<223> RXN00991

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<400> 467
acttcaagga aagacggtcc caagagctaa aactccccca cggcacgcga agctgaacag 60

gctttcacccg ctctctaaggc caacagctta aaccacgcta atg gac ata ctc ata 115
Met Asp Ile Leu Ile
      1              5

```

agc atc ctc tca ctg cta ggc ttc gtg ctt ctt acc gcg agc acc gga 163
 Ser Ile Leu Ser Leu Leu Gly Phe Val Leu Thr Ala Ser Thr Gly
 10 15 20

cta ttc gtg gcc att gag ttc gca ctc acc ggc tta gaa aaa tcc act 211
 Leu Phe Val Ala Ile Glu Phe Ala Leu Thr Gly Leu Glu Lys Ser Thr
 25 30 35

gta gaa aca cat gtg aag caa aaa ggc gac agc agc gcc cgc gca gtg 259
 Val Glu Thr His Val Lys Gln Lys Gly Asp Ser Ser Ala Arg Ala Val
 40 45 50

cag agg gat cat caa aat ctg tcg ttc gtg ctc tct ggt gcc cag ctg 307
 Gln Arg Asp His Gln Asn Leu Ser Phe Val Leu Ser Gly Ala Gln Leu
 55 60 65

ggc atc acg atc acg aca ctt gcc aca ggc ttc ctc gca gag ccg gtt 355
 Gly Ile Thr Thr Thr Leu Ala Thr Gly Phe Leu Ala Glu Pro Val
 70 75 80 85

ttg gcc aaa ttc ttc acc cca gca ctt gag ctg gtg gga tta aat gaa 403
 Leu Ala Lys Phe Phe Thr Pro Ala Leu Glu Leu Val Gly Leu Asn Glu
 90 95 100

tca gca agc tcc gca gta gcc ctc atc atc gca ctg ttg gtg gca act 451
 Ser Ala Ser Ser Ala Val Ala Leu Ile Ile Ala Leu Leu Ala Thr
 105 110 115

acc ctc tcc atg gtt ttt ggt gag ttg gtt ccc aaa aac tgg cgc atc 499
 Thr Leu Ser Met Val Phe Gly Glu Leu Val Pro Lys Asn Trp Ala Ile
 120 125 130

acc aac ccg ttg ggc gtg gca cgt ttt gtt gtc cac cct gtc aat tgg 547
 Thr Asn Pro Leu Gly Val Ala Arg Phe Val Val His Pro Val Asn Trp
 135 140 145

ttc aac atg gtt ctc aag ccg ttt att aac ggc atg aac aag tct gca 595
 Phe Asn Met Val Leu Lys Pro Phe Ile Asn Gly Met Asn Lys Ser Ala
 150 155 160 165

aac ttt att gtc cgc aaa ctt ggt att gaa cca gcc gaa gag ctt gcc 643
 Asn Phe Ile Val Arg Lys Leu Gly Ile Glu Pro Ala Glu Glu Leu Ala
 170 175 180

tct gcc cgt tcc tcc caa gag ctc acc gcc ttg gta cgc agc tcc gcg 691
 Ser Ala Arg Ser Ser Gln Glu Leu Thr Ala Leu Val Arg Ser Ser Ala
 185 190 195

gaa agc ggc gga ctg gat caa aac acc gca gcg gtg atc aac cga tcc 739
 Glu Ser Gly Gly Leu Asp Gln Asn Thr Ala Ala Val Ile Asn Arg Ser
 200 205 210

ctg cag ttc ggt gac gcc acc gct gat gaa ttc atg aca cct cgc tcc 787
 Leu Gln Phe Gly Asp Ala Thr Ala Asp Glu Phe Met Thr Pro Arg Ser
 215 220 225

acc att gaa tca ttg cgt gcc aca gac acc gtc aat gat ttg atc gag 835
 Thr Ile Glu Ser Ser Leu Arg Ala Thr Asp Thr Val Asn Asp Leu Ile Glu
 230 235 240 245

ctt gcc ctg gaa acg ggt cac tcc cgc ttc cca gtc acc gaa ggc gac 883

Leu Ala Leu Glu Thr Gly His Ser Arg Phe Pro Val Thr Glu Gly Asp
 250 255 260
 ttg gat gaa acc atc ggc atg gtc cac atc aag gac gca ttc tct gta 931
 Leu Asp Glu Thr Ile Gly Met Val His Ile Lys Asp Ala Phe Ser Val
 265 270
 gtg cag gca gaa cgc gcc acc acc atg gtg cgc gat cta gcc cgc aaa 979
 Val Gln Ala Glu Arg Ala Thr Thr Met Val Arg Asp Leu Ala Arg Lys
 280 285 290
 att cct gtg gta cca gcc agc ctt gac ggc gac tct gtc ctc aac gct 1027
 Ile Pro Val Val Pro Ala Ser Leu Asp Gly Asp Ser Val Leu Asn Ala
 295 300 305
 gtc cgc tcc gcc ggc tcc caa gtt att ttg gtt gcc gat gaa tac ggc 1075
 Val Arg Ser Ala Gly Ser Gln Val Ile Leu Val Ala Asp Glu Tyr Gly
 310 315 320 325
 gga acc gca ggc atg gtc acc atc gaa gac gtc gtg gag gaa atc ctc 1123
 Gly Thr Ala Gly Met Val Thr Ile Glu Asp Val Val Glu Glu Ile Leu
 330 335 340
 ggc gaa atc cac gat gag cac gac gac tcc gac gcc gaa cgc gat ttc 1171
 Gly Glu Ile His Asp Glu His Asp Asp Ser Asp Ala Glu Arg Asp Phe
 345 350 355
 caa caa ttc ggc gcc agc tgg gaa gtc tcc ggc ctg gtc cgc atc gat 1219
 Gln Gln Phe Gly Ala Ser Trp Glu Val Ser Gly Leu Val Arg Ile Asp
 360 365 370
 gaa ctc gaa aaa cgc gtc ggg tac gtc tcc cct gac ggc ccc tac gaa 1267
 Glu Leu Glu Lys Arg Val Gly Tyr Val Ser Pro Asp Gly Pro Tyr Glu
 375 380 385
 acc ctc ggc ggc ttg atc atg tac aca gtc ggc gcc att cct cgc gtc 1315
 Thr Leu Gly Gly Leu Ile Met Tyr Thr Val Gly Ala Ile Pro Arg Val
 390 395 400 405
 ggc gat gtc gcc cta ctc cca ctg acc gat acc cca acc atg gat gaa 1363
 Gly Asp Val Ala Leu Leu Pro Leu Thr Asp Thr Pro Thr Met Asp Glu
 410 415 420
 ttc gaa tcc ggc ttc tcc gga cgc tgg atc gca cga gta acg gtc atg 1411
 Phe Glu Ser Gly Phe Ser Gly Arg Trp Ile Ala Arg Val Thr Val Met
 425 430 435
 gaa gat cga cgc atc gac aaa gcc gtt ctc acc ccc atc acc cat gaa 1459
 Glu Asp Arg Arg Ile Asp Lys Ala Val Leu Thr Pro Ile Thr His Glu
 440 445 450
 gaa gca aag gag tac gaa aag tgagtatttg ggcaactgtc ctt 1503
 Glu Ala Lys Glu Tyr Glu Lys
 455 460

<210> 468

<211> 460

<212> PRT

<213> Corynebacterium glutamicum

<400> 468

Met Asp Ile Leu Ile Ser Ile Leu Ser Leu Leu Gly Phe Val Leu Leu
 1 5 10 15

Thr Ala Ser Thr Gly Leu Phe Val Ala Ile Glu Phe Ala Leu Thr Gly
 20 25 30

Leu Glu Lys Ser Thr Val Glu Thr His Val Lys Gln Lys Gly Asp Ser
 35 40 45

Ser Ala Arg Ala Val Gln Arg Asp His Gln Asn Leu Ser Phe Val Leu
 50 55 60

Ser Gly Ala Gln Leu Gly Ile Thr Ile Thr Thr Leu Ala Thr Gly Phe
 65 70 75 80

Leu Ala Glu Pro Val Leu Ala Lys Phe Phe Thr Pro Ala Leu Glu Leu
 85 90 95

Val Gly Leu Asn Glu Ser Ala Ser Ser Ala Val Ala Leu Ile Ile Ala
 100 105 110

Leu Leu Val Ala Thr Thr Leu Ser Met Val Phe Gly Glu Leu Val Pro
 115 120 125

Lys Asn Trp Ala Ile Thr Asn Pro Leu Gly Val Ala Arg Phe Val Val
 130 135 140

His Pro Val Asn Trp Phe Asn Met Val Leu Lys Pro Phe Ile Asn Gly
 145 150 155 160

Met Asn Lys Ser Ala Asn Phe Ile Val Arg Lys Leu Gly Ile Glu Pro
 165 170 175

Ala Glu Glu Leu Ala Ser Ala Arg Ser Ser Gln Glu Leu Thr Ala Leu
 180 185 190

Val Arg Ser Ser Ala Glu Ser Gly Gly Leu Asp Gln Asn Thr Ala Ala
 195 200 205

Val Ile Asn Arg Ser Leu Gln Phe Gly Asp Ala Thr Ala Asp Glu Phe
 210 215 220

Met Thr Pro Arg Ser Thr Ile Glu Ser Leu Arg Ala Thr Asp Thr Val
 225 230 235 240

Asn Asp Leu Ile Glu Leu Ala Leu Glu Thr Gly His Ser Arg Phe Pro
 245 250 255

Val Thr Glu Gly Asp Leu Asp Glu Thr Ile Gly Met Val His Ile Lys
 260 265 270

Asp Ala Phe Ser Val Val Gln Ala Glu Arg Ala Thr Thr Met Val Arg
 275 280 285

Asp Leu Ala Arg Lys Ile Pro Val Val Pro Ala Ser Leu Asp Gly Asp
 290 295 300

Ser Val Leu Asn Ala Val Arg Ser Ala Gly Ser Gln Val Ile Leu Val
 305 310 315 320

Ala Asp Glu Tyr Gly Gly Thr Ala Gly Met Val Thr Ile Glu Asp Val
 325 330 335

Val Glu Glu Ile Leu Gly Glu Ile His Asp Glu His Asp Asp Ser Asp
 340 345 350

Ala Glu Arg Asp Phe Gln Gln Phe Gly Ala Ser Trp Glu Val Ser Gly
 355 360 365

Leu Val Arg Ile Asp Glu Leu Glu Lys Arg Val Gly Tyr Val Ser Pro
 370 375 380

Asp Gly Pro Tyr Glu Thr Leu Gly Gly Leu Ile Met Tyr Thr Val Gly
 385 390 395 400

Ala Ile Pro Arg Val Gly Asp Val Ala Leu Leu Pro Leu Thr Asp Thr
 405 410 415

Pro Thr Met Asp Glu Phe Glu Ser Gly Phe Ser Gly Arg Trp Ile Ala
 420 425 430

Arg Val Thr Val Met Glu Asp Arg Arg Ile Asp Lys Ala Val Leu Thr
 435 440 445

Pro Ile Thr His Glu Glu Ala Lys Glu Tyr Glu Lys
 450 455 460

<210> 469
 <211> 1185
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1162)
 <223> RXN01004

<400> 469
 ccggacgctg gatcgacga gtaacggtca tggaaatcg acgcacgcac aaagccgttc 60

tcacccccat caccatgaa gaagcaaagg agtacgaaaa gtg agt att tgg gca 115
 Val Ser Ile Trp Ala
 1 5

act gtc ctt cta att atc gtc ctt ctt tcc gcc aac gcc ttc ttc gtg 163
 Thr Val Leu Leu Ile Ile Val Leu Leu Ser Ala Asn Ala Phe Phe Val
 10 15 20

gcc gcg gag ttc gca ctg att tcc tgg cgc cgg gac cgc ctg gat tcc 211
 Ala Ala Glu Phe Ala Leu Ile Ser Ser Arg Arg Asp Arg Leu Asp Ser
 25 30 35

ctg gta tcc cag ggt aaa aag gga gct gaa aag gtt ctc tac gca acc 259
 Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys Val Leu Tyr Ala Thr
 40 45 50

gag cac ctc tcc atc atg ttg gcg ggc gct cag ttc ggt att acg gtc 307
 Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln Phe Gly Ile Thr Val
 55 60 65

tgt tct ctg att ctg ggt aaa gtc gca gaa cct gcg atc gcc cac ttc	355
Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro Ala Ile Ala His Phe	
70 75 80 85	
att gag gtg cct ttc acc tcc tgg ggt gtt cca aat gat ttg atc cac	403
Ile Glu Val Pro Phe Thr Ser Trp Gly Val Pro Asn Asp Leu Ile His	
90 95 100	
cca att tcc ttc gtc atc gca ctg gcg atc atc acc tgg ttg cac att	451
Pro Ile Ser Phe Val Ile Ala Leu Ala Ile Ile Thr Trp Leu His Ile	
105 110 115	
ctc ttt ggt gaa atg gtg cca aag aac atc gct att gct gcc cct gaa	499
Leu Phe Gly Glu Met Val Pro Lys Asn Ile Ala Ile Ala Gly Pro Glu	
120 125 130	
acc tta ggc atg tgg ctt gct cca gtg ctc att gcg ttt gtg aag att	547
Thr Leu Gly Met Trp Leu Ala Pro Val Leu Ile Ala Phe Val Lys Ile	
135 140 145	
acc cgc ccg ttg atc gag ttc atg aac tgg atc gcc cgt ctg acc ctt	595
Thr Arg Pro Leu Ile Glu Phe Met Asn Trp Ile Ala Arg Leu Thr Leu	
150 155 160 165	
cgc gcc ttt ggt gtg gag caa aaa aac gag ctg gat tcc acc gtg gac	643
Arg Ala Phe Gly Val Glu Gln Lys Asn Glu Leu Asp Ser Thr Val Asp	
170 175 180	
cca gag cag ctg gca tca atg att tcc gag tcc cgt tcc gaa gcc ctc	691
Pro Glu Gln Leu Ala Ser Met Ile Ser Glu Ser Arg Ser Glu Gly Leu	
185 190 195	
ctt gat gct gaa gag cac gcc cgc ctg tcc aag gcg ctg cgc tct gag	739
Leu Asp Ala Glu Glu His Ala Arg Leu Ser Lys Ala Leu Arg Ser Glu	
200 205 210	
cag cgt tcc atc aag gaa ctg gtg att aag gat gag gac gtg cgc acg	787
Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp Glu Asp Val Arg Thr	
215 220 225	
ctg gcg ttc ggt aaa tct gcc ccg acc ttg cac cag ttg gag gaa gca	835
Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His Gln Leu Glu Glu Ala	
230 235 240 245	
gtc cgc gag acc ggt ttc tcc cgc ttc cct gtc acc gcc cgc gat gga	883
Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val Thr Gly Arg Asp Gly	
250 255 260	
tcc tac ttg ggt tat atc cac atc aag gat att ttg cct cgt ctg gct	931
Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile Leu Pro Arg Leu Ala	
265 270 275	
gat cct gag atg gat ccc tcc gag acc att ccg cgt tct gca ctg cgc	979
Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro Arg Ser Ala Leu Arg	
280 285 290	
cct ttg agc aat gtg gat gcc gac gcc ctc atg gat gac gtc ttg gat	1027
Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met Asp Asp Val Leu Asp	
295 300 305	
ttt atg cac tac cgc tcc gcg cac atg gct cag gtt cgc ctc aaa ggt	1075

Phe Met His Tyr Arg Ser Ala His Met Ala Gln Val Arg Leu Lys Gly
 310 315 320 325
 gag ctt ctc ggc gtg att acg ctg gag gat ctc atc gaa gaa tac gtg 1123
 Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu Ile Glu Glu Tyr Val
 330 335 340
 ggc acc gtc aac gat tgg act cac gaa agc tcc gac gac tagaaatagt 1172
 Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser Asp Asp
 345 350
 aactgtgttg gac 1185

<210> 470
 <211> 354
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 470
 Val Ser Ile Trp Ala Thr Val Leu Leu Ile Ile Val Leu Leu Ser Ala
 1 5 10 15
 Asn Ala Phe Phe Val Ala Ala Glu Phe Ala Leu Ile Ser Ser Arg Arg
 20 25 30
 Asp Arg Leu Asp Ser Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys
 35 40 45
 Val Leu Tyr Ala Thr Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln
 50 55 60
 Phe Gly Ile Thr Val Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro
 65 70 75 80
 Ala Ile Ala His Phe Ile Glu Val Pro Phe Thr Ser Trp Gly Val Pro
 85 90 95
 Asn Asp Leu Ile His Pro Ile Ser Phe Val Ile Ala Leu Ala Ile Ile
 100 105 110
 Thr Trp Leu His Ile Leu Phe Gly Glu Met Val Pro Lys Asn Ile Ala
 115 120 125
 Ile Ala Gly Pro Glu Thr Leu Gly Met Trp Leu Ala Pro Val Leu Ile
 130 135 140
 Ala Phe Val Lys Ile Thr Arg Pro Leu Ile Glu Phe Met Asn Trp Ile
 145 150 155 160
 Ala Arg Leu Thr Leu Arg Ala Phe Gly Val Glu Gln Lys Asn Glu Leu
 165 170 175
 Asp Ser Thr Val Asp Pro Glu Gln Leu Ala Ser Met Ile Ser Glu Ser
 180 185 190
 Arg Ser Glu Gly Leu Leu Asp Ala Glu Glu His Ala Arg Leu Ser Lys
 195 200 205
 Ala Leu Arg Ser Glu Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp
 210 215 220

Glu Asp Val Arg Thr Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His
225 230 235 240

Gln Leu Glu Glu Ala Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val
245 250 255

Thr Gly Arg Asp Gly Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile
260 265 270

Leu Pro Arg Leu Ala Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro
275 280 285

Arg Ser Ala Leu Arg Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met
290 295 300

Asp Asp Val Leu Asp Phe Met His Tyr Arg Ser Ala His Met Ala Gln
305 310 315 320

Val Arg Leu Lys Gly Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu
325 330 335

Ile Glu Glu Tyr Val Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser
340 345 350

Asp Asp

<210> 471

<211> 771

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(748)

<223> RXN01016

<400> 471

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gctcgccatc atccaccaaa ttctccagcc ggggtgaagca ttg ttg ccg tat gca 115
Leu Leu Pro Tyr Ala
1 5

ata gtc ggc ctg gtc att ttg ctg cca tcc tcc tgg ttg cct cgt tgg 163
Ile Val Gly Leu Val Ile Leu Leu Pro Ser Ser Trp Leu Pro Arg Trp
10 15 20

gct gtc gca gtc ctt ggc gaa gtg tgg ctt gtg cca gcg gtg gtt ttc 211
Ala Val Ala Val Leu Gly Glu Val Ser Leu Val Pro Ala Val Val Phe
25 30 35

ggc ggc ggc ttc ctg ctt atc ccc tca atg ttc ctg atc ggt tca gcg 259
Gly Gly Gly Phe Leu Leu Ile Pro Ser Met Phe Leu Ile Gly Ser Ala
40 45 50

ctc gtt agg tat gga gta gtc gat cgg gca gag aac gca ccg cgg gct 307
Leu Val Arg Tyr Gly Val Val Asp Arg Ala Glu Asn Ala Pro Arg Ala
55 60 65

atg gga gtc ttt ttc gcc gta agc gca gca atc gct ata cct acg ctg 355
Met Gly Val Phe Phe Ala Val Ser Ala Ala Ile Ala Ile Pro Thr Leu
70 75 80 85

atc atc cag gca cgt gac atc act tct tca ggc ttc tcg atc gtt tcc 403
Ile Ile Gln Ala Arg Asp Ile Thr Ser Ser Gly Phe Ser Ile Val Ser
90 95 100

aca gtg gcg gga ctc gcg ctt ggc ggc gtc tac att tct tta gtg ttg 451
Thr Val Ala Gly Leu Ala Leu Gly Gly Val Tyr Ile Ser Leu Val Leu
105 110 115

ctg gcc ttg cat aca ccg att cgc ggt gca ctc gct gca gtt ttc gca 499
Leu Ala Leu His Thr Pro Ile Arg Gly Ala Leu Ala Val Phe Ala
120 125 130

cct tta ggg cgt atg gcg cta acc aac tac att ggt gca acg atc ctc 547
Pro Leu Gly Arg Met Ala Leu Thr Asn Tyr Ile Gly Ala Thr Ile Leu
135 140 145

atg ctc att ggc ggg cta atc gtg gat ctt cca cac agc aca tca tgg 595
Met Leu Ile Gly Gly Leu Ile Val Asp Leu Pro His Ser Thr Ser Trp
150 155 160 165

aca gct acg gtg ctc cta gct gcg ggt att ctc att att caa gag cta 643
Thr Ala Thr Val Leu Leu Ala Ala Gly Ile Leu Ile Ile Gln Glu Leu
170 175 180

ctt tct gct tta tgg ttg cgc cac tac aca cag ggg cca ctt ggg tat 691
Leu Ser Ala Leu Trp Leu Arg His Tyr Thr Gln Gly Pro Leu Gly Tyr
185 190 195

cta tgg cgt tgg gtg act tgg gga agc cgt tcc ccc ttc ctt acc cgt 739
Leu Trp Arg Trp Val Thr Trp Gly Ser Arg Ser Pro Phe Leu Thr Arg
200 205 210

tcc gca tca tgacaggtag ggaagtgtcc tac 771
Ser Ala Ser
215

<210> 472

<211> 216

<212> PRT

<213> Corynebacterium glutamicum

<400> 472

Leu Leu Pro Tyr Ala Ile Val Gly Leu Val Ile Leu Leu Pro Ser Ser
1 5 10 15

Trp Leu Pro Arg Trp Ala Val Ala Val Leu Gly Glu Val Ser Leu Val
20 25 30

Pro Ala Val Val Phe Gly Gly Gly Phe Leu Leu Ile Pro Ser Met Phe
35 40 45

Leu Ile Gly Ser Ala Leu Val Arg Tyr Gly Val Val Asp Arg Ala Glu
50 55 60

Asn Ala Pro Arg Ala Met Gly Val Phe Phe Ala Val Ser Ala Ala Ile

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65              70              75              80
Ala Ile Pro Thr Leu Ile Ile Gln Ala Arg Asp Ile Thr Ser Ser Gly
                        85                      90                      95

Phe Ser Ile Val Ser Thr Val Ala Gly Leu Ala Leu Gly Gly Val Tyr
                100                105                110

Ile Ser Leu Val Leu Leu Ala Leu His Thr Pro Ile Arg Gly Ala Leu
                115                120                125

Ala Ala Val Phe Ala Pro Leu Gly Arg Met Ala Leu Thr Asn Tyr Ile
                130                135                140

Gly Ala Thr Ile Leu Met Leu Ile Gly Gly Leu Ile Val Asp Leu Pro
                145                150                155                160

His Ser Thr Ser Trp Thr Ala Thr Val Leu Leu Ala Ala Gly Ile Leu
                165                170                175

Ile Ile Gln Glu Leu Leu Ser Ala Leu Trp Leu Arg His Tyr Thr Gln
                180                185                190

Gly Pro Leu Gly Tyr Leu Trp Arg Trp Val Thr Trp Gly Ser Arg Ser
                195                200                205

Pro Phe Leu Thr Arg Ser Ala Ser
                210                215

<210> 473
<211> 771
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(748)
<223> FRXA01016

<400> 473
tgcccgtcga ggtgaacgcc caagaatagt tctctttcgt cgactttcga cgttgatacc 60

gctcggcatc atccacaaaa ttctccagcc ggggtgaagca ttg ttg ccg tat gca 115
                1                      5

ata gtc ggc ctg gtc att ttg ctg cca tcc tcc ttg cct cgt tgg 163
Ile Val Gly Leu Val Ile Leu Leu Pro Ser Ser Trp Leu Pro Arg Trp
                10                15                20

gct gtc gca gtc ctt ggc gaa gtg tcg ctt gtg cca gcg gtg gtt ttc 211
Ala Val Ala Val Leu Gly Glu Val Ser Leu Val Pro Ala Val Val Phe
                25                30                35

ggt ggc ggg ttc ctg ctt atc ccc tca atg ttc ctg atc ggt tca gcg 259
Gly Gly Gly Phe Leu Leu Ile Pro Ser Met Phe Leu Ile Gly Ser Ala
                40                45                50

ctc gtt agg tat gga gta gtc gat cgg gca gag aac gca ccg cgg gct 307
Leu Val Arg Tyr Gly Val Val Asp Arg Ala Glu Asn Ala Pro Arg Ala

```

55 60 65

atg gga gtc ttt ttc gcc gta agc gca gca atc gct ata cct acg ctg 355
 Met Gly Val Phe Phe Arg Ala Val Ser Ala Ala Ile Ala Ile Pro Thr Leu 85
 70 75 80

atc atc cag gca cgt gac atc act tct tca ggc ttc tgg atc gtt tcc 403
 Ile Ile Gln Ala Arg Asp Ile Thr Ser Gly Phe Ser Ile Val Ser 100
 90 95

aca gtg gcg gga ctc gcg ctt ggc ggc gtc tac att tct tta gtg ttg 451
 Thr Val Ala Gly Leu Ala Leu Gly Gly Val Tyr Ile Ser Leu Val Leu 115
 105 110

ctg gcc ttg cat aca cgg att cgc ggt gca ctc gct gca gtt ttc gca 499
 Leu Ala Leu His Thr Pro Ile Arg Gly Ala Leu Ala Ala Val Phe Ala 130
 120 125

cct tta ggg cgt atg gcg cta acc aac tac att ggt gca acg atc ctc 547
 Pro Leu Gly Arg Met Ala Leu Thr Asn Tyr Ile Gly Ala Thr Ile Leu 145
 135 140

atg ctc att ggc ggg cta atc gtg gat ctt cca cac agc aca tca tgg 595
 Met Leu Ile Gly Gly Leu Ile Val Asp Leu Pro His Ser Thr Ser Trp 165
 150 155 160

aca gct acg gtg ctc cta gct gcg ggt att ctc att att caa gag cta 643
 Thr Ala Thr Val Leu Leu Ala Ala Gly Ile Leu Ile Ile Gln Glu Leu 180
 170 175

ctt tct gct tta tgg ttg cgc cac tac aca cag ggg cca ctt ggg tat 691
 Leu Ser Ala Leu Trp Leu Arg His Tyr Thr Gln Gly Pro Leu Gly Tyr 195
 185 190

cta tgg cgt tgg gtg act tgg gga agc cgt tcc ccc ttc ctt acc cgt 739
 Leu Trp Arg Trp Val Thr Trp Gly Ser Arg Ser Pro Phe Leu Thr Arg 210
 200 205

tcc gca tca tgacaggtac ggaagtgtcc tac 771
 Ser Ala Ser 215

<210> 474
 <211> 216
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 474
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Trp Leu Pro Arg Trp Ala Val Ala Val Leu Gly Glu Val Ser Leu Val 30
 20 25

Pro Ala Val Val Phe Gly Gly Gly Phe Leu Leu Ile Pro Ser Met Phe 45
 35 40

Leu Ile Gly Ser Ala Leu Val Arg Tyr Gly Val Val Asp Arg Ala Glu 60
 50 55

Asn Ala Pro Arg Ala Met Gly Val Phe Phe Ala Val Ser Ala Ala Ile
65 70 75 80

Ala Ile Pro Thr Leu Ile Ile Gln Ala Arg Asp Ile Thr Ser Ser Gly
85 90 95

Phe Ser Ile Val Ser Thr Val Ala Gly Leu Ala Leu Gly Gly Val Tyr
100 105 110

Ile Ser Leu Val Leu Leu Ala Leu His Thr Pro Ile Arg Gly Ala Leu
115 120 125

Ala Ala Val Phe Ala Pro Leu Gly Arg Met Ala Leu Thr Asn Tyr Ile
130 135 140

Gly Ala Thr Ile Leu Met Leu Ile Gly Gly Leu Ile Val Asp Leu Pro
145 150 155 160

His Ser Thr Ser Trp Thr Ala Thr Val Leu Leu Ala Ala Gly Ile Leu
165 170 175

Ile Ile Gln Glu Leu Leu Ser Ala Leu Trp Leu Arg His Tyr Thr Gln
180 185 190

Gly Pro Leu Gly Tyr Leu Trp Arg Trp Val Thr Trp Gly Ser Arg Ser
195 200 205

Pro Phe Leu Thr Arg Ser Ala Ser
210 215

<210> 475

<211> 1101

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1078)

<223> RXN01023

<400> 475

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atttttctag tctatcgccc cacaggtagg ctcaggacac atg agt gcc gtg aac 115
Met Ser Ala Val Asn 5
1

agt gct ggt cgc cca gcc aac ggg gga att aac aaa acc ccc atg att 163
Ser Ala Gly Arg Pro Ala Asn Gly Gly Ile Asn Lys Thr Pro Met Ile 20
10 15

att gcc cta gtg tta tot att gtg ttg gtt ttg gcg gtg ctg ttc gcc 211
Ile Ala Leu Val Leu Ser Ile Val Leu Val Leu Ala Val Leu Phe Gly 35
25 30

gcc cga gtc ctc ctt gcc ccc gcc gcc cag caa cag ata gcc atg agt 259
Ala Arg Val Leu Leu Gly Pro Ala Gly Gln Gln Gln Ile Ala Met Ser 50
40 45

ggg ctt ccc gcc cca gac gca gaa tct gct gag tgc gcc gca tta ctc 307

Gly	Leu	Pro	Ala	Pro	Asp	Ala	Glu	Ser	Ala	Glu	Cys	Ala	Ala	Leu	Leu	
55						60				65						
gag	gat	ctc	ccc	ggc	gag	gcc	ttc	ggg	cac	acc	cgt	gca	gaa	atc	atg	355
Glu	Asp	Leu	Pro	Gly	Glu	Ala	Phe	Gly	His	Thr	Arg	Ala	Glu	Ile	Met	
70				75						80				85		
gat	cct	gtt	cca	ccg	ggc	gct	gcc	tggt	tcc	acc	tca	gac	ctc	gag		403
Asp	Pro	Val	Pro	Pro	Gly	Ala	Ala	Ala	Trp	Ser	Thr	Ser	Asp	Leu	Glu	
				90					95					100		
cgt	gtg	acg	ctg	cgt	tgt	ggc	gtc	gat	atg	cca	ttc	cag	tac	acc	gcg	451
Arg	Val	Thr	Leu	Arg	Cys	Gly	Val	Asp	Met	Pro	Phe	Gln	Tyr	Thr	Ala	
			105					110					115			
ctc	gcc	aac	acc	gtc	gac	gtc	gac	ggc	acc	acc	tggt	cta	cct	gtc	tcc	499
Leu	Ala	Asn	Thr	Val	Asp	Val	Asp	Gly	Thr	Thr	Trp	Leu	Pro	Val	Ser	
		120					125					130				
gac	atg	acc	ccc	ggc	tcc	tcc	ctg	gag	acc	tggt	tac	tcc	gtc	aac	cgc	547
Asp	Met	Thr	Pro	Gly	Ser	Ser	Leu	Glu	Thr	Trp	Tyr	Ser	Val	Asn	Arg	
		135				140					145					
ttc	ccc	gtc	gtc	gcc	atc	acc	gcc	gat	gac	atc	agc	acc	gac	agc	gcc	595
Phe	Pro	Val	Val	Ala	Ile	Thr	Ala	Asp	Asp	Ile	Ser	Thr	Asp	Ser	Ala	
150					155					160				165		
gac	aac	ccc	gtc	gcc	ccc	ttc	agc	agc	gcc	gtc	gac	aag	cta	gaa	aag	643
Asp	Asn	Pro	Val	Ala	Pro	Phe	Ser	Ser	Ala	Val	Asp	Lys	Leu	Glu	Lys	
				170				175						180		
cgc	gac	ggc	cag	ccc	ttc	gac	gcc	cca	ctt	acc	ggc	ttg	agc	tca	gcc	691
Arg	Asp	Gly	Gln	Pro	Phe	Asp	Ala	Pro	Leu	Thr	Gly	Leu	Ser	Ser	Ala	
			185					190					195			
ggc	acc	aca	tgc	act	tgc	ctt	ttc	gac	gcc	ctc	ccc	cgc	caa	ctc	gaa	739
Gly	Thr	Thr	Cys	Thr	Ser	Leu	Phe	Asp	Ala	Leu	Pro	Arg	Gln	Leu	Glu	
		200				205						210				
gtc	ggc	ggc	gac	gac	ggc	aca	acg	tac	gaa	cgc	atc	gag	gag	gac	cgc	787
Val	Gly	Gly	Asp	Asp	Gly	Thr	Thr	Tyr	Glu	Arg	Ile	Glu	Glu	Asp	Arg	
		215				220					225					
atg	cag	gcc	gcc	gga	tac	tcc	gac	gac	gca	gtc	gcg	tggt	gac	acg	ccg	835
Met	Gln	Ala	Ala	Gly	Tyr	Ser	Asp	Asp	Ala	Val	Ala	Trp	Asp	Thr	Pro	
230					235					240				245		
gga	tta	gaa	ccc	att	gtg	atc	cgt	tgc	ggc	gtg	gag	cct	tct	gag	aac	883
Gly	Leu	Glu	Pro	Ile	Val	Ile	Arg	Cys	Gly	Val	Glu	Pro	Ser	Glu	Asn	
				250					255					260		
tac	gca	gcc	ggt	gcc	atg	ttg	cag	cag	atc	gat	gac	atc	ccg	tggt	ttc	931
Tyr	Ala	Ala	Gly	Ala	Met	Leu	Gln	Gln	Ile	Asp	Asp	Ile	Pro	Trp	Phe	
			265					270					275			
gag	gac	acc	att	ttg	gcc	tcc	ggt	acc	acc	tgc	tct	acc	tggt	tat	gcc	979
Glu	Asp	Thr	Ile	Leu	Ala	Ser	Gly	Thr	Thr	Ser	Ser	Thr	Trp	Tyr	Ala	
		280					285					290				
ctt	gga	cgc	gag	atc	gac	atc	gcc	gtg	tct	ctg	cct	cag	gct	gct	tcc	1027
Leu	Gly	Arg	Glu	Ile	Asp	Ile	Ala	Val	Ser	Leu	Pro	Gln	Ala	Ala	Ser	

295

300

305

tct tcc ctg att act atc tcc ggt ttc att gaa gac acg gtt cct gcg 1075
 Ser Ser Leu Ile Thr Ile Ser Gly Phe Ile Glu Asp Thr Val Pro Ala
 310 315 320 325

gaa taagacataa aaaatcgccc cac 1101
 Glu

<210> 476

<211> 326

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 476

Met Ser Ala Val Asn Ser Ala Gly Arg Pro Ala Asn Gly Gly Ile Asn
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Lys Thr Pro Met Ile Ile Ala Leu Val Leu Ser Ile Val Leu Val Leu
 20 25 30

Ala Val Leu Phe Gly Ala Arg Val Leu Leu Gly Pro Ala Gly Gln Gln
 35 40 45

Gln Ile Ala Met Ser Gly Leu Pro Ala Pro Asp Ala Glu Ser Ala Glu
 50 55 60

Cys Ala Ala Leu Leu Glu Asp Leu Pro Gly Glu Ala Phe Gly His Thr
 65 70 75 80

Arg Ala Glu Ile Met Asp Pro Val Pro Pro Gly Ala Ala Ala Trp Ser
 85 90 95

Thr Ser Asp Leu Glu Arg Val Thr Leu Arg Cys Gly Val Asp Met Pro
 100 105 110

Phe Gln Tyr Thr Ala Leu Ala Asn Thr Val Asp Val Asp Gly Thr Thr
 115 120 125

Trp Leu Pro Val Ser Asp Met Thr Pro Gly Ser Ser Leu Glu Thr Trp
 130 135 140

Tyr Ser Val Asn Arg Phe Pro Val Val Ala Ile Thr Ala Asp Asp Ile
 145 150 155 160

Ser Thr Asp Ser Ala Asp Asn Pro Val Ala Pro Phe Ser Ser Ala Val
 165 170 175

Asp Lys Leu Glu Lys Arg Asp Gly Gln Pro Phe Asp Ala Pro Leu Thr
 180 185 190

Gly Leu Ser Ser Ala Gly Thr Thr Cys Thr Ser Leu Phe Asp Ala Leu
 195 200 205

Pro Arg Gln Leu Glu Val Gly Gly Asp Asp Gly Thr Thr Tyr Glu Arg
 210 215 220

Ile Glu Glu Asp Arg Met Gln Ala Ala Gly Tyr Ser Asp Asp Ala Val
 225 230 235 240

Ala Trp Asp Thr Pro Gly Leu Glu Pro Ile Val Ile Arg Cys Gly Val
 245 250 255

Glu Pro Ser Glu Asn Tyr Ala Ala Gly Ala Met Leu Gln Gln Ile Asp
 260 265 270

Asp Ile Pro Trp Phe Glu Asp Thr Ile Leu Ala Ser Gly Thr Thr Ser
 275 280 285

Ser Thr Trp Tyr Ala Leu Gly Arg Glu Ile Asp Ile Ala Val Ser Leu
 290 295 300

Pro Gln Ala Ala Ser Ser Ser Leu Ile Thr Ile Ser Gly Phe Ile Glu
 305 310 315 320

Asp Thr Val Pro Ala Glu
 325

<210> 477

<211> 974

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(951)

<223> FRXA01023

<400> 477

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 Pro Ala Asn Gly Gly Ile Asn Lys Thr Pro Met Ile Ile Ala Leu Val
 1 5 10 15

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 Leu Ser Ile Val Leu Val Leu Ala Val Leu Phe Gly Ala Arg Val Leu
 20 25 30

ctt ggc ccc gcc ggc cag caa cag ata gcc atg agt ggg ctt ccc gcc 144
 Leu Gly Pro Ala Gly Gln Gln Ile Ala Met Ser Gly Leu Pro Ala
 35 40 45

cca gac gca gaa tct gct gag tgc gcc gca tta ctc gag gat ctc ccc 192
 Pro Asp Ala Glu Ser Ala Glu Cys Ala Ala Leu Leu Glu Asp Leu Pro
 50 55 60

ggc gag gcc ttc ggg cac acc cgt gca gaa atc atg gat cct gtt cca 240
 Gly Glu Ala Phe Gly His Thr Arg Ala Glu Ile Met Asp Pro Val Pro
 65 70 75 80

cgg ggc gct gcc gcc tgg tcc acc tca gac ctc gag cgt gtg acg ctg 288
 Pro Gly Ala Ala Ala Trp Ser Thr Ser Asp Leu Glu Arg Val Thr Leu
 85 90 95

cgt tgt ggc gtc gat atg cca ttc cag tac acc gcg ctc gcc aac acc 336
 Arg Cys Gly Val Asp Met Pro Phe Gln Tyr Thr Ala Leu Ala Asn Thr
 100 105 110

gtc gac gtc gac gcc acc acc tgg cta cct gtc tcc gac atg acc ccc 384
 Val Asp Val Asp Gly Thr Thr Trp Leu Pro Val Ser Asp Met Thr Pro

115	120	125	
ggc tcc tcc ctg gag acc tgg tac tcc gtc aac cgc ttc ccc gtc gtc			432
Gly Ser Ser Leu Glu Thr Trp Tyr Ser Val Asn Arg Phe Pro Val Val			
130	135	140	
gcc atc acc gcc gat gac atc agc acc gac agc gcc gac aac ccc gtc			480
Ala Ile Thr Ala Asp Asp Ile Ser Thr Asp Ser Ala Asp Asn Pro Val			
145	150	155	160
gac ccc ttc agc agc gcc gtc gac aag cta gaa aag cgc gac gcc cag			528
Asp Pro Phe Ser Ser Ala Val Asp Lys Leu Glu Lys Arg Asp Gly Gln			
165	170	175	
ccc ttc gac gcc cca ctt acc ggc ttg agc tca gcc gcc acc aca tgc			576
Pro Phe Asp Ala Pro Leu Thr Gly Leu Ser Ser Ala Gly Thr Thr Cys			
180	185	190	
act tgg ctt ttc gac gcc ctc ccc cgc caa ctc gaa gtc gcc gcc gac			624
Thr Ser Leu Phe Asp Ala Leu Pro Arg Gln Leu Glu Val Gly Gly Asp			
195	200	205	
gac gcc aca acg tac gaa cgc atc gag gag gac cgc atg cag gcc gcc			672
Asp Gly Thr Thr Tyr Glu Arg Ile Glu Glu Asp Arg Met Gln Ala Ala			
210	215	220	
gga tac tcc gac gac gca gtc gcg tgg gac acg ccg gga tta gaa ccc			720
Gly Tyr Ser Asp Asp Ala Val Ala Trp Asp Thr Pro Gly Leu Glu Pro			
225	230	235	240
att gtg atc cgt tgc gcc gtg gag cct tct gag aac tac gca gcc ggt			768
Ile Val Ile Arg Cys Gly Val Glu Pro Ser Glu Asn Tyr Ala Ala Gly			
245	250	255	
gcc atg ttg cag cag atc gat gac atc ccg tgg ttc gag gac acc att			816
Ala Met Leu Gln Gln Ile Asp Asp Ile Pro Trp Phe Glu Asp Thr Ile			
260	265	270	
ttg gcc tcc ggt acc acc tgg tct acc tgg tat gcc ctt gga cgc gag			864
Leu Ala Ser Gly Thr Thr Ser Ser Thr Trp Tyr Ala Leu Gly Arg Glu			
275	280	285	
atc gac atc gcc gtg tct ctg cct cag gct gct tcc tct tcc ctg att			912
Ile Asp Ile Ala Val Ser Leu Pro Gln Ala Ala Ser Ser Ser Leu Ile			
290	295	300	
act atc tcc ggt ttc att gaa gac acg gtt cct gcg gaa taagacataa			961
Thr Ile Ser Gly Phe Ile Glu Asp Thr Val Pro Ala Glu			
305	310	315	
aaaatcgccc cac			974
<210> 478			
<211> 317			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 478			
Pro Ala Asn Asn Gly Gly Ile Asn Lys Thr Pro Met Ile Ile Ala Leu Val			
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Leu Ser Ile Val Leu Val Leu Ala Val Leu Phe Gly Ala Arg Val Leu
 20 25 30
 Leu Gly Pro Ala Gly Gln Gln Gln Ile Ala Met Ser Gly Leu Pro Ala
 35 40 45
 Pro Asp Ala Glu Ser Ala Glu Cys Ala Ala Leu Leu Glu Asp Leu Pro
 50 55 60
 Gly Glu Ala Phe Gly His Thr Arg Ala Glu Ile Met Asp Pro Val Pro
 65 70 75 80
 Pro Gly Ala Ala Ala Trp Ser Thr Ser Asp Leu Glu Arg Val Thr Leu
 85 90 95
 Arg Cys Gly Val Asp Met Pro Phe Gln Tyr Thr Ala Leu Ala Asn Thr
 100 105 110
 Val Asp Val Asp Gly Thr Thr Trp Leu Pro Val Ser Asp Met Thr Pro
 115 120 125
 Gly Ser Ser Leu Glu Thr Trp Tyr Ser Val Asn Arg Phe Pro Val Val
 130 135 140
 Ala Ile Thr Ala Asp Asp Ile Ser Thr Asp Ser Ala Asp Asn Pro Val
 145 150 155 160
 Asp Pro Phe Ser Ser Ala Val Asp Lys Leu Glu Lys Arg Asp Gly Gln
 165 170 175
 Pro Phe Asp Ala Pro Leu Thr Gly Leu Ser Ser Ala Gly Thr Thr Cys
 180 185 190
 Thr Ser Leu Phe Asp Ala Leu Pro Arg Gln Leu Glu Val Gly Gly Asp
 195 200 205
 Asp Gly Thr Thr Tyr Glu Arg Ile Glu Glu Asp Arg Met Gln Ala Ala
 210 215 220
 Gly Tyr Ser Asp Asp Ala Val Ala Trp Asp Thr Pro Gly Leu Glu Pro
 225 230 235 240
 Ile Val Ile Arg Cys Gly Val Glu Pro Ser Glu Asn Tyr Ala Ala Gly
 245 250 255
 Ala Met Leu Gln Gln Ile Asp Asp Ile Pro Trp Phe Glu Asp Thr Ile
 260 265 270
 Leu Ala Ser Gly Thr Thr Ser Ser Thr Trp Tyr Ala Leu Gly Arg Glu
 275 280 285
 Ile Asp Ile Ala Val Ser Leu Pro Gln Ala Ala Ser Ser Ser Leu Ile
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 305 310 315

<210> 479

<211> 2172

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(2149)

<223> RXN01028

<400> 479

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caatgaacgct gaccacagcgg tgacccatcc gcatctcaca	gtg atc tac cca ccg	115
	Val Ile Tyr Pro Pro	
	1 5	

ctc acc cct gca tcc gaa gag aaa ttc aac aag atc acc tca gtc gct	163
Leu Thr Pro Ala Ser Glu Glu Lys Phe Asn Lys Ile Thr Ser Val Ala	
10 15 20	

gct gtg agc aag cgc cca acc acc ctg ccg tat ttc cgt gca gat ggt	211
Ala Val Ser Lys Arg Pro Thr Thr Leu Pro Tyr Phe Arg Ala Asp Gly	
25 30 35	

tca cct act cgt ggc ttt gct aac ttc tcc aca gga ggt att cac ggt	259
Ser Pro Thr Arg Gly Phe Ala Asn Phe Ser Thr Gly Gly Ile His Gly	
40 45 50	

gog gaa tac aac gaa gat cgt ttt gac cat gat caa gat cta cac aca	307
Ala Glu Tyr Asn Glu Asp Arg Phe Asp His Asp Gln Asp Leu His Thr	
55 60 65	

gtg gca acc cgt gaa ttc ttc gcc att ctt gat gog aca tta gog gct	355
Val Ala Thr Arg Glu Phe Phe Ala Ile Leu Asp Ala Thr Leu Ala Ala	
70 75 80 85	

ctc tac gca gcc cac caa gcc gaa cct gaa tcg gog gac tac cag att	403
Leu Tyr Ala Ala His Gln Ala Glu Pro Glu Ser Ala Asp Tyr Gln Ile	
90 95 100	

gca caa gac gca ctc gcc tgg gca aag aat gta ctt agc gat caa aaa	451
Ala Gln Asp Ala Leu Ala Trp Ala Lys Asn Val Leu Ser Asp Gln Lys	
105 110 115	

ctc atc gct aag tcg cct cag tta tac aac ccc gaa acc ggg gtc acc	499
Leu Ile Ala Lys Ser Pro Gln Leu Tyr Asn Pro Glu Thr Gly Val Thr	
120 125 130	

tat gag tgg gag ttt gtc gct caa gca gca tgg tgg att cgc aac aaa	547
Tyr Glu Trp Glu Phe Val Ala Gln Ala Ala Trp Trp Ile Arg Asn Lys	
135 140 145	

ccg gtt gag gtt att tta cca aca ggt gaa tca atg acc gta aaa cac	595
Pro Val Glu Val Ile Leu Pro Thr Gly Glu Ser Met Thr Val Lys His	
150 155 160 165	

aaa tct gta ttg gca tct gcg tcc tac cca ctc cga gac aac gtg gcg	643
Lys Ser Val Leu Ala Ser Ala Ser Tyr Pro Leu Arg Asp Asn Val Ala	
170 175 180	

tac tgg cgt agc gaa ccc aaa aca cca cag ctg ttt ccc gta gca aaa	691
Tyr Trp Arg Ser Glu Pro Lys Thr Pro Gln Leu Phe Pro Val Ala Lys	

185	190	195	
tct ggt ggt tcc tcg ctt gag aag aag tac aac tac acc tct gtg ggt Ser Gly Gly Ser Ser Leu Glu Lys Lys Tyr Asn Tyr Thr Ser Val Gly 200 205 210			739
act gct att cac gag gac ttt agc agt tac tat ccg ctc ttg ctc acc Thr Ala Ile His Glu Asp Phe Thr Ser Ser Tyr Tyr Pro Leu Leu Leu Thr 215 220 225			787
aat atg gct gca ttt acc aat gct gac tta ggt att gat gag aaa acc Asn Met Ala Ala Phe Thr Asn Ala Asp Leu Gly Ile Asp Glu Lys Thr 230 235 240 245			835
ggg cgc cct cgt gac cgc tac cgt gaa atc tac gaa caa aaa gag atc Gly Arg Pro Arg Asp Arg Tyr Arg Glu Ile Tyr Glu Gln Lys Glu Ile 250 255 260			883
tat ggc gca cag cgc aaa gac ccc tcc att gat gaa gaa aca aag caa Tyr Gly Ala Gln Arg Lys Asp Pro Ser Ile Asp Glu Glu Thr Lys Gln 265 270 275			931
cgt cta ggg att ttg cgc gaa ggt acc aag ttg att ctt aac tcg gcc Arg Leu Gly Ile Leu Arg Glu Gly Thr Lys Leu Ile Leu Asn Ser Ala 280 285 290			979
acc ggt gct gct gat gct ggt cac gac acc ccg atc ctc atg aac aat Thr Gly Ala Ala Asp Ala Gly His Asp Thr Pro Ile Leu Met Asn Asn 295 300 305			1027
cgc gtt att gcc atg agg att att ggg cag cta ttt tct tgg aga att Arg Val Ile Ala Met Arg Ile Ile Gly Gln Leu Phe Ser Trp Arg Ile 310 315 320 325			1075
ggg caa gct caa tca ctg gct ggt gca acg att att tcc act aac act Gly Gln Ala Gln Ser Leu Ala Gly Ala Thr Ile Ile Ser Thr Asn Thr 330 335 340			1123
gat ggc ctg tat tcc gta ctc gat atg ggg act aac cag cgc gtt ctt Asp Gly Leu Tyr Ser Val Leu Asp Met Gly Thr Asn Gln Arg Val Leu 345 350 355			1171
gat gaa cac gct aca gcc atc ggt gtg caa att gag cct gaa gaa ctg Asp Glu His Ala Thr Ala Ile Gly Val Gln Ile Glu Pro Glu Glu Leu 360 365 370			1219
gat att gtc tcc aag gat tcc aac tca cgt gcc gaa ttt ctc ggc aat Asp Ile Val Ser Lys Asp Ser Asn Ser Arg Ala Glu Phe Leu Gly Asn 375 380 385			1267
ggc tac atc aat gcg gcc ggt gac ttg gcg tgt tgg gat gga ccc aac Gly Tyr Ile Asn Ala Ala Gly Asp Leu Ala Cys Trp Asp Gly Pro Asn 390 395 400 405			1315
tct cgg aac tca cta gat cac ccg gcc ttt gtt gac cat gtg ctg gtg Ser Arg Asn Ser Leu Asp His Pro Ala Phe Val Asp His Val Leu Val 410 415 420			1363
aag tat ttc cag ctc gtc gtc aac aac act gtg cca gag att cca gaa Lys Tyr Phe Gln Leu Val Val Asn Asn Thr Val Pro Glu Ile Pro Glu 425 430 435			1411

aca cct gag ctt gag ggt gta ccg ctg gct ctt gat caa ccc atg aac 1459
 Thr Pro Glu Leu Glu Gly Val Pro Leu Ala Leu Asp Gln Pro Met Asn
 440 445 450

cgc cac gaa gtc tcg aag att gtc gcc act atg cac aag gaa ttc gag 1507
 Arg His Glu Val Ser Lys Ile Val Ala Thr Met His Lys Glu Phe Glu
 455 460 465

ccg aaa aag ctg ctg tcg ttt tac caa aac att ttg gcc tct tca cgc 1555
 Pro Lys Lys Leu Leu Ser Phe Tyr Gln Asn Ile Leu Ala Ser Ser Arg
 470 475 480 485

ggt tct aat acc ttc cta ttc tct gtc ccc tat atc cct gca aca gaa 1603
 Gly Ser Asn Thr Phe Leu Phe Ser Val Pro Tyr Ile Pro Ala Thr Glu
 490 495 500

gga gaa gaa acc cac cct gca aca gat acc agc act att gcg aca cca 1651
 Gly Glu Glu Thr His Pro Ala Thr Asp Thr Ser Thr Ile Ala Thr Pro
 505 510 515

acc ttg agc ttt gat gct tat ggt aat aag gcc gag gtc atg ccg act 1699
 Thr Leu Ser Phe Asp Ala Tyr Gly Asn Lys Ala Glu Val Met Pro Thr
 520 525 530

caa tcc act gtg gat aag cgc gtg ccc tct ttg ctg cag tat tac acg 1747
 Gln Ser Thr Val Asp Lys Arg Val Pro Ser Leu Leu Gln Tyr Tyr Thr
 535 540 545

cgt aca ttc cat gtg cga caa gat acg cag cag gct gtc ttt gat gtt 1795
 Arg Thr Phe His Val Arg Gln Asp Thr Gln Gln Ala Val Phe Asp Val
 550 555 560 565

att ggc gcc aac ccc gtg ctc atc gcc gca gca aaa gct gca tcc ata 1843
 Ile Gly Ala Asn Pro Val Leu Ile Ala Ala Ala Lys Ala Ala Ser Ile
 570 575 580

tca ccg gct tct gct gat tca cgt aga aag aag ggc ctg gcc tcc acc 1891
 Ser Pro Ala Ser Ala Asp Ser Arg Arg Lys Lys Gly Leu Ala Ser Thr
 585 590 595

aac gct gac cca gta gcc aag cat gta cta gaa att gca gga gct gat 1939
 Asn Ala Asp Pro Val Ala Lys His Val Leu Glu Ile Ala Gly Ala Asp
 600 605 610

gtg gaa tcg ctg cgc cat gaa aag gat ctc aag gtc acc aag cac act 1987
 Val Glu Ser Leu Arg His Glu Lys Asp Leu Lys Val Thr Lys His Thr
 615 620 625

ggc caa gac cca gca ctg cct gtc gtg gtc ttt aac caa acc att tgg 2035
 Gly Gln Asp Pro Ala Leu Pro Val Val Val Phe Asn Gln Thr Ile Trp
 630 635 640 645

cat aac ccc aac gac gat gtg att aat gca tta ctg ggc gct att gac 2083
 His Asn Pro Asn Asp Asp Val Ile Asn Ala Leu Leu Gly Ala Ile Asp
 650 655 660

cag gat gcc tac att gac atg gcg atc tcg tcc tac aac aag tcc tgg 2131
 Gln Asp Ala Tyr Ile Asp Met Ala Ile Ser Ser Tyr Asn Lys Ser Trp
 665 670 675

cac aac att atc ccg gct taactaccgc tgggtagacc cct
His Asn Ile Ile Pro Ala
680

2172

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<211> 683
<212> PRT
<213> Corynebacterium glutamicum

<400> 480
Val Ile Tyr Pro Pro Leu Thr Pro Ala Ser Glu Glu Lys Phe Asn Lys
1 5 10 15
Ile Thr Ser Val Ala Ala Val Ser Lys Arg Pro Thr Thr Leu Pro Tyr
20 25 30
Phe Arg Ala Asp Gly Ser Pro Thr Arg Gly Phe Ala Asn Phe Ser Thr
35 40 45
Gly Gly Ile His Gly Ala Glu Tyr Asn Glu Asp Arg Phe Asp His Asp
50 55 60
Gln Asp Leu His Thr Val Ala Thr Arg Glu Phe Phe Ala Ile Leu Asp
65 70 75 80
Ala Thr Leu Ala Ala Leu Tyr Ala Ala His Gln Ala Glu Pro Glu Ser
85 90 95
Ala Asp Tyr Gln Ile Ala Gln Asp Ala Leu Ala Trp Ala Lys Asn Val
100 105 110
Leu Ser Asp Gln Lys Leu Ile Ala Lys Ser Pro Gln Leu Tyr Asn Pro
115 120 125
Glu Thr Gly Val Thr Tyr Glu Trp Glu Phe Val Ala Gln Ala Ala Trp
130 135 140
Trp Ile Arg Asn Lys Pro Val Glu Val Ile Leu Pro Thr Gly Glu Ser
145 150 155 160
Met Thr Val Lys His Lys Ser Val Leu Ala Ser Ala Ser Tyr Pro Leu
165 170 175
Arg Asp Asn Val Ala Tyr Trp Arg Ser Glu Pro Lys Thr Pro Gln Leu
180 185 190
Phe Pro Val Ala Lys Ser Gly Gly Ser Ser Leu Glu Lys Lys Tyr Asn
195 200 205
Tyr Thr Ser Val Gly Thr Ala Ile His Glu Asp Phe Ser Ser Tyr Tyr
210 215 220
Pro Leu Leu Leu Thr Asn Met Ala Ala Phe Thr Asn Ala Asp Leu Gly
225 230 235 240
Ile Asp Glu Lys Thr Gly Arg Pro Arg Asp Arg Tyr Arg Glu Ile Tyr
245 250 255
Glu Gln Lys Glu Ile Tyr Gly Ala Gln Arg Lys Asp Pro Ser Ile Asp
260 265 270

Glu Glu Thr Lys Gln Arg Leu Gly Ile Leu Arg Glu Gly Thr Lys Leu
 275 280 285
 Ile Leu Asn Ser Ala Thr Gly Ala Ala Asp Ala Gly His Asp Thr Pro
 290 295 300
 Ile Leu Met Asn Asn Arg Val Ile Ala Met Arg Ile Ile Gly Gln Leu
 305 310 315 320
 Phe Ser Trp Arg Ile Gly Gln Ala Gln Ser Leu Ala Gly Ala Thr Ile
 325 330 335
 Ile Ser Thr Asn Thr Asp Gly Leu Tyr Ser Val Leu Asp Met Gly Thr
 340 345 350
 Asn Gln Arg Val Leu Asp Glu His Ala Thr Ala Ile Gly Val Gln Ile
 355 360 365
 Glu Pro Glu Glu Leu Asp Ile Val Ser Lys Asp Ser Asn Ser Arg Ala
 370 375 380
 Glu Phe Leu Gly Asn Gly Tyr Ile Asn Ala Ala Gly Asp Leu Ala Cys
 385 390 395 400
 Trp Asp Gly Pro Asn Ser Arg Asn Ser Leu Asp His Pro Ala Phe Val
 405 410 415
 Asp His Val Leu Val Lys Tyr Phe Gln Leu Val Val Asn Asn Thr Val
 420 425 430
 Pro Glu Ile Pro Glu Thr Pro Glu Leu Glu Gly Val Pro Leu Ala Leu
 435 440 445
 Asp Gln Pro Met Asn Arg His Glu Val Ser Lys Ile Val Ala Thr Met
 450 455 460
 His Lys Glu Phe Glu Pro Lys Lys Leu Leu Ser Phe Tyr Gln Asn Ile
 465 470 475 480
 Leu Ala Ser Ser Arg Gly Ser Asn Thr Phe Leu Phe Ser Val Pro Tyr
 485 490 495
 Ile Pro Ala Thr Glu Gly Glu Glu Thr His Pro Ala Thr Asp Thr Ser
 500 505 510
 Thr Ile Ala Thr Pro Thr Leu Ser Phe Asp Ala Tyr Gly Asn Lys Ala
 515 520 525
 Glu Val Met Pro Thr Gln Ser Thr Val Asp Lys Arg Val Pro Ser Leu
 530 535 540
 Leu Gln Tyr Tyr Thr Arg Thr Phe His Val Arg Gln Asp Thr Gln Gln
 545 550 555 560
 Ala Val Phe Asp Val Ile Gly Ala Asn Pro Val Leu Ile Ala Ala Ala
 565 570 575
 Lys Ala Ala Ser Ile Ser Pro Ala Ser Ala Asp Ser Arg Arg Lys Lys
 580 585 590

Gly Leu Ala Ser Thr Asn Ala Asp Pro Val Ala Lys His Val Leu Glu
595 600 605

Ile Ala Gly Ala Asp Val Glu Ser Leu Arg His Glu Lys Asp Leu Lys
610 615 620

Val Thr Lys His Thr Gly Gln Asp Pro Ala Leu Pro Val Val Val Phe
625 630 635 640

Asn Gln Thr Ile Trp His Asn Pro Asn Asp Asp Val Ile Asn Ala Leu
645 650 655

Leu Gly Ala Ile Asp Gln Asp Ala Tyr Ile Asp Met Ala Ile Ser Ser
660 665 670

Tyr Asn Lys Ser Trp His Asn Ile Ile Pro Ala
675 680

<210> 481
<211> 647
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(624)
<223> FRXA01028

<400> 481
ttt tac caa aac att ttg gcc tct tca cgc ggt tct aat acc ttc cta 48
Phe Tyr Gln Asn Ile Leu Ala Ser Ser Arg Gly Ser Asn Thr Phe Leu
1 5 10 15

ttc tct gtc ccc tat atc cct gca aca gaa gga gaa gaa acc cac cct 96
Phe Ser Val Pro Tyr Ile Pro Ala Thr Glu Gly Glu Glu Thr His Pro
20 25 30

gca aca gat acc agc act att gcg aca cca acc ttg agc ttt gat gct 144
Ala Thr Asp Thr Ser Thr Ile Ala Thr Pro Thr Leu Ser Phe Asp Ala
35 40 45

tat ggt aat aag gcc gag gtc atg ccg act caa tcc act gtg gat aag 192
Tyr Gly Asn Lys Ala Glu Val Met Pro Thr Gln Ser Thr Val Asp Lys
50 55 60

cgc gtg ccc tct ttg ctg cag tat tac acg cgt aca ttc cat gtg cga 240
Arg Val Pro Ser Leu Leu Gln Tyr Tyr Thr Arg Thr Phe His Val Arg
65 70 75 80

caa gat acg cag cag gct gtc ttt gat gtt att ggc gcc aac ccc gtg 288
Gln Asp Thr Gln Gln Ala Val Phe Asp Val Ile Gly Ala Asn Pro Val
85 90 95

ctc atc gcc gca gca aaa gct gca tcc ata tca ccg gct tct gct gat 336
Leu Ile Ala Ala Ala Lys Ala Ala Ser Ile Ser Pro Ala Ser Ala Asp
100 105 110

tca cgt aga aag aag ggc ctg gcc tcc acc aac gct gac cca gta gcc 384
Ser Arg Arg Lys Lys Gly Leu Ala Ser Thr Asn Ala Asp Pro Val Ala
115 120 125

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aag cat gta cta gaa att gca gga gct gat gtg gaa tcg ctg cgc cat 432
Lys His Val Leu Glu Ile Ala Gly Ala Asp Val Glu Ser Leu Arg His
130 135 140

gaa aag gat ctc aag gtc acc aag cac act ggc caa gac cca gca ctg 480
Glu Lys Asp Leu Lys Val Thr Lys His Thr Gly Gln Asp Pro Ala Leu
145 150 155 160

cct gtc gtg gtc ttt aac caa acc att tgg cat aac ccc aac gac gat 528
Pro Val Val Val Phe Asn Gln Thr Ile Trp His Asn Pro Asn Asp Asp
165 170 175

gtg att aat gca tta ctg ggc gct att gac cag gat gcc tac att gac 576
Val Ile Asn Ala Leu Leu Gly Ala Ile Asp Gln Asp Ala Tyr Ile Asp
180 185 190

atg gcg atc tcg tcc tac aac aag tcc tgg cac aac att atc ccg gct 624
Met Ala Ile Ser Ser Tyr Asn Lys Ser Trp His Asn Ile Ile Pro Ala
195 200 205

taactaccgc tgggtagacc cct 647

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<210> 482
<211> 208
<212> PRT
<213> Corynebacterium glutamicum

<400> 482
Phe Tyr Gln Asn Ile Leu Ala Ser Ser Arg Gly Ser Asn Thr Phe Leu
1 5 10 15

Phe Ser Val Pro Tyr Ile Pro Ala Thr Glu Gly Glu Glu Thr His Pro
20 25 30

Ala Thr Asp Thr Ser Thr Ile Ala Thr Pro Thr Leu Ser Phe Asp Ala
35 40 45

Tyr Gly Asn Lys Ala Glu Val Met Pro Thr Gln Ser Thr Val Asp Lys
50 55 60

Arg Val Pro Ser Leu Leu Gln Tyr Tyr Thr Arg Thr Phe His Val Arg
65 70 75 80

Gln Asp Thr Gln Gln Ala Val Phe Asp Val Ile Gly Ala Asn Pro Val
85 90 95

Leu Ile Ala Ala Ala Lys Ala Ala Ser Ile Ser Pro Ala Ser Ala Asp
100 105 110

Ser Arg Arg Lys Lys Gly Leu Ala Ser Thr Asn Ala Asp Pro Val Ala
115 120 125

Lys His Val Leu Glu Ile Ala Gly Ala Asp Val Glu Ser Leu Arg His
130 135 140

Glu Lys Asp Leu Lys Val Thr Lys His Thr Gly Gln Asp Pro Ala Leu
145 150 155 160

Pro Val Val Val Phe Asn Gln Thr Ile Trp His Asn Pro Asn Asp Asp

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165

170

175

Val Ile Asn Ala Leu Leu Gly Ala Ile Asp Gln Asp Ala Tyr Ile Asp
180 185 190

Met Ala Ile Ser Ser Tyr Asn Lys Ser Trp His Asn Ile Ile Pro Ala
195 200 205

<210> 483

<211> 1230

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1230)

<223> FRXA01812

<400> 483

agc ttc aat gac gtt gac cca gcg gtg acc cat ccg cat ctc aca gtg 48
Ser Phe Asn Asp Val Asp Pro Ala Val Thr His Pro His Leu Thr Val
1 5 10 15

atc tac cca ccg ctc acc cct gca tcc gaa gag aaa ttc aac aag atc 96
Ile Tyr Pro Pro Leu Thr Pro Ala Ser Glu Glu Lys Phe Asn Lys Ile
20 25 30

acc tca gtc gct gct gtg agc aag cgc cca acc acc ctg ccg tat ttc 144
Thr Ser Val Ala Ala Val Ser Lys Arg Pro Thr Thr Leu Pro Tyr Phe
35 40 45

cgt gca gat ggt tca cct act cgt ggc ttt gct aac ttc tcc aca gga 192
Arg Ala Asp Gly Ser Pro Thr Arg Gly Phe Ala Asn Phe Ser Thr Gly
50 55 60

ggt att cac ggt gcg gaa tac aac gaa gat cgt ttt gac cat gat caa 240
Gly Ile His Gly Ala Glu Tyr Asn Glu Asp Arg Phe Asp His Asp Gln
65 70 75 80

gat cta cac aca gtg gca acc cgt gaa ttc ttc gcc att ctt gat gcg 288
Asp Leu His Thr Val Ala Thr Arg Glu Phe Phe Ala Ile Leu Asp Ala
85 90 95

aca tta gcg gct ctc tac gca gcc cac caa gcc gaa cct gaa tcg gcg 336
Thr Leu Ala Ala Leu Tyr Ala Ala His Gln Ala Glu Pro Glu Ser Ala
100 105 110

gac tac cag att gca caa gac gca ctc gcc tgg gca aag aat gta ctt 384
Asp Tyr Gln Ile Ala Gln Asp Ala Leu Ala Trp Ala Lys Asn Val Leu
115 120 125

agc gat Caa aaa ctc atc gct aag tcg cct cag tta tac aac ccc gaa 432
Ser Asp Gln Lys Leu Ile Ala Lys Ser Pro Gln Leu Tyr Asn Pro Glu
130 135 140

acc ggg gtc acc tat gag tgg gag ttt gtc gct caa gca gca tgg tgg 480
Thr Gly Val Thr Tyr Glu Trp Glu Phe Val Ala Gln Ala Ala Trp Trp

145	150	155	160	
att cgc aac aaa ccg gtt gag gtt att tta cca aca ggt gaa tca atg	528			
Ile Arg Asn Lys Pro Val Glu Val Ile Leu Pro Thr Gly Glu Ser Met				
165	170	175		
acc gta aaa cac aaa tct gta ttg gca tct gcg tcc tac cca ctc cga	576			
Thr Val Lys His Lys Ser Val Leu Ala Ser Ala Ser Tyr Pro Leu Arg				
180	185	190		
gac aac gtg gcg tac tgg cgt agc gaa ccc aaa aca cca cag ctg ttt	624			
Asp Asn Val Ala Tyr Trp Arg Ser Glu Pro Lys Thr Pro Gln Leu Phe				
195	200	205		
ccc gta gca aaa tct ggt ggt tcc tcg ctt gag aag aag tac aac tac	672			
Pro Val Ala Lys Ser Gly Gly Ser Ser Leu Glu Lys Lys Tyr Asn Tyr				
210	215	220		
acc tct gtg ggt act gct att cac gag gac ttt agc agt tac tat ccg	720			
Thr Ser Val Gly Thr Ala Ile His Glu Asp Phe Ser Ser Tyr Tyr Pro				
225	230	235	240	
ctc ttg ctc acc aat atg gct gca ttt acc aat gct gac tta ggt att	768			
Leu Leu Leu Thr Asn Met Ala Ala Phe Thr Asn Ala Asp Leu Gly Ile				
245	250	255		
gat gag aaa acc ggg cgc cct cgt gac cgc tac cgt gaa atc tac gaa	816			
Asp Glu Lys Thr Gly Arg Pro Arg Asp Arg Tyr Arg Glu Ile Tyr Glu				
260	265	270		
caa aaa gag atc tat ggc gca cag cgc aaa gac ccc tcc att gat gaa	864			
Gln Lys Glu Ile Tyr Gly Ala Gln Arg Lys Asp Pro Ser Ile Asp Glu				
275	280	285		
gaa aca aag caa cgt cta ggg att ttg cgc gaa ggt acc aag ttg att	912			
Glu Thr Lys Gln Arg Leu Gly Ile Leu Arg Glu Gly Thr Lys Leu Ile				
290	295	300		
ctt aac tcg gcc acc ggt gct gct gat gct ggt cac gac acc ccg atc	960			
Leu Asn Ser Ala Thr Gly Ala Ala Asp Ala Gly His Asp Thr Pro Ile				
305	310	315	320	
ctc atg aac aat cgc gtt att gcc atg agg att att ggg cag cta ttt	1008			
Leu Met Asn Asn Arg Val Ile Ala Met Arg Ile Ile Gly Gln Leu Phe				
325	330	335		
tct tgg aga att ggg caa gct caa tca ctg gct ggt gca acg att att	1056			
Ser Trp Arg Ile Gly Gln Ala Gln Ser Leu Ala Gly Ala Thr Ile Ile				
340	345	350		
tcc act aac act gat ggc ctg tat tcc gta ctc gat atg ggg act aac	1104			
Ser Thr Asn Thr Asp Gly Leu Tyr Ser Val Leu Asp Met Gly Thr Asn				
355	360	365		
cag cgc gtt ctt gat gaa cac gct aca gcc atc ggt gtg caa att gag	1152			
Gln Arg Val Leu Asp Glu His Ala Thr Ala Ile Gly Val Gln Ile Glu				
370	375	380		
cct gaa gaa ctg gat att gtc tcc aag gat tcc aac tca cgt gcc gaa	1200			
Pro Glu Glu Leu Asp Ile Val Ser Lys Asp Ser Asn Ser Arg Ala Glu				
385	390	395	400	

ttt ctc ggc aat ggc tac atc aat gcg gcc 1230
 Phe Leu Gly Asn Gly Tyr Ile Asn Ala Ala
 405 410

<210> 484

<211> 410

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 484

Ser Phe Asn Asp Val Asp Pro Ala Val Thr His Pro His Leu Thr Val
 1 5 10 15

Ile Tyr Pro Pro Leu Thr Pro Ala Ser Glu Glu Lys Phe Asn Lys Ile
 20 25 30

Thr Ser Val Ala Ala Val Ser Lys Arg Pro Thr Thr Leu Pro Tyr Phe
 35 40 45

Arg Ala Asp Gly Ser Pro Thr Arg Gly Phe Ala Asn Phe Ser Thr Gly
 50 55 60

Gly Ile His Gly Ala Glu Tyr Asn Glu Asp Arg Phe Asp His Asp Gln
 65 70 75 80

Asp Leu His Thr Val Ala Thr Arg Glu Phe Phe Ala Ile Leu Asp Ala
 85 90 95

Thr Leu Ala Ala Leu Tyr Ala Ala His Gln Ala Glu Pro Glu Ser Ala
 100 105 110

Asp Tyr Gln Ile Ala Gln Asp Ala Leu Ala Trp Ala Lys Asn Val Leu
 115 120 125

Ser Asp Gln Lys Leu Ile Ala Lys Ser Pro Gln Leu Tyr Asn Pro Glu
 130 135 140

Thr Gly Val Thr Tyr Glu Trp Glu Phe Val Ala Gln Ala Ala Trp Trp
 145 150 155 160

Ile Arg Asn Lys Pro Val Glu Val Ile Leu Pro Thr Gly Glu Ser Met
 165 170 175

Thr Val Lys His Lys Ser Val Leu Ala Ser Ala Ser Tyr Pro Leu Arg
 180 185 190

Asp Asn Val Ala Tyr Trp Arg Ser Glu Pro Lys Thr Pro Gln Leu Phe
 195 200 205

Pro Val Ala Lys Ser Gly Gly Ser Ser Leu Glu Lys Lys Tyr Asn Tyr
 210 215 220

Thr Ser Val Gly Thr Ala Ile His Glu Asp Phe Ser Ser Tyr Tyr Pro
 225 230 235 240

Leu Leu Leu Thr Asn Met Ala Ala Phe Thr Asn Ala Asp Leu Gly Ile
 245 250 255

Asp Glu Lys Thr Gly Arg Pro Arg Asp Arg Tyr Arg Glu Ile Tyr Glu

260 265 270

Gln Lys Glu Ile Tyr Gly Ala Gln Arg Lys Asp Pro Ser Ile Asp Glu
275 280 285

Glu Thr Lys Gln Arg Leu Gly Ile Leu Arg Glu Gly Thr Lys Leu Ile
290 295 300

Leu Asn Ser Ala Thr Gly Ala Ala Asp Ala Gly His Asp Thr Pro Ile
305 310 315 320

Leu Met Asn Asn Arg Val Ile Ala Met Arg Ile Ile Gly Gln Leu Phe
325 330 335

Ser Trp Arg Ile Gly Gln Ala Gln Ser Leu Ala Gly Ala Thr Ile Ile
340 345 350

Ser Thr Asn Thr Asp Gly Leu Tyr Ser Val Leu Asp Met Gly Thr Asn
355 360 365

Gln Arg Val Leu Asp Glu His Ala Thr Ala Ile Gly Val Gln Ile Glu
370 375 380

Pro Glu Glu Leu Asp Ile Val Ser Lys Asp Ser Asn Ser Arg Ala Glu
385 390 395 400

Phe Leu Gly Asn Gly Tyr Ile Asn Ala Ala
405 410

<210> 485
<211> 837
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(814)
<223> RXN01069

<400> 485
tcctaagctc tcttgagtc ctgagacctt ctcagcaaaa cacaaagtgc cttcacccaa 60
cctgggggtgg aggcactttc tcattgctaa ggtgtgcac gtg aac gat tta ccg 115
Val Asn Asp Leu Pro 5
1

aac cta cca aag ctg ccc ttc aac tgg aca tgg gtg ctg gca act gtt 163
Asn Leu Pro Lys Leu Pro Phe Asn Trp Thr Trp Val Leu Ala Thr Val 20
10 15

gcc acg aca gtg gtg ttg gcg ggt att ggt ttg tat gtg tat tac ccg 211
Ala Thr Thr Val Val Leu Ala Gly Ile Gly Leu Tyr Val Tyr Tyr Pro 35
25 30

tcg ttg cca gat cct atg ccg gtg cat tgg aat gga tcc ggg gag gcg 259
Ser Leu Pro Asp Pro Met Pro Val His Trp Asn Gly Ser Gly Glu Ala 50
40 45

gat aat tgg acg cct aaa tcg gtg ggt tcg ttt ctt tca ctg att ttg 307
Asp Asn Trp Thr Pro Lys Ser Val Gly Ser Phe Leu Ser Leu Ile Leu

55 60 65

ata ggg cca ggc att att ttg ctg acc ctg tgg ggt atg cag gcg ttg 355
 Ile Gly Pro Gly Ile Ile Leu Leu Thr Leu Ser Gly Met Gln Ala Leu
 70 75 80 85

ctg acc atg cag tct gga gtg atc acg caa cgc ggt ggg gcg aaa tgg 403
 Leu Thr Met Gln Ser Gly Val Ile Thr Gln Arg Gly Gly Ala Lys Ser
 90 95 100

gcg aat gaa gcg cac cgg cag tgg gaa acc tac aag gca aca agc atg 451
 Ala Asn Glu Ala His Arg Gln Trp Glu Thr Tyr Lys Ala Thr Ser Met
 105 110 115

cac atg ggt tgg tac atg ttt gtg ctc aac gct ttg att ttg gtg atg 499
 His Met Gly Trp Tyr Met Phe Val Leu Asn Ala Leu Ile Leu Val Met
 120 125 130

atc ctc aat gag ttc cgc cca aac cct ctg cct ggt gga ttt atc atc 547
 Ile Leu Asn Glu Phe Arg Pro Asn Pro Leu Pro Gly Gly Phe Ile Ile
 135 140 145

ggg ctt att gga att att gct gcc acg att gtc ctg ttg gtt ctg att 595
 Gly Leu Ile Gly Ile Ile Ala Ala Thr Ile Val Leu Leu Val Leu Ile
 150 155 160 165

gga aaa aca acc acg agt ttg gca aag aaa tac ccc atg cct gac caa 643
 Gly Lys Thr Thr Thr Ser Leu Ala Lys Lys Tyr Pro Met Pro Asp Gln
 170 175 180

gat gga aag acg tgg ggg att ttc tac aac gat ccg gac gat aat cgg 691
 Asp Gly Lys Thr Trp Gly Ile Phe Tyr Asn Asp Pro Asp Asp Asn Arg
 185 190 195

atc tta gtg gac acc ggg atg ggg atg aat tac acg ttt aac att gcc 739
 Ile Leu Val Asp Thr Gly Met Gly Met Asn Tyr Thr Phe Asn Ile Ala
 200 205 210

cat acg tgg ggc aag atc ttc gcg gtt ttg atc ttc gcg gtg cca gta 787
 His Thr Trp Gly Lys Ile Phe Ala Val Leu Ile Phe Ala Val Pro Val
 215 220 225

ctc atc gtt tta tta acc gtt ctc ctt taacctcgat ccaccgatgt 834
 Leu Ile Val Leu Leu Thr Val Leu Leu
 230 235

gcc 837

<210> 486
 <211> 238
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 486
 Val Asn Asp Leu Pro Asn Leu Pro Lys Leu Pro Phe Asn Trp Thr Trp
 1 5 10 15
 Val Leu Ala Thr Val Ala Thr Thr Val Val Leu Ala Gly Ile Gly Leu
 20 25 30

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Tyr Val Tyr Tyr Pro Ser Leu Pro Asp Pro Met Pro Val His Trp Asn
      35                      40                      45

Gly Ser Gly Glu Ala Asp Asn Trp Thr Pro Lys Ser Val Gly Ser Phe
      50                      55                      60

Leu Ser Leu Ile Leu Ile Gly Pro Gly Ile Ile Leu Leu Thr Leu Ser
      65                      70                      75                      80

Gly Met Gln Ala Leu Leu Thr Met Gln Ser Gly Val Ile Thr Gln Arg
      85                      90                      95

Gly Gly Ala Lys Ser Ala Asn Glu Ala His Arg Gln Trp Glu Thr Tyr
      100                     105                     110

Lys Ala Thr Ser Met His Met Gly Trp Tyr Met Phe Val Leu Asn Ala
      115                     120                     125

Leu Ile Leu Val Met Ile Leu Asn Glu Phe Arg Pro Asn Pro Leu Pro
      130                     135                     140

Gly Gly Phe Ile Ile Gly Leu Ile Gly Ile Ile Ala Ala Thr Ile Val
      145                     150                     155                     160

Leu Leu Val Leu Ile Gly Lys Thr Thr Thr Ser Leu Ala Lys Lys Tyr
      165                     170                     175

Pro Met Pro Asp Gln Asp Gly Lys Thr Trp Gly Ile Phe Tyr Asn Asp
      180                     185                     190

Pro Asp Asp Asn Arg Ile Leu Val Asp Thr Gly Met Gly Met Asn Tyr
      195                     200                     205

Thr Phe Asn Ile Ala His Thr Trp Gly Lys Ile Phe Ala Val Leu Ile
      210                     215                     220

Phe Ala Val Pro Val Leu Ile Val Leu Leu Thr Val Leu Leu
      225                     230                     235

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<210> 487

<211> 703

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(703)

<223> FRXA01069

<400> 487

tcctaagctc tcttgagtac ctgagacctt ctcagcaaaa cacaaagtgc cttcacccaa 60

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cctgggggtgg aggcactttc tcattgctaa ggtgtgcatc gtg aac gat tta ccg 115
              Val Asn Asp Leu Pro
              1                      5

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aac cta cca aag ctg ccc ttc aac tgg aca tgg gtg ctg gca act gtt 163
Asn Leu Pro Lys Leu Pro Phe Asn Trp Trp Val Leu Ala Thr Val
      10                      15                      20

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gcc acg aca gtg gtg ttg gcg ggt att ggt ttg tat gtg tat tac cgg 211
Ala Thr Thr Val Val Leu Ala Gly Ile Gly Leu Tyr Val Tyr Tyr Pro
25 30 35

tcg ttg cca gat cct atg ccg gtg cat tgg aat gga tcc ggg gag gcg 259
Ser Leu Pro Asp Pro Met Pro Val His Trp Asn Gly Ser Gly Glu Ala
40 45 50

gat aat tgg acg cct aaa tcg gtg ggt tcg ttt ctt tca ctg att ttg 307
Asp Asn Trp Thr Pro Lys Ser Val Gly Ser Phe Leu Ser Leu Ile Leu
55 60 65

ata ggg cca ggc att att ttg ctg acc ctg tcg ggt atg cag gcg ttg 355
Ile Gly Pro Gly Ile Ile Leu Leu Thr Leu Ser Gly Met Gln Ala Leu
70 75 80 85

ctg acc atg cag tct gga gtg atc acg caa cgc ggt ggg gcg aaa tcg 403
Leu Thr Met Gln Ser Gly Val Ile Thr Gln Arg Gly Gly Ala Lys Ser
90 95 100

gcg aat gaa gcg cac cgg cag tgg gaa acc tac aag gca aca agc atg 451
Ala Asn Glu Ala His Arg Gln Trp Glu Thr Tyr Lys Ala Thr Ser Met
105 110 115

cac atg ggt tgg tac atg ttt gtg ctc aac gct ttg att ttg gtg atg 499
His Met Gly Trp Tyr Met Phe Val Leu Asn Ala Leu Ile Leu Val Met
120 125 130

atc ctc aat gag ttc cgc cca aac cct ctg cct ggt gga ttt atc atc 547
Ile Leu Asn Glu Phe Arg Pro Asn Pro Leu Pro Gly Gly Phe Ile Ile
135 140 145

ggg ctt att gga att att gct gcc acg att gtc ctg ttg gtt ctg att 595
Gly Leu Ile Gly Ile Ile Ala Ala Thr Ile Val Leu Leu Val Leu Ile
150 155 160 165

gga aaa aca acc acg agt ttg gca aag aaa tac ccc atg cct gac caa 643
Gly Lys Thr Thr Thr Ser Leu Ala Lys Lys Tyr Pro Met Pro Asp Gln
170 175 180

gat gga aag acg tgg ggg att ttc tac aac gat ccg gac gat aat cgg 691
Asp Gly Lys Thr Trp Gly Ile Phe Tyr Asn Asp Pro Asp Asp Asn Arg
185 190 195

atc tta gtg gac 703
Ile Leu Val Asp
200

<210> 488
<211> 201
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 488
Val Asn Asp Leu Pro Asn Leu Pro Lys Leu Pro Phe Asn Trp Thr Trp
1 5 10 15
Val Leu Ala Thr Val Ala Thr Thr Val Val Leu Ala Gly Ile Gly Leu
20 25 30

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Tyr Val Tyr Tyr Pro Ser Leu Pro Asp Pro Met Pro Val His Trp Asn
      35                      40                      45
Gly Ser Gly Glu Ala Asp Asn Trp Thr Pro Lys Ser Val Gly Ser Phe
      50                      55                      60
Leu Ser Leu Ile Leu Ile Gly Pro Gly Ile Ile Leu Leu Thr Leu Ser
      65                      70                      75                      80
Gly Met Gln Ala Leu Leu Thr Met Gln Ser Gly Val Ile Thr Gln Arg
      85                      90                      95
Gly Gly Ala Lys Ser Ala Asn Glu Ala His Arg Gln Trp Glu Thr Tyr
      100                     105                     110
Lys Ala Thr Ser Met His Met Gly Trp Tyr Met Phe Val Leu Asn Ala
      115                     120                     125
Leu Ile Leu Val Met Ile Leu Asn Glu Phe Arg Pro Asn Pro Leu Pro
      130                     135                     140
Gly Gly Phe Ile Ile Gly Leu Ile Gly Ile Ile Ala Ala Thr Ile Val
      145                     150                     155                     160
Leu Leu Val Leu Ile Gly Lys Thr Thr Thr Ser Leu Ala Lys Lys Tyr
      165                     170                     175
Pro Met Pro Asp Gln Asp Gly Lys Thr Trp Gly Ile Phe Tyr Asn Asp
      180                     185                     190
Pro Asp Asp Asn Arg Ile Leu Val Asp
      195                     200

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<210> 489

<211> 2187

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2164)

<223> RXN01071

<400> 489

cacctgaatt ggctgagggga gaggcaccga ctggcaccga agaggtgctt gcctcgaagg 60

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cgggcgctga ggcgaatggc ctggagtagg ggaccagatc ttg gtc gtg gac tcc 115
                Leu Val Val Asp Ser
                1                      5

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agt ggc cgc tac aac gtc acc atc aca ggc ctg acc acc act gag acg 163
Ser Gly Arg Tyr Asn Val Thr Ile Thr Gly Leu Thr Thr Thr Glu Thr
                10                      15                      20

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aat acc ttc tcc atg att gtg gct cag cgc atg cgt gag ttc gct ctc Asn Thr Phe Ser Met Ile Val Ala Gln Arg Met Arg Glu Phe Ala Leu 120 125 130			499
ctg cga gcc ctg ggt gcg gcg cca gga cag atc act cgc tct gtg gtg Leu Arg Ala Leu Gly Ala Ala Pro Gly Gln Ile Thr Arg Ser Val Val 135 140 145			547
ctg gaa gca acc atc gtt ggc ctc ttc ggc tct gct ctt ggt gtg ctg Leu Glu Ala Thr Ile Val Gly Leu Phe Gly Ser Ala Leu Gly Val Leu 150 155 160 165			595
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acc gcg ctc gta ttg ggc acc gtt gtc acc att gtg agc gcg tgg gct Thr Ala Leu Val Leu Gly Thr Val Val Thr Ile Val Ser Ala Trp Ala 200 205 210			739
ccg gct cgt cgt gca ggt gag gtt aag cct gtt gaa gcg atg cgc aac Pro Ala Arg Arg Ala Gly Glu Val Lys Pro Val Glu Ala Met Arg Asn 215 220 225			787
atg gaa acc acc act atg cgt tcc atg atg ggg gcg acg atc acc ggt Met Glu Thr Thr Thr Met Arg Ser Met Met Gly Arg Thr Ile Thr Gly 230 235 240 245			835
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 Met Pro Val Val Gly Gly Leu Gly Lys Val Ile Gly Ala Pro Phe Gly
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agc gtt gga agc ctt gct gcg acc aac tcc aag cga aac cct cgc cgt 1075
 Ser Val Gly Ser Leu Ala Ala Thr Asn Ser Lys Arg Asn Pro Arg Arg
 310 315 320 325

acc gca act aca gcg ttc gca ctg acg ttg ggc att gcc tta gtg act 1123
 Thr Ala Thr Thr Ala Phe Ala Leu Thr Gly Ile Ala Leu Val Thr
 330 335 340

gca att ggc atg ctt tct gca acc atg aag gac gca gtc tcc gac atg 1171
 Ala Ile Gly Met Leu Ser Ala Thr Met Lys Asp Ala Val Ser Asp Met
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 Met Ala Gln Tyr Thr Ala Asp Tyr Ile Leu Gln Pro Thr Asn
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ggt tcc atc acc atg ccg aag gaa tct gtc aat gat gtt cgc gat gct 1267
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 Ala Asp Gly Asp Leu Ser Lys Val Ile Ser Thr Glu Ser Ile Asp Gly
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 Ser Leu Asp Leu Ser Asn Pro Gly Val Val Thr Asn Gln Thr Phe Ala
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gaa ggc ttt gat aag gaa caa ctg cgc acc aac ttg gaa gac gca gtc 1699
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Ala Asp Tyr Ile Val Ile Ser Val Lys Ser Ala Thr Glu Phe Ala Gly
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Glu Thr Val Ala Met Ile Asp Thr Met Met Asn Ile Leu Tyr Ala Leu
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Leu Ala Leu Ser Val Ile Val Ala Ile Ile Gly Ile Ile Asn Thr Leu
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630 635 640 645

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Ala Ala Val Ser Ile Pro Trp Gly Gln Val Gly Leu Met Leu Val Gly
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tcc gct gta gtc ggt gtt atc gcc gcg ctg tgg ccg gca gtc aag gca 2131
Ser Ala Val Val Gly Val Ile Ala Ala Leu Trp Pro Ala Val Lys Ala
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35 40 45

Val Met Leu Ser Ala Ala Asp Gly Thr Thr Pro Gln Glu Leu Val Asp
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Ala Leu Ala Ala Glu Leu Gly Ser Asn Phe Asp Val Glu Thr Gly Glu
 65 70 75 80
 Ala Leu Val Glu Gln Ala Thr Gly Met Ile Thr Gln Ala Leu Ser Phe
 85 90 95
 Val Gln Tyr Phe Leu Val Ala Phe Gly Leu Ile Ala Leu Leu Val Gly
 100 105 110
 Thr Phe Ile Ile Ala Asn Thr Phe Ser Met Ile Val Ala Gln Arg Met
 115 120 125
 Arg Glu Phe Ala Leu Leu Arg Ala Leu Gly Ala Ala Pro Gly Gln Ile
 130 135 140
 Thr Arg Ser Val Val Leu Glu Ala Thr Ile Val Gly Leu Phe Gly Ser
 145 150 155 160
 Ala Leu Gly Val Leu Gly Gly Met Gly Leu Val Ala Ile Ile Ser Ala
 165 170 175
 Val Leu Asn Asn Leu Gly Met Pro Met Gly Ser Ser Val Gly Leu Thr
 180 185 190
 Pro Ser Ala Val Val Thr Ala Leu Val Leu Gly Thr Val Val Thr Ile
 195 200 205
 Val Ser Ala Trp Ala Pro Ala Arg Arg Ala Gly Glu Val Lys Pro Val
 210 215 220
 Glu Ala Met Arg Asn Met Glu Thr Thr Thr Met Arg Ser Met Met Gly
 225 230 235 240
 Arg Thr Ile Thr Gly Gly Ile Val Leu Ala Leu Gly Ile Ile Phe Ala
 245 250 255
 Ile Ala Gly Ala Met Met Thr Asp Ser Ser Thr Ala Thr Arg Ser Ile
 260 265 270
 Leu Val Gly Ile Gly Ala Leu Phe Val Ile Val Gly Thr Phe Leu Phe
 275 280 285
 Ser Pro Ala Leu Ser Met Pro Val Val Gly Gly Leu Gly Lys Val Ile
 290 295 300
 Gly Ala Pro Phe Gly Ser Val Gly Ser Leu Ala Ala Thr Asn Ser Lys
 305 310 315 320
 Arg Asn Pro Arg Arg Thr Ala Thr Thr Ala Phe Ala Leu Thr Leu Gly
 325 330 335
 Ile Ala Leu Val Thr Ala Ile Gly Met Leu Ser Ala Thr Met Lys Asp
 340 345 350
 Ala Val Ser Asp Met Met Ala Glu Gln Tyr Thr Ala Asp Tyr Ile Leu
 355 360 365
 Gln Gly Pro Thr Asn Gly Ser Ile Thr Met Pro Lys Glu Ser Val Asn
 370 375 380
 Asp Val Arg Asp Ala Glu Gly Val Ala Asp Val Val Leu Val Ser Met

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Asn Ser Ala	Ser Val	Asn Gly	Gln Ala	Ser Tyr	Ser Gln	Leu Gly Gln
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Ser Val Thr	Phe Val	Ala Asp	Gly Asp	Leu Ser	Lys Val	Ile Ser Thr
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Glu Ser Ile	Asp Gly	Ser Leu	Asp Leu	Ser Asn	Pro Gly	Val Val Thr
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Gln Leu Glu	Ser Met	Gly Gln	Thr Ile	Gly Asp	Ile Glu	Leu Ile Gly
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Thr Phe Thr	Gly Asn	Asp Ala	Ile Gly	Asn Met	Ile Ile	Ser Glu Ser
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Ser Leu Ala	Asp Thr	Pro Ala	Ala Asp	Thr Ala	Val Pro	Gln Met Met
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Ile Leu Tyr	Ala Leu	Leu Ala	Leu Ser	Val Ile	Val Ala	Ile Ile Gly
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Ile Ile Asn	Thr Leu	Ala Leu	Asn Val	Ile Glu	Arg Arg	Gln Glu Ile
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Gly Met Leu	Arg Ala	Val Gly	Val Lys	Arg Gly	Gln Val	Arg Thr Met
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Ile Thr Leu	Glu Ser	Val Gln	Ile Ala	Ile Tyr	Gly Ala	Val Ile Gly
	610		615		620	
Ile Ala Ile	Gly Leu	Gly Leu	Gly Trp	Ala Phe	Val Thr	Val Met Ser
	625		630		635	640
Gly Glu Gly	Leu Asp	Ala Ala	Val Ser	Ile Pro	Trp Gly	Gln Val Gly
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Leu Met Leu	Val Gly	Ser Ala	Val Val	Gly Val	Ile Ala	Ala Leu Trp
	660		665		670	
Pro Ala Val	Lys Ala	Ser Arg	Thr Pro	Pro Leu	Asp Ala	Ile Thr Asp
	675		680		685	

ggc atg ccg atg qga tcc agc qtt qgc ttg act cct tct qca qtq qtt 691

Gly	Met	Pro	Met	Gly	Ser	Ser	Val	Gly	Leu	Thr	Pro	Ser	Ala	Val	Val	
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Thr	Ala	Leu	Val	Leu	Gly	Thr	Val	Val	Thr	Ile	Val	Ser	Ala	Trp	Ala	
			200				205					210				
cgc	gct	cgt	cgt	gca	ggc	gag	gtt	aag	cct	gtt	gaa	gcg	atg	cgc	aac	787
Pro	Ala	Arg	Arg	Ala	Gly	Glu	Val	Lys	Pro	Val	Glu	Ala	Met	Arg	Asn	
			215			220					225					
atg	gaa	acc	acc	act	atg	cgt	tcc	atg	atg	ggg	cgc	acg	atc	acc	ggc	835
Met	Glu	Thr	Thr	Thr	Met	Arg	Ser	Met	Met	Gly	Arg	Thr	Ile	Thr	Gly	
						235				240					245	
ggc	atc	gtt	cta	gca	ctc	ggc	atc	atc	ttt	gcg	att	gcc	ggc	gcg	atg	883
Gly	Ile	Val	Leu	Ala	Leu	Gly	Ile	Ile	Phe	Ala	Ile	Ala	Gly	Ala	Met	
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atg	act	gat	tct	tcc	acc	gct	act	cgt	tcc	atc	ctg	gtg	ggc	att	ggc	931
Met	Thr	Asp	Ser	Ser	Thr	Ala	Thr	Arg	Ser	Ile	Leu	Val	Gly	Ile	Gly	
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gca	ctg	ttt	gtc	atc	gtg	ggc	acg	ttc	ctc	ttc	tca	cca	gcg	ctc	tcc	979
Ala	Leu	Phe	Val	Ile	Val	Gly	Thr	Phe	Leu	Phe	Ser	Pro	Ala	Leu	Ser	
							285					290				
atg	cct	gtg	gtg	ggc	ctg	ggc	aag	gtt	atc	ggc	gca	ccg	ttt	ggc		1027
Met	Pro	Val	Val	Gly	Gly	Leu	Gly	Lys	Val	Ile	Gly	Ala	Pro	Phe	Gly	
						300					305					
agc	gtt	gga	agc	ctt	gct	gcg	acc	aac	tcc	aag	cga	aac	cct	cgc	cgt	1075
Ser	Val	Gly	Ser	Leu	Ala	Ala	Thr	Asn	Ser	Lys	Arg	Asn	Pro	Arg	Arg	
						315				320					325	
acc	gca	act	aca	gcg	ttc	gca	ctg	acg	ttg	ggc	att	gcc	tta	gtg	act	1123
Thr	Ala	Thr	Thr	Ala	Phe	Ala	Leu	Thr	Leu	Gly	Ile	Ala	Leu	Val	Thr	
					330				335						340	
gca	att	ggc	atg	ctt	tct	gca	acc	atg	aag	gac	gca	gtc	tcc	gac	atg	1171
Ala	Ile	Gly	Met	Leu	Ser	Ala	Thr	Met	Lys	Asp	Ala	Val	Ser	Asp	Met	
								350						355		
atg	gcg	gag	cag	tac	acc	gca	gat	tac	atc	ctg	cag	gga	cca	acc	aac	1219
Met	Ala	Glu	Gln	Tyr	Thr	Ala	Asp	Tyr	Ile	Leu	Gln	Gly	Pro	Thr	Asn	
							365					370				
ggc	tcc	atc	acc	atg	cgc	aag	gaa	tct	gtc	aat	gat	gtt	cgc	gat	gct	1267
Gly	Ser	Ile	Thr	Met	Pro	Lys	Glu	Ser	Val	Asn	Asp	Val	Arg	Asp	Ala	
							380				385					
gag	ggc	gtt	gcc	gat	gtc	gtg	ctc	gtt	tcc	atg	aac	tct	gcc	tgc	gtg	1315
Glu	Gly	Val	Ala	Asp	Val	Val	Leu	Val	Ser	Met	Asn	Ser	Ala	Ser	Val	
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aac	ggc	cag	gct	tca	tac	agc	cag	ctg	ggc	cag	tct	gta	acc	ttt	gtc	1363
Asn	Gly	Gln	Ala	Ser	Tyr	Ser	Gln	Leu	Gly	Gln	Ser	Val	Thr	Phe	Val	
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gct	gac	ggc	gac	ctg	agc	aag	gtc	atc	agc	aca	gaa	agc	att	gat	ggc	1411
Ala	Asp	Gly	Asp	Leu	Ser	Lys	Val	Ile	Ser	Thr	Glu	Ser	Ile	Asp	Gly	

	425	430	435	
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	Ser Leu Asp Leu Ser Asn Pro Gly Val Val Thr Asn Gln Thr Phe Ala			
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	gat gaa aac ggc tgg gca gta ggc gat act ctg cag ctt gaa tca atg			1507
	Asp Glu Asn Gly Trp Ala Val Gly Asp Thr Leu Gln Leu Glu Ser Met			
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	ggg cag acc atc ggc gat atc gag ttg atc ggt acc ttc acc gga aac			1555
	Gly Gln Thr Ile Gly Asp Ile Glu Leu Ile Gly Thr Phe Thr Gly Asn			
	470	475	480	485
	gac gcc atc gga aat atg atc atc tcc gaa agt tcc ttg gct gat aca			1603
	Asp Ala Ile Gly Asn Met Ile Ile Ser Glu Ser Ser Leu Ala Asp Thr			
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	cca gcg gca gac act gct gtt cct cag atg atg ctg gtg gta ggc gaa			1651
	Pro Ala Ala Asp Thr Ala Val Pro Gln Met Met Leu Val Val Gly Glu			
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	gaa ggc ttt gat aag gaa caa ctg cgc acc aac ttg gaa gac gca gtc			1699
	Glu Gly Phe Asp Lys Glu Gln Leu Arg Thr Asn Leu Glu Asp Ala Val			
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	Glu Ala Gly Tyr Leu Glu Arg Tyr Thr Asp Gly Ala Thr Val Pro Ser			
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	Val Met Leu Ser Ala Ala Asp Gly Thr Thr Pro Gln Glu Leu Val Asp			
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	Ala Leu Ala Ala Glu Leu Gly Ser Asn Phe Asp Val Glu Thr Gly Glu			
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	Ala Leu Val Glu Gln Ala Thr Gly Met Ile Thr Gln Ala Leu Ser Phe			
	85	90	95	
	Val Gln Tyr Phe Leu Val Ala Phe Gly Leu Ile Ala Leu Leu Val Gly			
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	Thr Phe Ile Ile Ala Asn Thr Phe Ser Met Ile Val Ala Gln Arg Met			
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 Ala Leu Gly Val Leu Gly Gly Met Gly Leu Val Ala Ile Ile Ser Ala
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 Val Leu Asn Asn Leu Gly Met Pro Met Gly Ser Ser Val Gly Leu Thr
 180 185 190
 Pro Ser Ala Val Val Thr Ala Leu Val Leu Gly Thr Val Val Thr Ile
 195 200 205
 Val Ser Ala Trp Ala Pro Ala Arg Arg Ala Gly Glu Val Lys Pro Val
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 Ile Ala Gly Ala Met Met Thr Asp Ser Ser Thr Ala Thr Arg Ser Ile
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 Ser Pro Ala Leu Ser Met Pro Val Val Gly Gly Leu Gly Lys Val Ile
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 Arg Asn Pro Arg Arg Thr Ala Thr Thr Ala Phe Ala Leu Thr Leu Gly
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 Gln Gly Pro Thr Asn Gly Ser Ile Thr Met Pro Lys Glu Ser Val Asn
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 385 390 395 400
 Asn Ser Ala Ser Val Asn Gly Gln Ala Ser Tyr Ser Gln Leu Gly Gln
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 Ser Val Thr Phe Val Ala Asp Gly Asp Leu Ser Lys Val Ile Ser Thr
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Thr Phe Thr Gly Asn Asp Ala Ile Gly Asn Met Ile Ile Ser Glu Ser				
	485		490	495
Ser Leu Ala Asp Thr Pro Ala Ala Asp Thr Ala Val Pro Gln Met Met				
	500		505	510
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Ile Gly Met Leu Arg Ala Val Gly Val Lys Arg Gly Gln Val Arg Thr	
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85 90 95	

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Gly Leu Met Leu Val Gly Ser Ala Val Val Gly Val Ile Ala Ala Leu	
100 105 110	

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Trp Pro Ala Val Lys Ala Ser Arg Thr Pro Pro Leu Asp Ala Ile Thr	
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Ile Gly Met Leu Arg Ala Val Gly Val Lys Arg Gly Gln Val Arg Thr
35 40 45
Met Ile Thr Leu Glu Ser Val Gln Ile Ala Ile Tyr Gly Ala Val Ile
50 55 60
Gly Ile Ala Ile Gly Leu Gly Leu Gly Trp Ala Phe Val Thr Val Met
65 70 75 80
Ser Gly Glu Gly Leu Asp Ala Ala Val Ser Ile Pro Trp Gly Gln Val
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Met Asp Asn Pro Val
1 5
aac atc ctc aat gag cag gaa gct ttg gag cgc ctg cag tcg gtg tct 163
Asn Ile Leu Asn Glu Gln Glu Ala Leu Glu Arg Leu Gln Ser Val Ser
10 15 20
ctt ggt cgc gtg gtg gtt cgt cgc agc gat gag atg gac att ttc ccg 211

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Leu Gly Arg Val Val Val Arg Arg Ser Asp Glu Met Asp Ile Phe Pro
      25                      30                      35

gtg aac ttc att gtg gat aag ggc gca att tac att cgt aca gct gag 259
Val Asn Phe Ile Val Asp Lys Gly Ala Ile Tyr Ile Arg Thr Ala Glu
      40                      45                      50

ggc aac aag ttg ttc agc atg aat ctc aac cac gat gtg ctc ttt gaa 307
Gly Asn Lys Leu Phe Ser Met Asn Leu Asn His Asp Val Leu Phe Glu
      55                      60                      65

gcc gat gag gtc aag gac gga aag gcc tgg tcc gtg gtg gtt cgt gcg 355
Ala Asp Glu Val Lys Asp Gly Lys Ala Trp Ser Val Val Val Arg Ala
      70                      75                      80                      85

acc gca gag att gtg cgc aag ctg gat gag atc gct act gcc gac act 403
Thr Ala Glu Ile Val Arg Lys Leu Asp Glu Ile Ala Thr Ala Asp Thr
      90                      95                      100

ttg gag ttg aag cct tgg att cca acc ctg aag tcc aac ttt gcc cgt 451
Leu Glu Leu Lys Pro Trp Ile Pro Thr Leu Lys Ser Asn Phe Ala Arg
      105                      110                      115

att gtt ccg aat gaa atc act ggg cgg gag ttc acc ctc gcc gag gag 499
Ile Val Pro Asn Glu Ile Thr Gly Arg Glu Phe Thr Leu Gly Glu Glu
      120                      125                      130

cct gag cgc tac tagctttgcc acatttcaact aaa 534
Pro Glu Arg Tyr
      135

<210> 496
<211> 137
<212> PRT
<213> Corynebacterium glutamicum

<400> 496
Met Asp Asn Pro Val Asn Ile Leu Asn Glu Gln Glu Ala Leu Glu Arg
  1          5          10          15

Leu Gln Ser Val Ser Leu Gly Arg Val Val Val Arg Arg Ser Asp Glu
      20          25          30

Met Asp Ile Phe Pro Val Asn Phe Ile Val Asp Lys Gly Ala Ile Tyr
      35          40          45

Ile Arg Thr Ala Glu Gly Asn Lys Leu Phe Ser Met Asn Leu Asn His
      50          55          60

Asp Val Leu Phe Glu Ala Asp Glu Val Lys Asp Gly Lys Ala Trp Ser
      65          70          75          80

Val Val Val Arg Ala Thr Ala Glu Ile Val Arg Lys Leu Asp Glu Ile
      85          90          95

Ala Thr Ala Asp Thr Leu Glu Leu Lys Pro Trp Ile Pro Thr Leu Lys
      100          105          110

Ser Asn Phe Ala Arg Ile Val Pro Asn Glu Ile Thr Gly Arg Glu Phe
      115          120          125

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Thr Leu Gly Glu Glu Pro Glu Arg Tyr
130 135

<210> 497

<211> 534

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(511)

<223> FRXA01075

<400> 497

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atattctttt tttcttttag ttgtgggagt ggagataact atg gac aat cca gtc 115
Met Asp Asn Pro Val
1 5

aac atc ctc aat gag cag gaa gct ttg gag cgc ctg cag tcg gtg tct 163
Asn Ile Leu Asn Glu Gln Glu Ala Leu Glu Arg Leu Gln Ser Val Ser
10 15 20

ctt ggt cgc gtg gtg gtt cgt cgc agc gat gag atg gac att ttc ccg 211
Leu Gly Arg Val Val Val Arg Arg Ser Asp Glu Met Asp Ile Phe Pro
25 30 35

gtg aac ttc att gtg gat aag ggc gca att tac att cgt aca gct gag 259
Val Asn Phe Ile Val Asp Lys Gly Ala Ile Tyr Ile Arg Thr Ala Glu
40 45 50

ggc aac aag ttg ttc agc atg aat ctc aac cac gat gtg ctc ttt gaa 307
Gly Asn Lys Leu Phe Ser Met Asn Leu Asn His Asp Val Leu Phe Glu
55 60 65

gcc gat gag gtc aag gac gga aag gcc tgg tcc gtg gtg gtt cgt gcg 355
Ala Asp Glu Val Lys Asp Gly Lys Ala Trp Ser Val Val Val Arg Ala
70 75 80 85

acc gca gag att gtg cgc aag ctg gat gag atc gct act gcc gac act 403
Thr Ala Glu Ile Val Arg Lys Leu Asp Glu Ile Ala Thr Ala Asp Thr
90 95 100

ttg gag ttg aag cct tgg att cca acc ctg aag tcc aac ttt gcc cgt 451
Leu Glu Leu Lys Pro Trp Ile Pro Thr Leu Lys Ser Asn Phe Ala Arg
105 110 115

att gtt ccg aat gaa atc act ggg cgg gag ttc acc ctc gcc gag gag 499
Ile Val Pro Asn Glu Ile Thr Gly Arg Glu Phe Thr Leu Gly Glu Glu
120 125 130

cct gag cgc tac tagctttgcc acatttcact aaa 534
Pro Glu Arg Tyr
135

<210> 498

<211> 137

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 498

Met Asp Asn Pro Val Asn Ile Leu Asn Glu Gln Glu Ala Leu Glu Arg
 1 5 10 15

Leu Gln Ser Val Ser Leu Gly Arg Val Val Val Arg Arg Ser Asp Glu
 20 25 30

Met Asp Ile Phe Pro Val Asn Phe Ile Val Asp Lys Gly Ala Ile Tyr
 35 40 45

Ile Arg Thr Ala Glu Gly Asn Lys Leu Phe Ser Met Asn Leu Asn His
 50 55 60

Asp Val Leu Phe Glu Ala Asp Glu Val Lys Asp Gly Lys Ala Trp Ser
 65 70 75 80

Val Val Val Arg Ala Thr Ala Glu Ile Val Arg Lys Leu Asp Glu Ile
 85 90 95

Ala Thr Ala Asp Thr Leu Glu Leu Lys Pro Trp Ile Pro Thr Leu Lys
 100 105 110

Ser Asn Phe Ala Arg Ile Val Pro Asn Glu Ile Thr Gly Arg Glu Phe
 115 120 125

Thr Leu Gly Glu Glu Pro Glu Arg Tyr
 130 135

<210> 499

<211> 1137

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1114)

<223> RXN01128

<400> 499

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tattgcttta gcgaaagtaa cttccatgca tcaacgttcg atg agc ttc act ttc 115
 Met Ser Phe Thr Phe
 1 5

att cgt act ttt ttc gta ctt ttt ggc atc acg ttg tta gtg tca tgc 163
 Ile Arg Thr Phe Phe Val Leu Phe Gly Ile Thr Leu Leu Val Ser Cys
 10 15 20

gtt cca gag cct cct gac tcc tac act aaa gaa tcc act gtg ctg cgg 211
 Val Pro Glu Pro Pro Asp Ser Tyr Thr Lys Glu Ser Thr Val Leu Arg
 25 30 35

tat cag gtc tct gat ttc aat cta aac ttc gtg gaa tta gca gtt gcg 259
 Tyr Gln Val Ser Asp Phe Asn Leu Asn Phe Val Glu Leu Ala Val Ala
 40 45 50

ctt ggg tat ttg aac aac att gag ctc caa gta gtc gga tct gta caa 307
 Leu Gly Tyr Leu Asn Asn Ile Glu Leu Gln Val Val Gly Ser Val Gln
 55 60 65

ggc ggc gtt gag tcc att gaa tcg ctc aaa aag gat gac att gac ttc 355
 Gly Gly Val Glu Ser Ile Glu Ser Leu Lys Lys Asp Asp Ile Asp Phe
 70 75 80 85

gcg gca gtc ccc ttc att ggc ctt gtt gca gga gag ata gcc acc ggt 403
 Ala Ala Val Pro Phe Ile Gly Leu Val Ala Gly Glu Ile Ala Thr Gly
 90 95 100

gcg ccc atc aaa gca gtg gcc gca agt tac gga att tcc cac gat tct 451
 Ala Pro Ile Lys Ala Val Ala Ala Ser Tyr Gly Ile Ser His Asp Ser
 105 110 115

tct tct gca ctt cta gtc ctt aaa agt gag ata cac gaa gtg cac 499
 Ser Ser Ala Leu Leu Val Leu Lys Asp Ser Glu Ile His Glu Val His
 120 125 130

gat ctc att ggc aaa aca gtt ggc ata aac acc ctc ggt gct ctg gga 547
 Asp Leu Ile Gly Lys Thr Val Gly Ile Asn Thr Thr Gly Ala Leu Gly
 135 140 145

tct gcg atg gtt gag cgt cat cta ttc gac gcc ggt ctc acc gaa cct 595
 Ser Ala Met Val Glu Arg His Leu Phe Asp Ala Gly Leu Thr Glu Pro
 150 155 160 165

gag atc gtg agc gtc act caa cgt gca tta ccc ggt gag tac tta gaa 643
 Glu Ile Val Ser Val Thr Gln Arg Ala Leu Pro Gly Glu Tyr Leu Glu
 170 175 180

caa cgc ctc tac cag ggg caa gtt gat gca att tgg gtc acc gat agc 691
 Gln Arg Leu Tyr Gln Gly Gln Val Asp Ala Ile Trp Val Thr Asp Ser
 185 190 195

gct aaa cac caa gcg ctt gaa act gga gat ttt cgg atc ttg gca gag 739
 Ala Lys His Gln Ala Leu Glu Thr Gly Asp Phe Arg Ile Leu Ala Glu
 200 205 210

gat tca gac ctt gtg cag gaa ctc aac act ggc tgc atg gtg gtg tgc 787
 Asp Ser Asp Leu Val Gln Glu Leu Asn Thr Gly Cys Met Val Val Ser
 215 220 225

caa aaa ctc atc gac gag cac ccc gca gtg gtt gga gaa tta gtg gat 835
 Gln Lys Leu Ile Asp Glu His Pro Ala Val Val Gly Glu Leu Val Asp
 230 235 240 245

gga gta gct cag gca atc gag ttt gaa cga tcc cac tcc cct gaa gaa 883
 Gly Val Ala Gln Ala Ile Glu Phe Glu Arg Ser His Ser Pro Glu Glu
 250 255 260

gtg cgc gaa gtt tat ttc aac tac ctc gaa gcc cat ggt cag agt gat 931
 Val Arg Glu Val Tyr Phe Asn Tyr Leu Glu Ala His Gly Gln Ser Asp
 265 270 275

aga ata tcc agc ttt aga tat tgg gag cat tcg ggc atc gca acc cga 979
 Arg Ile Ser Ser Phe Arg Tyr Trp Glu His Ser Gly Ile Ala Thr Arg
 280 285 290

ggt gga gtg ctc agt gat agg gag ttc agc atg tgg tcc cac tgg att 1027

Gly Gly Val Leu Ser Asp Arg Glu Phe Ser Met Trp Ser His Trp Ile
 295 300 305
 gac cgc caa tac gac gtc ccc gat atc aat cca gca agt att tac acc 1075
 Asp Arg Gln Tyr Asp Val Pro Asp Ile Asn Pro Ala Ser Ile Tyr Thr
 310 315 320 325
 aac caa ttc aac cca tac cga aaa gta aac ccc tcg cca taaaaggcaa 1124
 Asn Gln Phe Asn Pro Tyr Arg Lys Val Asn Pro Ser Pro
 330 335
 gggggctcggc gtt 1137

<210> 500
 <211> 338
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 500
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 20 25 30
 Ser Thr Val Leu Arg Tyr Gln Val Ser Asp Phe Asn Leu Asn Phe Val
 35 40 45
 Glu Leu Ala Val Ala Leu Gly Tyr Leu Asn Asn Ile Glu Leu Gln Val
 50 55 60
 Val Gly Ser Val Gln Gly Gly Val Glu Ser Ile Glu Ser Leu Lys Lys
 65 70 75 80
 Asp Asp Ile Asp Phe Ala Ala Val Pro Phe Ile Gly Leu Val Ala Gly
 85 90 95
 Glu Ile Ala Thr Gly Ala Pro Ile Lys Ala Val Ala Ala Ser Tyr Gly
 100 105 110
 Ile Ser His Asp Ser Ser Ser Ala Leu Leu Val Leu Lys Asp Ser Glu
 115 120 125
 Ile His Glu Val His Asp Leu Ile Gly Lys Thr Val Gly Ile Asn Thr
 130 135 140
 Leu Gly Ala Leu Gly Ser Ala Met Val Glu Arg His Leu Phe Asp Ala
 145 150 155 160
 Gly Leu Thr Glu Pro Glu Ile Val Ser Val Thr Gln Arg Ala Leu Pro
 165 170 175
 Gly Glu Tyr Leu Glu Gln Arg Leu Tyr Gln Gly Gln Val Asp Ala Ile
 180 185 190
 Trp Val Thr Asp Ser Ala Lys His Gln Ala Leu Glu Thr Gly Asp Phe
 195 200 205
 Arg Ile Leu Ala Glu Asp Ser Asp Leu Val Gln Glu Leu Asn Thr Gly
 210 215 220

Cys Met Val Val Ser Gln Lys Leu Ile Asp Glu His Pro Ala Val Val
 225 230 235 240
 Gly Glu Leu Val Asp Gly Val Ala Gln Ala Ile Glu Phe Glu Arg Ser
 245 250 255
 His Ser Pro Glu Glu Val Arg Glu Val Tyr Phe Asn Tyr Leu Glu Ala
 260 265 270
 His Gly Gln Ser Asp Arg Ile Ser Ser Phe Arg Tyr Trp Glu His Ser
 275 280 285
 Gly Ile Ala Thr Arg Gly Gly Val Leu Ser Asp Arg Glu Phe Ser Met
 290 295 300
 Trp Ser His Trp Ile Asp Arg Gln Tyr Asp Val Pro Asp Ile Asn Pro
 305 310 315 320
 Ala Ser Ile Tyr Thr Asn Gln Phe Asn Pro Tyr Arg Lys Val Asn Pro
 325 330 335

Ser Pro

<210> 501
 <211> 1137
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1114)
 <223> FRXA01128

<400> 501
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 Met Ser Phe Thr Phe
 1 5
 att cgt act ttt ttc gta ctt ttt ggc atc acg ttg tta gtg tca tgc 163
 Ile Arg Thr Phe Phe Val Leu Phe Gly Ile Thr Leu Leu Val Ser Cys
 10 15 20
 gtt cca gag cct cct gac tcc tac act aaa gaa tcc act gtg ctg cgg 211
 Val Pro Glu Val Pro Asp Ser Tyr Thr Lys Glu Ser Thr Val Leu Arg
 25 30 35
 tat cag gtc tct gat ttc aat cta aac ttc gtg gaa tta gca gtt gcg 259
 Tyr Gln Val Ser Asp Phe Asn Leu Asn Phe Val Glu Leu Ala Val Ala
 40 45 50
 ctt ggg tat ttg aac aac att gag ctc caa gta gtc gga tct gta caa 307
 Leu Gly Tyr Leu Asn Asn Ile Glu Leu Gln Val Val Gly Ser Val Gln
 55 60 65
 ggc ggc gtt gag tcc att gaa tgc ctc aaa aag gat gac att gac ttc 355
 Gly Gly Val Glu Ser Ile Glu Ser Leu Lys Lys Asp Asp Ile Asp Phe

70	75	80	85	
gcg gca gtc ccc ttc att ggc ctt gtt gca gga gag ata gcc acc ggt				403
Ala Ala Val Pro Phe	Ile Gly Leu Val	Ala Gly Glu Ile	Ala Thr Gly	
	90	95	100	
gcg ccc atc aaa gca gtg gcc gca agt tac gga att tcc cac gat tct				451
Ala Pro Ile Lys	Ala Val Ala Ala	Ser Tyr Gly Ile	Ser His Asp Ser	
	105	110	115	
tct tct gca ctt cta gtc ctt aaa gac agt gag ata cac gaa gtg cac				499
Ser Ser Ala Leu	Leu Val Leu Lys	Asp Ser Glu Ile	His Glu Val His	
	120	125	130	
gat ctc att ggc aaa aca gtt ggc ata aac acc ctc ggt gct ctg gga				547
Asp Leu Ile Gly Lys Thr	Val Gly Ile Asn Thr	Leu Gly Ala Leu Gly		
	135	140	145	
tct gcg atg gtt gag cgt cat cta ttc gac gcc ggt ctc acc gaa cct				595
Ser Ala Met Val Glu Arg	His Leu Phe Asp	Ala Gly Leu Thr	Glu Pro	
	155	160	165	
gag atc gtg agc gtc act caa cgt gca tta ccc ggt gag tac tta gaa				643
Glu Ile Val Ser	Val Thr Gln Arg	Ala Leu Pro Gly	Glu Tyr Leu Glu	
	170	175	180	
caa cgc ctc tac cag ggg caa gtt gat gca att tgg gtc acc gat agc				691
Gln Arg Leu Tyr	Gln Gly Gln Val Asp	Ala Ile Trp Val	Thr Asp Ser	
	185	190	195	
gct aaa cac caa gcg ctt gaa act gga gat ttt cgg atc ttg gca gag				739
Ala Lys His Gln Ala Leu Glu Thr	Gly Asp Phe Arg	Ile Leu Ala Glu		
	200	205	210	
gat tca gac ctt gtg cag gaa ctc aac act ggc tgc atg gtg gtg tgc				787
Asp Ser Asp Leu Val Gln Glu Leu Asn Thr	Gly Cys Met Val Val Ser			
	215	220	225	
caa aaa ctc atc gac gag cac ccc gca gtg gtt gga gaa tta gtg gat				835
Gln Lys Leu Ile Asp Glu His Pro Ala Val Val	Gly Glu Leu Val Asp			
	235	240	245	
gga gta gct cag gca atc gag ttt gaa cga tcc cac tcc cct gaa gaa				883
Gly Val Ala Gln Ala Ile Glu Phe Glu Arg Ser His Ser Pro Glu Glu				
	250	255	260	
gtg cgc gaa gtt tat ttc aac tac ctc gaa gcc cat ggt cag agt gat				931
Val Arg Glu Val Tyr Phe Asn Tyr Leu Glu Ala His Gly Gln Ser Asp				
	265	270	275	
aga ata tcc agc ttt aga tat tgg gag cat tog ggc atc gca acc cga				979
Arg Ile Ser Ser Phe Arg Tyr Trp Glu His Ser Gly Ile Ala Thr Arg				
	280	285	290	
ggt gga gtg ctc agt gat agg gag ttc agc atg tgg tcc cac tgg att				1027
Gly Gly Val Leu Ser Asp Arg Glu Phe Ser Met Trp Ser His Trp Ile				
	295	300	305	
gac cgc caa tac gac gtc ccc gat atc aat cca gca agt att tac acc				1075
Asp Arg Gln Tyr Asp Val Pro Asp Ile Asn Pro Ala Ser Ile Tyr Thr				
	315	320	325	

aac caa ttc aac cca tac cga aaa gta aac ccc tcg cca taaaaggcaa 1124
 Asn Gln Phe Asn Pro Tyr Arg Lys Val Asn Pro Ser Pro
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gggggtcggc gtt 1137

<210> 502

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 502

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 20 25 30

Ser Thr Val Leu Arg Tyr Gln Val Ser Asp Phe Asn Leu Asn Phe Val
 35 40 45

Glu Leu Ala Val Ala Leu Gly Tyr Leu Asn Asn Ile Glu Leu Gln Val
 50 55 60

Val Gly Ser Val Gln Gly Gly Val Glu Ser Ile Glu Ser Leu Lys Lys
 65 70 75 80

Asp Asp Ile Asp Phe Ala Ala Val Pro Phe Ile Gly Leu Val Ala Gly
 85 90 95

Glu Ile Ala Thr Gly Ala Pro Ile Lys Ala Val Ala Ala Ser Tyr Gly
 100 105 110

Ile Ser His Asp Ser Ser Ser Ala Leu Leu Val Leu Lys Asp Ser Glu
 115 120 125

Ile His Glu Val His Asp Leu Ile Gly Lys Thr Val Gly Ile Asn Thr
 130 135 140

Leu Gly Ala Leu Gly Ser Ala Met Val Glu Arg His Leu Phe Asp Ala
 145 150 155 160

Gly Leu Thr Glu Pro Glu Ile Val Ser Val Thr Gln Arg Ala Leu Pro
 165 170 175

Gly Glu Tyr Leu Glu Gln Arg Leu Tyr Gln Gly Gln Val Asp Ala Ile
 180 185 190

Trp Val Thr Asp Ser Ala Lys His Gln Ala Leu Glu Thr Gly Asp Phe
 195 200 205

Arg Ile Leu Ala Glu Asp Ser Asp Leu Val Gln Glu Leu Asn Thr Gly
 210 215 220

Cys Met Val Val Ser Gln Lys Leu Ile Asp Glu His Pro Ala Val Val
 225 230 235 240

Gly Glu Leu Val Asp Gly Val Ala Gln Ala Ile Glu Phe Glu Arg Ser
 245 250 255

His Ser Pro Glu Glu Val Arg Glu Val Tyr Phe Asn Tyr Leu Glu Ala
260 265 270

His Gly Gln Ser Asp Arg Ile Ser Phe Arg Tyr Trp Glu His Ser
275 280 285

Gly Ile Ala Thr Arg Gly Gly Val Leu Ser Asp Arg Glu Phe Ser Met
290 295 300

Trp Ser His Trp Ile Asp Arg Gln Tyr Asp Val Pro Asp Ile Asn Pro
305 310 315 320

Ala Ser Ile Tyr Thr Asn Gln Phe Asn Pro Tyr Arg Lys Val Asn Pro
325 330 335

Ser Pro

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<210> 503
<211> 871
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(871)
<223> RXN01134
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4400> 503																		
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ttcgaagagg cggtgaatt cctgcgtcag cgatgcattt																		115
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gtt cca tac acc gcg cag att gtt cca ctg gcc gtg atc ctc acc ctg																		163
<div style="display: flex; justify-content: space-between;"> <div>Val Pro Tyr Thr Ala Gln Ile Val Pro Leu Ala Val Ile Leu Thr Leu</div> </div> <div style="display: flex; justify-content: space-between;"> <div>10</div> <div>15</div> <div>20</div> </div>																		
ctt gat gca gaa gaa atg gcc acc gca cgt tca tgg gat cgt ttg aat																		211
<div style="display: flex; justify-content: space-between;"> <div>Leu Asp Ala Glu Glu Met Ala Thr Ala Arg Ser Trp Asp Arg Leu Asn</div> </div> <div style="display: flex; justify-content: space-between;"> <div>25</div> <div>30</div> <div>35</div> </div>																		
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<div style="display: flex; justify-content: space-between;"> <div>Gln Trp Phe Trp Ser Gly Val Leu Gly Glu Leu Tyr Gly Ser Pro Ala</div> </div> <div style="display: flex; justify-content: space-between;"> <div>40</div> <div>45</div> <div>50</div> </div>																		
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<div style="display: flex; justify-content: space-between;"> <div>Val Ile Ala Arg Ser Gly Arg Asp Thr Asp Gln Val Ala Ala Trp Ile</div> </div> <div style="display: flex; justify-content: space-between;"> <div>55</div> <div>60</div> <div>65</div> </div>																		
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<div style="display: flex; justify-content: space-between;"> <div>Arg Glu Gly Ala Gly Glu Thr Ala Val Val Pro Lys Thr Ile Arg Asp</div> </div> <div style="display: flex; justify-content: space-between;"> <div>70</div> <div>75</div> <div>80</div> <div>85</div> </div>																		
acc gtt ttc cac gaa tca cgt ctt ctc agt gca acc caa gac acc gga																		403
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gtg tgg aag ggt atc ttc gca ctg ctc atg ggc agg gga gca cgc gac 451
Val Trp Lys Gly Ile Phe Ala Leu Leu Met Gly Arg Gly Ala Arg Asp
105 110 115

tgg cgc acc gga cag cag ttt gat cgc tgg act ttt gat gag ctg ggt 499
Trp Arg Thr Gly Gln Gln Phe Asp Arg Trp Thr Phe Asp Glu Leu Gly
120 125 130

tgc aat ttc cac cag att ttc ccc acc aaa tgg tgc aag gaa cgc ggc 547
Cys Asn Phe His Gln Ile Phe Pro Thr Lys Trp Cys Lys Glu Arg Gly
135 140 145

atc gat cct gtc ctt acg gaa tca gta ctg aac cgc acc ccg atg ggt 595
Ile Asp Pro Val Leu Thr Glu Ser Val Leu Asn Arg Thr Pro Met Gly
150 155 160 165

cgc cgt acc gaa gta gtc atc ggc gat acc cct cca tcc cgc tac ctg 643
Arg Arg Thr Glu Val Ile Gly Asp Thr Pro Pro Ser Arg Tyr Leu
170 175 180

tct cgt gtt caa tcc aag tcg ctc atg ggt gat gag gaa ttc gat cag 691
Ser Arg Val Gln Ser Lys Ser Leu Met Gly Asp Glu Glu Phe Asp Gln
185 190 195

atg ctg gat acc cac ctg ctc agc gcg gaa gac ctg cac agt tcc aac 739
Met Leu Asp Thr His Leu Leu Ser Ala Glu Asp Leu His Ser Ser Asn
200 205 210

acc acg cac ttc ttt gct tct cga cgc acc aac ttc atc gac atg gtc 787
Thr Thr His Phe Phe Ala Ser Arg Arg Thr Asn Phe Ile Asp Met Val
215 220 225

gag gat gcc atc ggt aaa gcg gtg atc agg gac gtc aac gag tca gat 835
Glu Asp Ala Ile Gly Lys Ala Val Ile Arg Asp Val Asn Glu Ser Asp
230 235 240 245

ctc acc ggt gga cac gat ggt ccc tcg gta cac ggg 871
Leu Thr Gly Gly His Asp Gly Pro Ser Val His Gly
250 255

<210> 504
<211> 257
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 504
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Val Ile Leu Thr Leu Leu Asp Ala Glu Glu Met Ala Thr Ala Arg Ser
20 25 30

Trp Asp Arg Leu Asn Gln Trp Phe Trp Ser Gly Val Leu Gly Glu Leu
35 40 45

Tyr Gly Ser Pro Ala Val Ile Ala Arg Ser Gly Arg Asp Thr Asp Gln
50 55 60

Val Ala Ala Trp Ile Arg Glu Gly Ala Gly Glu Thr Ala Val Val Pro
65 70 75 80

Lys Thr Ile Arg Asp Thr Val Phe His Glu Ser Arg Leu Leu Ser Ala
85 95

Thr Gln Asp Thr Gly Val Trp Lys Gly Ile Phe Ala Leu Leu Met Gly
100 105 110

Arg Gly Ala Arg Asp Trp Arg Thr Gly Gln Gln Phe Asp Arg Trp Thr
115 120 125

Phe Asp Glu Leu Gly Cys Asn Phe His Gln Ile Phe Pro Thr Lys Trp
130 135 140

Cys Lys Glu Arg Gly Ile Asp Pro Val Leu Thr Glu Ser Val Leu Asn
145 150 155 160

Arg Thr Pro Met Gly Arg Arg Thr Glu Val Val Ile Gly Asp Thr Pro
165 170 175

Pro Ser Arg Tyr Leu Ser Arg Val Gln Ser Lys Ser Leu Met Gly Asp
180 185 190

Glu Glu Phe Asp Gln Met Leu Asp Thr His Leu Leu Ser Ala Glu Asp
195 200 205

Leu His Ser Ser Asn Thr Thr His Phe Phe Ala Ser Arg Arg Thr Asn
210 215 220

Phe Ile Asp Met Val Glu Asp Ala Ile Gly Lys Ala Val Ile Arg Asp
225 230 235 240

Val Asn Glu Ser Asp Leu Thr Gly Gly His Asp Gly Pro Ser Val His
245 250 255

Gly

<210> 505

<211> 459

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(459)

<223> FRXA01134

<400> 505

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Ser Ala Thr Gln Asp Thr Gly Val Trp Lys Gly Ile Phe Ala Leu Leu
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atg ggc agg gga gca cgc gac tgg cgc acc gga cag cag ttt gat cgc 96
Met Gly Arg Gly Ala Arg Asp Trp Arg Thr Gly Gln Gln Phe Asp Arg
20 25 30

tgg act ttt gat gag ctg ggt tgc aat ttc cac cag att ttc ccc acc 144
Trp Thr Phe Asp Glu Leu Gly Cys Asn Phe His Gln Ile Phe Pro Thr
35 40 45


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aaa tgg tgc aag gaa cgc ggc atc gat cct gtc ctt acg gaa tca gta 192
Lys Trp Cys Lys Glu Arg Gly Ile Asp Pro Val Leu Thr Glu Ser Val
50 55 60

ctg aac cgc acc ccg atg ggt cgc cgt acc gaa gta gtc atc ggc gat 240
Leu Asn Arg Thr Pro Met Gly Arg Arg Thr Glu Val Val Ile Gly Asp
65 70 75 80

acc cct cca tcc cgc tac ctg tct cgt gtt caa tcc aag tcg ctc atg 288
Thr Pro Pro Ser Arg Tyr Leu Ser Arg Val Gln Ser Lys Ser Leu Met
85 90 95

ggg gat gag gaa ttc gat cag atg ctg gat acc cac ctg ctc agc gcg 336
Gly Asp Glu Glu Phe Asp Gln Met Leu Asp Thr His Leu Leu Ser Ala
100 105 110

gaa gac ctg cac agt tcc aac acc acg cac ttc ttt gct tct cga cgc 384
Glu Asp Leu His Ser Ser Asn Thr Thr His Phe Phe Ala Ser Arg Arg
115 120 125

acc aac ttc atc gac atg gtc gag gat gcc atc ggt aaa gcg gtg atc 432
Thr Asn Phe Ile Asp Met Val Glu Asp Ala Ile Gly Lys Ala Val Ile
130 135 140

agg gac gtc aac gag tca gat ctc acc 459
Arg Asp Val Asn Glu Ser Asp Leu Thr
145 150

<210> 506
<211> 153
<212> PRT
<213> Corynebacterium glutamicum

<400> 506
Ser Ala Thr Gln Asp Thr Gly Val Trp Lys Gly Ile Phe Ala Leu Leu
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Met Gly Arg Gly Ala Arg Asp Trp Arg Thr Gly Gln Gln Phe Asp Arg
20 25 30

Trp Thr Phe Asp Glu Leu Gly Cys Asn Phe His Gln Ile Phe Pro Thr
35 40 45

Lys Trp Cys Lys Glu Arg Gly Ile Asp Pro Val Leu Thr Glu Ser Val
50 55 60

Leu Asn Arg Thr Pro Met Gly Arg Arg Thr Glu Val Val Ile Gly Asp
65 70 75 80

Thr Pro Pro Ser Arg Tyr Leu Ser Arg Val Gln Ser Lys Ser Leu Met
85 90 95

Gly Asp Glu Glu Phe Asp Gln Met Leu Asp Thr His Leu Leu Ser Ala
100 105 110

Glu Asp Leu His Ser Ser Asn Thr Thr His Phe Phe Ala Ser Arg Arg
115 120 125

Thr Asn Phe Ile Asp Met Val Glu Asp Ala Ile Gly Lys Ala Val Ile
130 135 140

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Arg Asp Val Asn Glu Ser Asp Leu Thr
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<210> 507

<211> 1056

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1033)

<223> RXN01140

<400> 507

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tataaccact gttcttcgtg gttttccagt aggtgtgctg atg gca cta gac acc 115
Met Ala Leu Asp Thr
1 5

cgc ggc gag gaa atg cgt ttc cgg cca cgc gcg ctg tcc ggc gcc cca 163
Arg Gly Glu Glu Met Arg Phe Arg Pro Arg Ala Leu Ser Gly Ala Pro
10 15 20

gat acg ggc aag gat cca ggt ctt ttg ctt ctc gac gga caa cag cgc 211
Asp Thr Gly Lys Asp Pro Gly Leu Leu Leu Asp Gly Gln Gln Arg
25 30 35

ctc acc acc ctt tat cat tgc ttc agt ggc gat ggc tat gta aat acg 259
Leu Thr Thr Leu Tyr His Cys Phe Ser Gly Asp Gly Tyr Val Asn Thr
40 45 50

gtg gac ttc cga tca aag aaa gtg acc cgg aag ttt tat att gat gtt 307
Val Asp Phe Arg Ser Lys Lys Val Thr Arg Lys Phe Tyr Ile Asp Val
55 60 65

gct aag gct gtt gaa tct cgg gtc atg tcc gat gag gct att ttt tca 355
Ala Lys Ala Val Glu Ser Pro Val Met Ser Asp Glu Ala Ile Phe Ser
70 75 80 85

gtc gac gaa acc ggc aaa atc atc tcc cac ttc ggt cca gtg atc gac 403
Val Asp Glu Thr Gly Lys Ile Ile Ser His Phe Gly Pro Val Ile Asp
90 95 100

ggc ggc atc acc gat tta gaa aca gca ctt gct cat ggt tgc ctt cca 451
Gly Gly Ile Thr Asp Leu Glu Thr Ala Leu Ala His Gly Cys Leu Pro
105 110 115

gtt tct gtg ctg ctg gat gat aac ggc act gat ttc ctc ttt gac ctc 499
Val Ser Val Leu Leu Asp Asp Asn Gly Thr Asp Phe Leu Phe Asp Leu
120 125 130

gcc gat atg gca gga gaa ggc gct cgc gaa cac gcg aag cgc ttc caa 547
Ala Asp Met Ala Gly Glu Gly Ala Arg Glu His Ala Lys Arg Phe Gln
135 140 145

tca caa atc gtt aag acc tta gtt agt tac gac atc cca atg atc cga 595
Ser Gln Ile Val Lys Thr Leu Val Ser Tyr Asp Ile Pro Met Ile Arg
150 155 160 165

ctg gat cgt gaa acc gcc aag ggt gga att ggt tcc atc ttt gct cag 643
 Leu Asp Arg Glu Thr Ala Lys Gly Gly Ile Gly Ser Ile Phe Ala Gln
 170 175 180

gcc aat agc tct ggc ttg cag atg gat gtc ttt gat ttg ctc acc gcg 691
 Ala Asn Ser Ser Gly Leu Gln Met Asp Val Phe Asp Leu Leu Thr Ala
 185 190 195

gtg ttc gca gcc gat gaa tcg gtg gag acc gaa ttc tca ctg cgt gat 739
 Val Phe Ala Ala Asp Glu Ser Val Glu Thr Glu Phe Ser Leu Arg Asp
 200 205 210

gac tgg gtg cgg gtt gaa cga aac ctt cgc caa cac tcc gca ctt gat 787
 Asp Trp Val Arg Val Glu Arg Asn Leu Arg Gln His Ser Ala Leu Asp
 215 220 225

ggc atc ggc agc acg gag ttc ctc acc gca gta gcc ctg ttg gtc agt 835
 Gly Ile Gly Ser Thr Glu Phe Leu Thr Ala Val Ala Leu Leu Val Ser
 230 235 240 245

gcc cgc aag gga cat gcg tct ggt tac cgt gaa gat atc ttg aac ttg 883
 Ala Arg Lys Gly His Ala Ser Gly Tyr Arg Glu Asp Ile Leu Asn Leu
 250 255 260

acg ctg gct gaa tac att cct gct gcc gat gaa atg atc aag ggc ttc 931
 Thr Leu Ala Glu Tyr Ile Pro Ala Ala Asp Glu Met Ile Lys Gly Phe
 265 270 275

gac gag gcg gct gaa ttc ctg cgt cag cga tgc att ttt gag tct cga 979
 Asp Glu Ala Ala Glu Phe Leu Arg Gln Arg Cys Ile Phe Glu Ser Arg
 280 285 290

cca ggt tcc ata cac cgc gca gat tgt tcc act ggc cgt gat cct cac 1027
 Pro Gly Ser Ile His Arg Ala Asp Cys Ser Thr Gly Arg Asp Pro His
 295 300 305

cct gct tgatgcagaa gaaatggcca ccg 1056
 Pro Ala
 310

<210> 508

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 508

Met Ala Leu Asp Thr Arg Gly Glu Glu Met Arg Phe Arg Pro Arg Ala
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20 25 30

Asp Gly Gln Gln Arg Leu Thr Thr Leu Tyr His Cys Phe Ser Gly Asp
35 40 45

Gly Tyr Val Asn Thr Val Asp Phe Arg Ser Lys Lys Val Thr Arg Lys
50 55 60

Phe Tyr Ile Asp Val Ala Lys Ala Val Glu Ser Pro Val Met Ser Asp

65	70	75	80
Glu Ala Ile Phe	Ser Val Asp	Glu Thr Gly Lys	Ile Ile Ser His Phe
	85	90	95
Gly Pro Val Ile	Asp Gly Gly Ile	Thr Asp Leu	Glu Thr Ala Leu Ala
	100	105	110
His Gly Cys Leu	Pro Val Ser	Val Leu Leu Asp	Asp Asn Gly Thr Asp
	115	120	125
Phe Leu Phe Asp	Leu Ala Asp	Met Ala Gly	Glu Gly Ala Arg Glu His
	130	135	140
Ala Lys Arg Phe	Gln Ser Gln	Ile Val Lys	Thr Leu Val Ser Tyr Asp
	145	150	155
Ile Pro Met Ile	Arg Leu Asp	Arg Glu Thr	Ala Lys Gly Gly Ile Gly
	165	170	175
Ser Ile Phe Ala	Gln Ala Asn	Ser Ser Gly	Leu Gln Met Asp Val Phe
	180	185	190
Asp Leu Leu Thr	Ala Val Phe	Ala Ala Asp	Glu Ser Val Glu Thr Glu
	195	200	205
Phe Ser Leu Arg	Asp Asp Trp	Val Arg Val	Glu Arg Asn Leu Arg Gln
	210	215	220
His Ser Ala Leu	Asp Gly Ile	Gly Ser Thr	Glu Phe Leu Thr Ala Val
	225	230	235
Ala Leu Leu Val	Ser Ala Arg	Lys Gly His	Ala Ser Gly Tyr Arg Glu
	245	250	255
Asp Ile Leu Asn	Leu Thr Leu	Ala Glu Tyr	Ile Pro Ala Ala Asp Glu
	260	265	270
Met Ile Lys Gly	Phe Asp Glu	Ala Ala Glu	Phe Leu Arg Gln Arg Cys
	275	280	285
Ile Phe Glu Ser	Arg Pro Gly	Ser Ile His	Arg Ala Asp Cys Ser Thr
	290	295	300
Gly Arg Asp Pro	His Pro Ala		
	305	310	

<210> 509

<211> 886

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(886)

<223> FRXA01140

<400> 509

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Met Ala Leu Asp Thr
1 5

cgc ggc gag gaa atg cgt ttc cgg cca cgc gcg ctg tcc ggc gcc cca 163
Arg Gly Glu Glu Met Arg Phe Arg Pro Arg Ala Leu Ser Gly Ala Pro
10 15 20

gat acg ggc aag gat cca ggt ctt ttg ctt ctc gac gga caa cag cgc 211
Asp Thr Gly Lys Asp Pro Gly Leu Leu Leu Asp Gly Gln Gln Arg
25 30 35

ctc acc acc ctt tat cat tgc ttc agt ggc gat ggc tat gta aat acg 259
Leu Thr Thr Leu Tyr His Cys Phe Ser Gly Asp Gly Tyr Val Asn Thr
40 45 50

gtg gac ttc cga tca aag aaa gtg acc cgg aag ttt tat att gat gtt 307
Val Asp Phe Arg Ser Lys Lys Val Thr Arg Lys Phe Tyr Ile Asp Val
55 60 65

gct aag gct gtt gaa tct ccg gtc atg tcc gat gag gct att ttt tca 355
Ala Lys Ala Val Glu Ser Pro Val Met Ser Asp Glu Ala Ile Phe Ser
70 75 80 85

gtc gac gaa acc ggc aaa atc atc tcc cac ttc ggt cca gtg atc gac 403
Val Asp Glu Thr Gly Lys Ile Ile Ser His Phe Gly Pro Val Ile Asp
90 95 100

ggc ggc atc acc gat tta gaa aca gca ctt gct cat ggt tgc ctt cca 451
Gly Gly Ile Thr Asp Leu Glu Thr Ala Leu Ala His Gly Cys Leu Pro
105 110 115

gtt tct gtg ctg ctg gat gat aac ggc act gat ttc ctc ttt gac ctc 499
Val Ser Val Leu Leu Asp Asp Asn Gly Thr Asp Phe Leu Phe Asp Leu
120 125 130

gcc gat atg gca gga gaa ggc gct cgc gaa cac gcg aag cgc ttc caa 547
Ala Asp Met Ala Gly Glu Gly Ala Arg Glu His Ala Lys Arg Phe Gln
135 140 145

tca caa atc gtt aag acc tta gtt agt tac gac atc cca atg atc cga 595
Ser Gln Ile Val Lys Thr Leu Val Ser Tyr Asp Ile Pro Met Ile Arg
150 155 160 165

ctg gat cgt gaa acc gcc aag ggt gga att ggt tcc atc ttt gct cag 643
Leu Asp Arg Glu Thr Ala Lys Gly Gly Ile Gly Ser Ile Phe Ala Gln
170 175 180

gcc aat agc tct ggc ttg cag atg gat gtc ttt gat ttg ctc acc gcg 691
Ala Asn Ser Ser Gly Leu Gln Met Asp Val Phe Asp Leu Leu Thr Ala
185 190 195

gtg ttc gca gcc gat gaa tcg gtg gag acc gaa ttc tca ctg cgt gat 739
Val Phe Ala Ala Asp Glu Ser Val Glu Thr Glu Phe Ser Leu Arg Asp
200 205 210

gac tgg gtg cgg gtt gaa cga aac ctt cgc caa cac tcc gca ctt gat 787
Asp Trp Val Arg Val Glu Arg Asn Leu Arg Gln His Ser Ala Leu Asp
215 220 225

ggc atc ggc agc acg gag ttc ctc acc gca gta gcc ctg ttg gtc agt 835

Gly Ile Gly Ser Thr Glu Phe Leu Thr Ala Val Ala Leu Leu Val Ser
 230 235 240 245

gcc cgc aag gga cat gcg tct ggt tac cgt gaa gat atc ttg aac ttg 883
 Ala Arg Lys Gly His Ala Ser Gly Tyr Arg Glu Asp Ile Leu Asn Leu
 250 255 260

acg 886
 Thr

<210> 510
 <211> 262
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 510
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Asp Gly Gln Gln Arg Leu Thr Thr Leu Tyr His Cys Phe Ser Gly Asp
 35 40 45

Gly Tyr Val Asn Thr Val Asp Phe Arg Ser Lys Lys Val Thr Arg Lys
 50 55 60

Phe Tyr Ile Asp Val Ala Lys Ala Val Glu Ser Pro Val Met Ser Asp
 65 70 75 80

Glu Ala Ile Phe Ser Val Asp Glu Thr Gly Lys Ile Ile Ser His Phe
 85 90 95

Gly Pro Val Ile Asp Gly Gly Ile Thr Asp Leu Glu Thr Ala Leu Ala
 100 105 110

His Gly Cys Leu Pro Val Ser Val Leu Leu Asp Asp Asn Gly Thr Asp
 115 120 125

Phe Leu Phe Asp Leu Ala Asp Met Ala Gly Glu Gly Ala Arg Glu His
 130 135 140

Ala Lys Arg Phe Gln Ser Gln Ile Val Lys Thr Leu Val Ser Tyr Asp
 145 150 155 160

Ile Pro Met Ile Arg Leu Asp Arg Glu Thr Ala Lys Gly Gly Ile Gly
 165 170 175

Ser Ile Phe Ala Gln Ala Asn Ser Ser Gly Leu Gln Met Asp Val Phe
 180 185 190

Asp Leu Leu Thr Ala Val Phe Ala Ala Asp Glu Ser Val Glu Thr Glu
 195 200 205

Phe Ser Leu Arg Asp Asp Trp Val Arg Val Glu Arg Asn Leu Arg Gln
 210 215 220

His Ser Ala Leu Asp Gly Ile Gly Ser Thr Glu Phe Leu Thr Ala Val

gac act gtg ctg ccc aac ggc gtt cct gtt cgt ggt ttt atc gac cgt 547
Asp Thr Val Leu Pro Asn Gly Val Pro Val Arg Gly Phe Ile Asp Arg
135 140 145

gtg gat acc gcc cca ccg gcc aag tcc gag tta tcg act aca aga ctg 595
 Val Asp Thr Ala Pro Pro Ala Lys Ser Glu Leu Ser Thr Thr Arg Leu
 150 155 160 165

gca aga aac caa agc cgc agt gga gcc agc aag cgc agt tcc aga tgc 643
 Ala Arg Asn Gln Ser Arg Ser Gly Ala Ser Lys Arg Ser Ser Arg Cys
 170 175 180

tgt tct atg cac tgg tct act ggc gca tgt tca atg aaa tcc cag ctg 691
 Cys Ser Met His Trp Ser Thr Gly Ala Cys Ser Met Lys Ser Gln Leu
 185 190 195

agc ttc gtt taatgtacct caaagtcaac gat 723
 Ser Phe Val
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<210> 512

<211> 200

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 512

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 20 25 30

Arg Phe Arg Ala Ile Asp Arg Leu Pro Glu Pro Lys Thr Val Ala Gln
 35 40 45

Val Lys Gly Thr Leu Val His Ala Val Leu Glu Tyr Met His Lys Leu
 50 55 60

Pro Arg Glu Glu Arg Glu Tyr Pro Ala Met Val Lys Gln Leu Lys Pro
 65 70 75 80

Thr Trp Ala Gln Met Cys Glu Glu Asp Ala Glu Leu Lys Glu Leu Val
 85 90 95

Pro Glu Asp Glu Leu Tyr Asp Phe Leu Val Asp Ser Arg Thr Leu Leu
 100 105 110

Arg Gly Tyr Phe Glu Met Glu Asn Pro Gln Gly Phe Asp Ala Thr Glu
 115 120 125

Cys Glu Met Tyr Val Asp Thr Val Leu Pro Asn Gly Val Pro Val Arg
 130 135 140

Gly Phe Ile Asp Arg Val Asp Thr Ala Pro Pro Ala Lys Ser Glu Leu
 145 150 155 160

Ser Thr Thr Arg Leu Ala Arg Asn Gln Ser Arg Ser Gly Ala Ser Lys
 165 170 175

Arg Ser Ser Arg Cys Cys Ser Met His Trp Ser Thr Gly Ala Cys Ser
 180 185 190

Met Lys Ser Gln Leu Ser Phe Val

195

200

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<222> (101)..(700)
<223> FRXA01148
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Met Thr Ser Pro Val																		5
gaa aac gtt aag aaa aag cca cgc cca ttg cgc ctg tca ccg tcg cgc																		163
Glu Asn Val Lys Lys Pro Arg Pro Leu Ala Leu Ser Pro Ser Arg																		20
gcc ggg gat tac cag cag tgt ccc ctg ttg tat cgc ttc cgc cgc att																		211
Ala Gly Asp Tyr Gln Gln Cys Pro Leu Leu Tyr Arg Phe Arg Ala Ile																		35
gat cgc ctg cca gag cct aag acc gtc gcc cag gtc aaa ggc acg ttg																		259
Asp Arg Leu Pro Glu Pro Lys Thr Val Ala Gln Val Lys Gly Thr Leu																		40
gtg cac gct gtg ttg gaa tat atg cac aag ttg ccg cgt gaa gaa cgc																		307
Val His Ala Val Leu Glu Tyr Met His Lys Leu Pro Arg Glu Glu Arg																		55
gaa tat cca gcc atg gtg aag caa ctc aag ccc acc tgg cgc cag atg																		355
Glu Tyr Pro Ala Met Val Lys Gln Leu Lys Pro Thr Trp Ala Gln Met																		70 75 80 85
tgt gaa gaa gac gca gag ctc aaa gag ctt gtt cca gaa gat gag ctt																		403
Cys Glu Glu Asp Ala Glu Leu Lys Glu Leu Val Pro Glu Asp Glu Leu																		90 95 100
tat gat ttc ctc gtg gat tcc cgc acc ctg ctg cgt ggc tac ttt gaa																		451
Tyr Asp Phe Leu Val Asp Ser Arg Thr Leu Leu Arg Gly Tyr Phe Glu																		105 110 115
atg gaa aat cct caa ggt ttc gac gcc acc gaa tgc gaa atg tac gtg																		499
Met Glu Asn Pro Gln Gly Phe Asp Ala Thr Glu Cys Glu Met Tyr Val																		120 125 130
gac act gtg ctg ccc aac ggc gtt cct gtt cgt ggt ttt atc gac cgt																		547
Asp Thr Val Leu Pro Asn Gly Val Pro Val Arg Gly Phe Ile Asp Arg																		135 140 145
gtg gat acc gcc cca ccg gcc aag tcc gag tta tcg act aca aga ctg																		595
Val Asp Thr Ala Pro Pro Ala Lys Ser Glu Leu Ser Thr Thr Arg Leu																		150 155 160 165
gca aga aac caa agc cgc agt gga gcc agc aag cgc agt tcc aga tgc																		643

Ala Arg Asn Gln Ser Arg Ser Gly Ala Ser Lys Arg Ser Ser Arg Cys
 170 175 180

tgt tct atg cac tgg tct act ggc gca tgt tca atg aaa tcc cag ctc 691
 Cys Ser Met His Trp Ser Thr Gly Ala Cys Ser Met Lys Ser Gln Leu
 185 190 195

agc ttc gtt taatgtacct caaagtcaac gat 723
 Ser Phe Val
 200

<210> 514
 <211> 200
 <212> PRT
 <213> *Corynebacterium glutamicum*

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 20 25 30

Arg Phe Arg Ala Ile Asp Arg Leu Pro Glu Pro Lys Thr Val Ala Gln
 35 40 45

Val Lys Gly Thr Leu Val His Ala Val Leu Glu Tyr Met His Lys Leu
 50 55 60

Pro Arg Glu Glu Arg Glu Tyr Pro Ala Met Val Lys Gln Leu Lys Pro
 65 70 75 80

Thr Trp Ala Gln Met Cys Glu Glu Asp Ala Glu Leu Lys Glu Leu Val
 85 90 95

Pro Glu Asp Glu Leu Tyr Asp Phe Leu Val Asp Ser Arg Thr Leu Leu
 100 105 110

Arg Gly Tyr Phe Glu Met Glu Asn Pro Gln Gly Phe Asp Ala Thr Glu
 115 120 125

Cys Glu Met Tyr Val Asp Thr Val Leu Pro Asn Gly Val Pro Val Arg
 130 135 140

Gly Phe Ile Asp Arg Val Asp Thr Ala Pro Pro Ala Lys Ser Glu Leu
 145 150 155 160

Ser Thr Thr Arg Leu Ala Arg Asn Gln Ser Arg Ser Gly Ala Ser Lys
 165 170 175

Arg Ser Ser Arg Cys Cys Ser Met His Trp Ser Thr Gly Ala Cys Ser
 180 185 190

Met Lys Ser Gln Leu Ser Phe Val
 195 200

<210> 515
 <211> 543
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<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(543)

<223> RXN01153

<400> 515

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Pro	Phe	Leu	Ser	Pro	Ile	Val	Thr	Ser	Thr	His	Ala	Val	Val	Ala	Tyr							

1					5					10					15							
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t	c	a	c	c	g	t	g	a	c	a	c	g	t	g	a	t	a	c	t		96	
Ser	Thr	Ala	Arg	Gly	Phe	Gly	Glu	His	Arg	Val	Arg	Trp	Asp	Tyr	Ala							

				20				25						30								
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c	a	a	g	a	c	a	c	g	a	t	a	c	t	g	c	a	c	a	t		144	
Gln	Glu	Ser	Pro	Leu	Arg	Asp	Thr	Arg	Gly	Phe	Asp	Leu	Arg	Arg	Tyr							

			35				40					45										
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c	a	c	a	c	c	t	g	t	a	c	a	c	a	t	a	c	a	c	a	t		192
His	Gln	Ala	Pro	Val	Val	Asp	Pro	His	Ala	Ile	Gly	Val	Ala	Asn	Val							

			50				55				60											
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t	t	t	c	c	a	a	t	g	a	c	a	c	g	a	c	c	a	a		240		
Phe	Val	Pro	Asn	Gly	Ala	Arg	Phe	Tyr	Val	Asp	His	Ala	His	Pro	Glu							

			65			70				75				80								
--	--	--	----	--	--	----	--	--	--	----	--	--	--	----	--	--	--	--	--	--	--	--

t	a	c	t	c	c	a	g	a	c	a	c	a	t	g	a	c	a	t	a	c		288
Tyr	Ser	Ser	Pro	Glu	Val	Thr	Asn	Ala	Trp	Asp	Ala	Met	Val	Tyr	Asp							

				85				90						95								
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g	c	c	a	c	a	c	a	t	a	c	a	c	a	t	a	c	a	c	a	t		336
Ala	Ala	Gly	Asp	His	Ile	Leu	Met	Gln	Ala	Val	Ser	Asp	Val	Ala	Ser							

			100				105						110									
--	--	--	-----	--	--	--	-----	--	--	--	--	--	-----	--	--	--	--	--	--	--	--	--

t	t	c	a	c	a	a	t	a	c	a	c	a	c	a	t	a	c	a	c	a		384
Phe	Thr	Ser	Gln	Asn	Arg	Ser	Val	Leu	Asp	Gly	His	Asp	Pro	Cys	Pro							

			115				120						125									
--	--	--	-----	--	--	--	-----	--	--	--	--	--	-----	--	--	--	--	--	--	--	--	--

g	c	t	a	a	a	c	a	t	a	c	a	c	a	c	a	t	a	c	a	c		432
Ala	Leu	Lys	Ile	Tyr	Lys	Asn	Asn	Val	Asp	Gly	Lys	Gly	Ala	Ser	Tyr							

			130				135						140									
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g	g	c	a	c	a	a	t	a	c	a	c	a	c	a	t	a	c	a	c	a		480
Gly	Phe	His	Glu	Asn	Tyr	Leu	Tyr	Ser	Arg	Glu	Thr	Asp	Phe	Asp	Val							

			145			150				155				160								
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c	t	a	c	a	c	a	c	a	c	a	c	a	c	a	c	a	c	a	c	a		528
Leu	Ala	Gln	Ala	Leu	Ile	Pro	Phe	Phe	Val	Cys	Arg	Gln	Val	Ile	Ile							

				165				170						175								
--	--	--	--	-----	--	--	--	-----	--	--	--	--	--	-----	--	--	--	--	--	--	--	--

g	g	c	a	c	a	c	a	c	a	c	a	c	a	c	a	c	a	c	a	c		543
Gly	Ala	Gly	Arg	Val																		

				180																		
--	--	--	--	-----	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

<210> 516

<211> 181

<212> FRT

<213> *Corynebacterium glutamicum*

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<400> 516
Pro Phe Leu Ser Pro Ile Val Thr Ser Thr His Ala Val Val Ala Tyr
 1              5              10              15

Ser Thr Ala Arg Gly Phe Gly Glu His Arg Val Arg Trp Asp Tyr Ala
              20              25              30

Gln Glu Ser Pro Leu Arg Asp Thr Arg Gly Phe Asp Leu Arg Arg Tyr
              35              40              45

His Gln Ala Pro Val Val Asp Pro His Ala Ile Gly Val Ala Asn Val
              50              55              60

Phe Val Pro Asn Gly Ala Arg Phe Tyr Val Asp His Ala His Pro Glu
 65              70              75              80

Tyr Ser Ser Pro Glu Val Thr Asn Ala Trp Asp Ala Met Val Tyr Asp
              85              90              95

Ala Ala Gly Asp His Ile Leu Met Gln Ala Val Ser Asp Val Ala Ser
              100              105              110

Phe Thr Ser Gln Asn Arg Ser Val Leu Asp Gly His Asp Pro Cys Pro
              115              120              125

Ala Leu Lys Ile Tyr Lys Asn Asn Val Asp Gly Lys Gly Ala Ser Tyr
              130              135              140

Gly Phe His Glu Asn Tyr Leu Tyr Ser Arg Glu Thr Asp Phe Asp Val
 145              150              155              160

Leu Ala Gln Ala Leu Ile Pro Phe Phe Val Cys Arg Gln Val Ile Ile
              165              170              175

Gly Ala Gly Arg Val
              180

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<210> 517
<211> 543
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (1)..(543)
<223> FRXA01153

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<400> 517
cgc ttt tta agc cgc atc gtt act tcc acg cac gcg gtg gtg gcg tat      48
Pro Phe Leu Ser Pro Ile Val Thr Ser Thr His Ala Val Val Ala Tyr
 1              5              10              15

tcc acc gcg cgt gga ttt ggt gag cac cgc gtg cgt tgg gac tat gcg      96
Ser Thr Ala Arg Gly Phe Gly Glu His Arg Val Arg Trp Asp Tyr Ala
              20              25              30

caa gag tcc cca ctg cgc gat act cgt ggc ttt gat ctg cgc cga tac      144
Gln Glu Ser Pro Leu Arg Asp Thr Arg Gly Phe Asp Leu Arg Arg Tyr
              35              40              45

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cac cag gcc cct gtg gtg gat ccg cac gcc att ggt gtg gcc aac gtg 192
 His Gln Ala Pro Val Val Asp Pro His Ala Ile Gly Val Ala Asn Val
 50 55 60

ttt gtg ccc aat ggt gcc agg ttt tat gtc gat cac gcg cac ccg gaa 240
 Phe Val Pro Asn Gly Ala Arg Phe Tyr Val Asp His Ala His Pro Glu
 65 70 75 80

tac tcc tcc cca gag gtc acc aat gcg tgg gat gcc atg gtt tac gac 288
 Tyr Ser Ser Pro Glu Val Thr Asn Ala Trp Asp Ala Met Val Tyr Asp
 85 90 95

gcc gct ggt gac cac atc ctt atg cag gcc gtc tct gat gtt gcg agt 336
 Ala Ala Gly Asp His Ile Leu Met Gln Ala Val Ser Asp Val Ala Ser
 100 105 110

ttc acc agc cag aat agg tct gtg ttg gac ggc cat gat ccg tgt cca 384
 Phe Thr Ser Gln Asn Arg Ser Val Leu Asp Gly His Asp Pro Cys Pro
 115 120 125

gct ttg aaa atc tac aaa aac aat gtc gac ggt aag ggt gct agc tac 432
 Ala Leu Lys Ile Tyr Lys Asn Asn Val Asp Gly Lys Gly Ala Ser Tyr
 130 135 140

ggg ttc cac gag aat tac ctc tac tca cgt gag acg gat ttt gat gtg 480
 Gly Phe His Glu Asn Tyr Leu Tyr Ser Arg Glu Thr Asp Phe Asp Val
 145 150 155 160

ctg gct cag gca ttg atc cca ttt ttt gtg tgc cgg cag gtc atc atc 528
 Leu Ala Gln Ala Leu Ile Pro Phe Phe Val Cys Arg Gln Val Ile Ile
 165 170 175

ggt gcc gga cgt gtg 543
 Gly Ala Gly Arg Val
 180

<210> 518
 <211> 181
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 518
 Pro Phe Leu Ser Pro Ile Val Thr Ser Thr His Ala Val Val Ala Tyr
 1 5 10 15

Ser Thr Ala Arg Gly Phe Gly Glu His Arg Val Arg Trp Asp Tyr Ala
 20 25 30

Gln Glu Ser Pro Leu Arg Asp Thr Arg Gly Phe Asp Leu Arg Arg Tyr
 35 40 45

His Gln Ala Pro Val Val Asp Pro His Ala Ile Gly Val Ala Asn Val
 50 55 60

Phe Val Pro Asn Gly Ala Arg Phe Tyr Val Asp His Ala His Pro Glu
 65 70 75 80

Tyr Ser Ser Pro Glu Val Thr Asn Ala Trp Asp Ala Met Val Tyr Asp
 85 90 95

Ala Ala Gly Asp His Ile Leu Met Gln Ala Val Ser Asp Val Ala Ser
 100 105 110

Phe Thr Ser Gln Asn Arg Ser Val Leu Asp Gly His Asp Pro Cys Pro
 115 120 125

Ala Leu Lys Ile Tyr Lys Asn Asn Val Asp Gly Lys Gly Ala Ser Tyr
 130 135 140

Gly Phe His Glu Asn Tyr Leu Tyr Ser Arg Glu Thr Asp Phe Asp Val
 145 150 155 160

Leu Ala Gln Ala Leu Ile Pro Phe Phe Val Cys Arg Gln Val Ile Ile
 165 170 175

Gly Ala Gly Arg Val
 180

<210> 519

<211> 677

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (39)..(677)

<223> RXN01154

<400> 519

ccggggaatt ccaggtcagt cagcgagcct gactaccattg agc aag aaa att tca 56
 Leu Ser Lys Lys Ile Ser
 1 5

ctg gaa acc aca ctc aac cgc ggc att atc aac acc cgc gat gaa cca 104
 Leu Glu Thr Thr Leu Asn Arg Gly Ile Ile Asn Thr Arg Asp Glu Pro
 10 15 20

cac acc gac gct gat cac tgg ggt cgc ctg cac gtg atc atc ggc gat 152
 His Thr Asp Ala Asp His Trp Gly Arg Leu His Val Ile Ile Gly Asp
 25 30 35

gcc aac atg tcg cag act gcg aat ttc ctc aaa ttc ggc atg acc tcc 200
 Ala Asn Met Ser Gln Thr Ala Asn Phe Leu Lys Phe Gly Met Thr Ser
 40 45 50

cta gtg ctg gat gcc att gag gct ggg gtg gat ttc tct gaa ctc aag 248
 Leu Val Leu Asp Ala Ile Glu Ala Gly Val Asp Phe Ser Glu Leu Lys
 55 60 65 70

ctg aag aac gca gtg agt gaa gta gca aag gtc tcc cat gat ctt tcc 296
 Leu Lys Asn Ala Val Ser Glu Val Ala Lys Val Ser His Asp Leu Ser
 75 80 85

ctt acc cac cag ctg cga ttg gcg gat ggt tca gag ctc acc gct att 344
 Leu Thr His Gln Leu Arg Leu Ala Asp Gly Ser Glu Leu Thr Ala Ile
 90 95 100

gat att ctg cgc cgc tat ttg gac aag gtg cag ccg ttt gca gaa acc 392
 Asp Ile Leu Arg Arg Tyr Leu Asp Lys Val Gln Pro Phe Ala Glu Thr

CCGGGGAATT CCAGGTCAGT CAGCGAGCCT GACTACCATTG AGC AAG AAA ATT TCA
 1 5
 CTG GAA ACC ACA CTC AAC CGC GGC ATT ATC AAC ACC CGC GAT GAA CCA
 10 15 20
 CAC ACC GAC GCT GAT CAC TGG GGT CGC CTG CAC GTG ATC ATC GGC GAT
 25 30 35
 GCC AAC ATG TCG CAG ACT GCG AAT TTC CTC AAA TTC GGC ATG ACC TCC
 40 45 50
 CTA GTG CTG GAT GCC ATT GAG GCT GGG GTG GAT TTC TCT GAA CTC AAG
 55 60 65 70
 CTG AAG AAC GCA GTG AGT GAA GTA GCA AAG GTC TCC CAT GAT CTT TCC
 75 80 85
 CTT ACC CAC CAG CTG CGA TTG GCG GAT GGT TCA GAG CTC ACC GCT ATT
 90 95 100
 GAT ATT CTG CGC CGC TAT TTG GAC AAG GTG CAG CCG TTT GCA GAA ACC
 392

105	110	115	
cca gtg gaa cag cgt gtc act gcg ctg tgg ggt gaa gtg ctg ggg ctc			440
Pro Val Glu Gln Arg Val Thr Ala Leu Trp Gly Glu Val Leu Gly Leu			
120	125	130	
ctg gag aat gat ctg ctc tcc acc agc cat ctc ctt gat tgg act gca			488
Leu Glu Asn Asp Leu Leu Ser Thr Ser His Leu Leu Asp Trp Thr Ala			
135	140	145	150
aaa ctt gcc ctg atc aag tct ttt gag gcg cgt ggg ctg tcc att aac			536
Lys Leu Ala Leu Ile Lys Ser Phe Glu Ala Arg Gly Leu Ser Ile Asn			
155	160	165	
gat ccc aag atg tac ctc att gac ctg cag tac agc gat att gat cca			584
Asp Pro Lys Met Tyr Leu Ile Asp Leu Gln Tyr Ser Asp Ile Asp Pro			
170	175	180	
cag aag agt ctg tat cac gca ctg gta tcc aag ggg cgg atg aaa aca			632
Gln Lys Ser Leu Tyr His Ala Leu Val Ser Lys Gly Arg Met Lys Thr			
185	190	195	
ctg tgc agt gcg cag gac att gca gat gca gcg gcc act tca ccg			677
Leu Cys Ser Ala Gln Asp Ile Ala Asp Ala Ala Thr Ser Pro			
200	205	210	
<210> 520			
<211> 213			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 520			
Leu Ser Lys Lys Ile Ser Leu Glu Thr Thr Leu Asn Arg Gly Ile Ile			
1	5	10	15
Asn Thr Arg Asp Glu Pro His Thr Asp Ala Asp His Trp Gly Arg Leu			
20	25	30	
His Val Ile Ile Gly Asp Ala Asn Met Ser Gln Thr Ala Asn Phe Leu			
35	40	45	
Lys Phe Gly Met Thr Ser Leu Val Leu Asp Ala Ile Glu Ala Gly Val			
50	55	60	
Asp Phe Ser Glu Leu Lys Leu Lys Asn Ala Val Ser Glu Val Ala Lys			
65	70	75	80
Val Ser His Asp Leu Ser Leu Thr His Gln Leu Arg Leu Ala Asp Gly			
85	90	95	
Ser Glu Leu Thr Ala Ile Asp Ile Leu Arg Arg Tyr Leu Asp Lys Val			
100	105	110	
Gln Pro Phe Ala Glu Thr Pro Val Glu Gln Arg Val Thr Ala Leu Trp			
115	120	125	
Gly Glu Val Leu Gly Leu Leu Glu Asn Asp Leu Leu Ser Thr Ser His			
130	135	140	
Leu Leu Asp Trp Thr Ala Lys Leu Ala Leu Ile Lys Ser Phe Glu Ala			

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145              150              155              160
Arg Gly Leu Ser Ile Asn Asp Pro Lys Met Tyr Leu Ile Asp Leu Gln
              165              170              175
Tyr Ser Asp Ile Asp Pro Gln Lys Ser Leu Tyr His Ala Leu Val Ser
              180              185              190
Lys Gly Arg Met Lys Thr Leu Cys Ser Ala Gln Asp Ile Ala Asp Ala
              195              200              205
Ala Ala Thr Ser Pro
              210

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<210> 521
<211> 603
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (1)..(603)
<223> PRXA01154

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<400> 521
gag ggc att atc aac acc cgc gat gaa cca cac acc gac gct gat cac 48
Glu Gly Ile Ile Asn Thr Arg Asp Glu Pro His Thr Asp Ala Asp His
1 5 10 15

tgg ggt cgc ctg cac gtg atc atc ggc gat gcc aac atg tgc cag act 96
Trp Gly Arg Leu His Val Ile Ile Gly Asp Ala Asn Met Ser Gln Thr
20 25 30

gcg aat ttc ctc aaa ttc ggc atg acc tcc cta gtg ctg gat gcc att 144
Ala Asn Phe Leu Lys Phe Gly Met Thr Ser Leu Val Leu Asp Ala Ile
35 40 45

gag gct ggg gtg gat ttc tct gaa ctc aag ctg aag aac gca gtg agt 192
Glu Ala Gly Val Asp Phe Ser Glu Leu Lys Leu Lys Asn Ala Val Ser
50 55 60

gaa gta gca aag gtc tcc cat gat ctt tcc ctt acc cac cag ctg cga 240
Glu Val Ala Lys Val Ser His Asp Leu Ser Leu Thr His Gln Leu Arg
65 70 75 80

ttg gcg gat ggt tca gag ctc acc gct att gat att ctg cgc cgc tat 288
Leu Ala Asp Gly Ser Glu Leu Thr Ala Ile Asp Ile Leu Arg Arg Tyr
85 90 95

ttg gac aag gtg cag ccg ttt gca gaa acc cca gtg gaa cag cgt gtc 336
Leu Asp Lys Val Gln Pro Phe Ala Glu Thr Pro Val Glu Gln Arg Val
100 105 110

act gcg ctg tgg ggt gaa gtg ctg ggg ctc ctg gag aat gat ctg ctc 384
Thr Ala Leu Trp Gly Glu Val Leu Gly Leu Leu Glu Asn Asp Leu Leu
115 120 125

tcc acc agc cat ctc ctt gat tgg act gca aaa ctt gcc ctg atc aag 432
Ser Thr Ser His Leu Leu Asp Trp Thr Ala Lys Leu Ala Leu Ile Lys
130 135 140

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tct ttt gag gcg cgt ggg ctg tcc att aac gat ccc aag atg tac ctc 480
 Ser Phe Glu Ala Arg Gly Leu Ser Ile Asn Asp Pro Lys Met Tyr Leu
 145 150 155 160

att gac ctg cag tac agc gat att gat cca cag aag agt ctg tat cac 528
 Ile Asp Leu Gln Tyr Ser Asp Ile Asp Pro Gln Lys Ser Leu Tyr His
 165 170 175

gca ctg gta tcc aag ggg cgg atg aaa aca ctg tgc agt gcg cag gac 576
 Ala Leu Val Ser Lys Gly Arg Met Lys Thr Leu Cys Ser Ala Gln Asp
 180 185 190

att gca gat gca gcg gcc act tca cgg 603
 Ile Ala Asp Ala Ala Ala Thr Ser Pro
 195 200

<210> 522

<211> 201

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 522

Glu Gly Ile Ile Asn Thr Arg Asp Glu Pro His Thr Asp Ala Asp His
 1 5 10 15

Trp Gly Arg Leu His Val Ile Ile Gly Asp Ala Asn Met Ser Gln Thr
 20 25 30

Ala Asn Phe Leu Lys Phe Gly Met Thr Ser Leu Val Leu Asp Ala Ile
 35 40 45

Glu Ala Gly Val Asp Phe Ser Glu Leu Lys Leu Lys Asn Ala Val Ser
 50 55 60

Glu Val Ala Lys Val Ser His Asp Leu Ser Leu Thr His Gln Leu Arg
 65 70 75 80

Leu Ala Asp Gly Ser Glu Leu Thr Ala Ile Asp Ile Leu Arg Arg Tyr
 85 90 95

Leu Asp Lys Val Gln Pro Phe Ala Glu Thr Pro Val Glu Gln Arg Val
 100 105 110

Thr Ala Leu Trp Gly Glu Val Leu Gly Leu Leu Glu Asn Asp Leu Leu
 115 120 125

Ser Thr Ser His Leu Leu Asp Trp Thr Ala Lys Leu Ala Leu Ile Lys
 130 135 140

Ser Phe Glu Ala Arg Gly Leu Ser Ile Asn Asp Pro Lys Met Tyr Leu
 145 150 155 160

Ile Asp Leu Gln Tyr Ser Asp Ile Asp Pro Gln Lys Ser Leu Tyr His
 165 170 175

Ala Leu Val Ser Lys Gly Arg Met Lys Thr Leu Cys Ser Ala Gln Asp
 180 185 190

Ile Ala Asp Ala Ala Ala Thr Ser Pro

195

200

<210> 523
 <211> 1570
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1570)
 <223> RXN01155

<400> 523
 acagcttgct ggatgaaatc gacggactgt tggaaaacaa cgccgaggaa ttcgttcgtt 60
 cctatgtaca aaaggggtggc gaatagtcac tgtgagtacc gtg gaa tcc gca ttg 115
 Val Glu Ser Ala Leu
 1 5
 acc cgc agg atc atg ggc att gaa acg gag tat ggc ctc acc ttt gtt 163
 Thr Arg Arg Ile Met Gly Ile Glu Thr Glu Tyr Gly Leu Thr Phe Val
 10 15 20
 gat ggt gat tcc aaa aag ctt cgc cca gat gag ata gct cga agg atg 211
 Asp Gly Asp Ser Lys Lys Leu Arg Pro Asp Glu Ile Ala Arg Arg Met
 25 30 35
 ttt cgt ccc atc gtg gag aaa tat tcc agc tct aat atc ttc ata ccc 259
 Phe Arg Pro Ile Val Glu Lys Tyr Ser Ser Ser Asn Ile Phe Ile Pro
 40 45 50
 aat ggt tcc cgg ttg tat ctt gat gtg ggt tcc cac ccg gag tac gcc 307
 Asn Gly Ser Arg Leu Tyr Leu Asp Val Gly Ser His Pro Glu Tyr Ala
 55 60 65
 acc gcc gag tgt gat aat ttg acc cag ctg atc aat ttt gaa aaa gct 355
 Thr Ala Glu Cys Asp Asn Leu Thr Gln Leu Ile Asn Phe Glu Lys Ala
 70 75 80 85
 ggc gat gtt att gca gat cgc atg gct gta gat gcc gaa gag tcg ctg 403
 Gly Asp Val Ile Ala Asp Arg Met Ala Val Asp Ala Glu Glu Ser Leu
 90 95 100
 gcg aaa gaa gac att gct ggg cag gtg tac ctg ttt aaa aac aat gtc 451
 Ala Lys Glu Asp Ile Ala Gly Gln Val Tyr Leu Phe Lys Asn Asn Val
 105 110 115
 gat tcc gtg ggc aat tct tat ggc tgc cac gaa aac tac ctt gtg ggt 499
 Asp Ser Val Gly Asn Ser Tyr Gly Cys His Glu Asn Tyr Leu Val Gly
 120 125 130
 cgc tcc atg ccg ttg aag gcg ttg ggt aaa agg ctg atg ccg ttt ctg 547
 Arg Ser Met Pro Leu Lys Ala Leu Gly Lys Arg Leu Met Pro Phe Leu
 135 140 145
 att acc cgc cag ctc atc tgc ggc gcc ggc agg atc cat cac ccc aat 595
 Ile Thr Arg Gln Leu Ile Cys Gly Ala Gly Arg Ile His His Pro Asn
 150 155 160 165
 cct ttg gat aaa ggc gaa tcc ttc ccc ttg ggc tac tgc ata tcc cag 643

Pro	Leu	Asp	Lys	Gly	Glu	Ser	Phe	Pro	Leu	Gly	Tyr	Cys	Ile	Ser	Gln	
				170					175					180		
cgc	tct	gac	cac	gtg	tgg	gag	ggc	gta	tca	agt	gcc	acc	act	aga	tca	691
Arg	Ser	Asp	His	Val	Trp	Glu	Gly	Val	Ser	Ser	Ala	Thr	Thr	Arg	Ser	
			185					190					195			
cgc	ccc	att	atc	aac	acc	cgt	gat	gag	cca	cat	gcg	gat	tcc	cat	tct	739
Arg	Pro	Ile	Ile	Asn	Thr	Arg	Asp	Glu	Pro	His	Ala	Asp	Ser	His	Ser	
		200					205					210				
tac	cgc	agg	ctg	cac	gtg	att	gtg	ggg	gat	gcc	aac	atg	gca	gag	ccc	787
Tyr	Arg	Arg	Leu	His	Val	Ile	Val	Gly	Asp	Ala	Asn	Met	Ala	Glu	Pro	
		215				220					225					
agc	atc	gcg	ttg	aag	gtc	ggc	tcc	acg	ttg	ctg	gtt	ctg	gaa	atg	att	835
Ser	Ile	Ala	Leu	Lys	Val	Gly	Ser	Thr	Leu	Leu	Val	Leu	Glu	Met	Ile	
		230			235					240					245	
gag	gca	gat	ttc	ggg	ttg	ccc	agc	tta	gag	ctt	gcc	aat	gat	att	gcc	883
Glu	Ala	Asp	Phe	Gly	Leu	Pro	Ser	Leu	Glu	Leu	Ala	Asn	Asp	Ile	Ala	
			250						255					260		
tca	att	agg	gaa	atc	tcc	cgc	gat	gca	aca	gga	tcc	aca	ctg	ttg	tcc	931
Ser	Ile	Arg	Glu	Ile	Ser	Arg	Asp	Ala	Thr	Gly	Ser	Thr	Leu	Leu	Ser	
			265					270					275			
ctg	aaa	gat	ggc	acc	acc	atg	act	gcc	ttg	cag	atc	cag	cag	gtg	gtc	979
Leu	Lys	Asp	Gly	Thr	Thr	Met	Thr	Ala	Leu	Gln	Ile	Gln	Gln	Val	Val	
		280					285					290				
ttt	gag	cat	gcc	tgc	aag	tgg	ttg	gag	cag	cgc	ccc	gaa	cca	gaa	ttt	1027
Phe	Glu	His	Ala	Ser	Lys	Trp	Leu	Glu	Gln	Arg	Pro	Glu	Pro	Glu	Phe	
		295				300					305					
tct	ggc	acc	tcc	aac	aca	gag	atg	gcc	cgc	gtg	ctg	gat	ctg	tgg	ggg	1075
Ser	Gly	Thr	Ser	Asn	Thr	Glu	Met	Ala	Arg	Val	Leu	Asp	Leu	Trp	Gly	
		310			315					320					325	
cgc	atg	ttg	aaa	gcg	att	gag	tcc	ggg	gat	ttc	agc	gaa	gtg	gat	aca	1123
Arg	Met	Leu	Lys	Ala	Ile	Glu	Ser	Gly	Asp	Phe	Ser	Glu	Val	Asp	Thr	
			330						335					340		
gaa	att	gac	tgg	gtg	atc	aaa	aag	aag	ctc	att	gat	cgt	ttc	att	cag	1171
Glu	Ile	Asp	Trp	Val	Ile	Lys	Lys	Lys	Leu	Ile	Asp	Arg	Phe	Ile	Gln	
			345					350					355			
cgc	ggc	aac	ctt	ggg	ttg	gat	gat	cca	aaa	ctt	gcc	caa	gtg	gac	ttg	1219
Arg	Gly	Asn	Leu	Gly	Leu	Asp	Asp	Pro	Lys	Leu	Ala	Gln	Val	Asp	Leu	
			360				365					370				
act	tat	cac	gat	att	agg	cca	ggg	aga	ggc	cta	ttt	agc	gtg	ctg	caa	1267
Thr	Tyr	His	Asp	Ile	Arg	Pro	Gly	Arg	Gly	Leu	Phe	Ser	Val	Leu	Gln	
			375			380					385					
agc	cgc	ggc	atg	atc	aaa	cgg	tgg	act	act	gat	gag	gcg	att	tta	gct	1315
Ser	Arg	Gly	Met	Ile	Lys	Arg	Trp	Thr	Thr	Asp	Glu	Ala	Ile	Leu	Ala	
			390			395				400					405	
gcg	gtg	gat	acc	gct	cct	gat	aca	aca	cgt	gct	cat	ttg	cgc	ggg	cga	1363
Ala	Val	Asp	Thr	Ala	Pro	Asp	Thr	Thr	Arg	Ala	His	Leu	Arg	Gly	Arg	

410										415										420										
atc	ctt	aaa	gcg	gcg	gat	act	ctg	gga	gta	cct	gtg	act	gtc	gat	tgg	1411														
Ile	Leu	Lys	Ala	Ala	Asp	Thr	Leu	Gly	Val	Pro	Val	Thr	Val	Asp	Trp															
			425						430						435															
atg	cgt	cac	aag	gtc	aac	cga	ccg	gag	cca	caa	tcg	gtg	gaa	ttg	ggg	1459														
Met	Arg	His	Lys	Val	Asn	Arg	Pro	Glu	Pro	Gln	Ser	Val	Glu	Leu	Gly															
			440						445						450															
gat	cct	ttt	tcc	ctt	tta	aat	cct	caa	caa	cca	gcc	caa	gaa	act	gct	1507														
Asp	Pro	Phe	Ser	Leu	Leu	Asn	Pro	Gln	Gln	Pro	Ala	Gln	Glu	Thr	Ala															
			455						460						465															
ttg	agc	att	ctt	ctc	cta	ggc	gga	acc	tct	tac	att	gcc	ggg	gag	att	1555														
Leu	Ser	Ile	Leu	Leu	Leu	Gly	Gly	Thr	Ser	Tyr	Ile	Ala	Gly	Glu	Ile															
			470						475						485															
gcc	acg	ttg	acg	ttt												1570														
Ala	Thr	Leu	Thr	Phe																										
					490																									

<210> 524
 <211> 490
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 524
 Val Glu Ser Ala Leu Thr Arg Arg Ile Met Gly Ile Glu Thr Glu Tyr
 1 5 10 15
 Gly Leu Thr Phe Val Asp Gly Asp Ser Lys Lys Leu Arg Pro Asp Glu
 20 25 30
 Ile Ala Arg Arg Met Phe Arg Pro Ile Val Glu Lys Tyr Ser Ser Ser
 35 40 45
 Asn Ile Phe Ile Pro Asn Gly Ser Arg Leu Tyr Leu Asp Val Gly Ser
 50 55 60
 His Pro Glu Tyr Ala Thr Ala Glu Cys Asp Asn Leu Thr Gln Leu Ile
 65 70 75 80
 Asn Phe Glu Lys Ala Gly Asp Val Ile Ala Asp Arg Met Ala Val Asp
 85 90 95
 Ala Glu Glu Ser Leu Ala Lys Glu Asp Ile Ala Gly Gln Val Tyr Leu
 100 105 110
 Phe Lys Asn Asn Val Asp Ser Val Gly Asn Ser Tyr Gly Cys His Glu
 115 120 125
 Asn Tyr Leu Val Gly Arg Ser Met Pro Leu Lys Ala Leu Gly Lys Arg
 130 135 140
 Leu Met Pro Phe Leu Ile Thr Arg Gln Leu Ile Cys Gly Ala Gly Arg
 145 150 155 160
 Ile His His Pro Asn Pro Leu Asp Lys Gly Glu Ser Phe Pro Leu Gly
 165 170 175

Tyr Cys Ile Ser Gln Arg Ser Asp His Val Trp Glu Gly Val Ser Ser
 180 185 190
 Ala Thr Thr Arg Ser Arg Pro Ile Ile Asn Thr Arg Asp Glu Pro His
 195 200 205
 Ala Asp Ser His Ser Tyr Arg Arg Leu His Val Ile Val Gly Asp Ala
 210 215 220
 Asn Met Ala Glu Pro Ser Ile Ala Leu Lys Val Gly Ser Thr Leu Leu
 225 230 235 240
 Val Leu Glu Met Ile Glu Ala Asp Phe Gly Leu Pro Ser Leu Glu Leu
 245 250 255
 Ala Asn Asp Ile Ala Ser Ile Arg Glu Ile Ser Arg Asp Ala Thr Gly
 260 265 270
 Ser Thr Leu Leu Ser Leu Lys Asp Gly Thr Thr Met Thr Ala Leu Gln
 275 280 285
 Ile Gln Gln Val Val Phe Glu His Ala Ser Lys Trp Leu Glu Gln Arg
 290 295 300
 Pro Glu Pro Glu Phe Ser Gly Thr Ser Asn Thr Glu Met Ala Arg Val
 305 310 315 320
 Leu Asp Leu Trp Gly Arg Met Leu Lys Ala Ile Glu Ser Gly Asp Phe
 325 330 335
 Ser Glu Val Asp Thr Glu Ile Asp Trp Val Ile Lys Lys Lys Leu Ile
 340 345 350
 Asp Arg Phe Ile Gln Arg Gly Asn Leu Gly Leu Asp Asp Pro Lys Leu
 355 360 365
 Ala Gln Val Asp Leu Thr Tyr His Asp Ile Arg Pro Gly Arg Gly Leu
 370 375 380
 Phe Ser Val Leu Gln Ser Arg Gly Met Ile Lys Arg Trp Thr Thr Asp
 385 390 395 400
 Glu Ala Ile Leu Ala Ala Val Asp Thr Ala Pro Asp Thr Thr Arg Ala
 405 410 415
 His Leu Arg Gly Arg Ile Leu Lys Ala Ala Asp Thr Leu Gly Val Pro
 420 425 430
 Val Thr Val Asp Trp Met Arg His Lys Val Asn Arg Pro Glu Pro Gln
 435 440 445
 Ser Val Glu Leu Gly Asp Pro Phe Ser Leu Leu Asn Pro Gln Gln Pro
 450 455 460
 Ala Gln Glu Thr Ala Leu Ser Ile Leu Leu Leu Gly Gly Thr Ser Tyr
 465 470 475 480
 Ile Ala Gly Glu Ile Ala Thr Leu Thr Phe
 485 490

<210> 525
 <211> 1465
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1465)
 <223> FRXA01155

<400> 525
 acagcttgct ggtgaaatc gacggactgt tggaaaaaca cgcgaggaa ttcgttcgtt 60
 cctatgtaca aaaggggtggc gaatagtcac tgtgagttacc gtg gaa tcc gca ttg 115
 Val Glu Ser Ala Leu
 1 5
 acc cgc agg atc atg ggc att gaa acg gag tat ggc ctc acc ttt gtt 163
 Thr Arg Arg Ile Met Gly Ile Glu Thr Glu Tyr Gly Leu Thr Phe Val
 10 15 20
 gat ggt gat tcc aaa aag ctt cgc cca gat gag ata gct cga agg atg 211
 Asp Gly Asp Ser Lys Lys Leu Arg Pro Asp Glu Ile Ala Arg Arg Met
 25 30 35
 ttt cgt ccc atc gtg gag aaa tat tcc agc tct aat atc ttc ata ccc 259
 Phe Arg Pro Ile Val Glu Lys Tyr Ser Ser Ser Asn Ile Phe Ile Pro
 40 45 50
 aat ggt tcc cgg ttg tat ctt gat gtg ggt tcc cac ccg gag tac gcc 307
 Asn Gly Ser Arg Leu Tyr Leu Asp Val Gly Ser His Pro Glu Tyr Ala
 55 60 65
 acc gcc gag tgt gat aat ttg acc cag ctg atc aat ttt gaa aaa gct 355
 Thr Ala Glu Cys Asp Asn Leu Thr Gln Leu Ile Asn Phe Glu Lys Ala
 70 75 80 85
 ggc gat gtt att gca gat cgc atg gct gta gat gcc gaa gag tgg ctg 403
 Gly Asp Val Ile Ala Asp Arg Met Ala Val Asp Ala Glu Glu Ser Leu
 90 95 100
 gcg aaa gaa gac att gct ggg cag gtg tac ctg ttt aaa aac aat gtc 451
 Ala Lys Glu Asp Ile Ala Gly Gln Val Tyr Leu Phe Lys Asn Asn Val
 105 110 115
 gat tcc gtg ggc aat tct tat ggc tgc cac gaa aac tac ctt gtg ggt 499
 Asp Ser Val Gly Asn Ser Tyr Gly Cys His Glu Asn Tyr Leu Val Gly
 120 125 130
 cgc tcc atg ccg ttg aag gcg ttg ggt aaa agg ctg atg ccg ttt ctg 547
 Arg Ser Met Pro Leu Lys Ala Leu Gly Lys Arg Leu Met Pro Phe Leu
 135 140 145
 att acc cgc cag ctc atc tgc ggc gcc ggc agg atc cat cac ccc aat 595
 Ile Thr Arg Gln Leu Ile Cys Gly Ala Gly Arg Ile His His Pro Asn
 150 155 160 165
 cct ttg gat aaa ggc gaa tcc ttc ccc ttg ggc tac tgc ata tcc cag 643
 Pro Leu Asp Lys Gly Glu Ser Phe Pro Leu Gly Tyr Cys Ile Ser Gln
 170 175 180

cgc tct gac cac gtg tgg gag ggc gta tca agt gcc acc act aga tca Arg Ser Asp His Val Trp Glu Gly Val Ser Ser Ala Thr Arg Ser	691
185 190 195	
cgc ccc att atc aac acc cgt gat gag cca cat gcg gat tcc cat tct Arg Pro Ile Ile Asn Thr Arg Asp Glu Pro His Ala Asp Ser His Ser	739
200 205 210	
tac cgc agg ctg cac gtg att gtg ggt gat gcc aac atg gca gag ccc Tyr Arg Arg Leu His Val Ile Val Gly Asp Ala Asn Met Ala Glu Pro	787
215 220 225	
agc atc gcg ttg aag gtc ggc tcc acg ttg ctg gtt ctg gaa atg att Ser Ile Ala Leu Lys Val Gly Ser Thr Leu Leu Val Leu Glu Met Ile	835
230 235 240 245	
gag gca gat ttc ggt ttg ccc agc tta gag ctt gcc aat gat att gcc Glu Ala Asp Phe Gly Leu Pro Ser Leu Leu Ala Asn Asp Ile Ala	883
250 255 260	
tca att agg gaa atc tcc cgc gat gca aca gga tcc aca ctg ttg tcc Ser Ile Arg Glu Ile Ser Arg Asp Ala Thr Gly Ser Thr Leu Leu Ser	931
265 270 275	
ctg aaa gat ggc acc acc atg act gcc ttg cag atc cag cag gtg gtc Leu Lys Asp Gly Thr Thr Met Thr Ala Leu Gln Ile Gln Gln Val Val	979
280 285 290	
ttt gag cat gcc tcg aag tgg ttg gag cag cgc ccc gaa cca gaa ttt Phe Glu His Ala Ser Lys Trp Leu Glu Gln Arg Pro Glu Pro Glu Phe	1027
295 300 305	
tct ggc acc tcc aac aca gag atg gcc cgc gtg ctg gat ctg tgg ggt Ser Gly Thr Ser Asn Thr Glu Met Ala Arg Val Leu Asp Leu Trp Gly	1075
310 315 320 325	
cgc atg ttg aaa gcg att gag tcc ggt gat ttc agc gaa gtg gat aca Arg Met Leu Lys Ala Ile Glu Ser Gly Asp Phe Ser Glu Val Asp Thr	1123
330 335 340	
gaa att gac tgg gtg atc aaa aag aag ctc att gat cgt ttc att cag Glu Ile Asp Trp Val Ile Lys Lys Lys Leu Ile Asp Arg Phe Ile Gln	1171
345 350 355	
cgc ggc aac ctt ggg ttg gat gat cca aaa ctt gcc caa gtg gac ttg Arg Gly Asn Leu Gly Leu Asp Asp Pro Lys Leu Ala Gln Val Asp Leu	1219
360 365 370	
act tat cac gat att agg cca ggt aga ggc cta ttt agc gtg ctg caa Thr Tyr His Asp Ile Arg Pro Gly Arg Gly Leu Phe Ser Val Leu Gln	1267
375 380 385	
agc cgc ggc atg atc aaa cgg tgg act act gat gag gcg att tta gct Ser Arg Gly Met Ile Lys Arg Trp Thr Thr Asp Glu Ala Ile Leu Ala	1315
390 395 400 405	
gcg gtg gat acc gct cct gat aca aca cgt gct cat ttg cgc ggg cga Ala Val Asp Thr Ala Pro Asp Thr Thr Arg Ala His Leu Arg Gly Arg	1363
410 415 420	

atc ctt aaa gcg gcg gat act ctg gga gta cct gtg act gtc gat tgg 1411
 Ile Leu Lys Ala Ala Asp Thr Leu Gly Val Pro Val Thr Val Asp Trp
 425 430 435

atg cgt cac aag gtc aac cga ccg gag cca caa tcg gtg gaa ttg ggg 1459
 Met Arg His Lys Val Asn Arg Pro Glu Pro Gln Ser Val Glu Leu Gly
 440 445 450

gat cct 1465
 Asp Pro
 455

<210> 526

<211> 455

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 526

Val Glu Ser Ala Leu Thr Arg Arg Ile Met Gly Ile Glu Thr Glu Tyr
 1 5 10 15

Gly Leu Thr Phe Val Asp Gly Asp Ser Lys Lys Leu Arg Pro Asp Glu
 20 25 30

Ile Ala Arg Arg Met Phe Arg Pro Ile Val Glu Lys Tyr Ser Ser Ser
 35 40 45

Asn Ile Phe Ile Pro Asn Gly Ser Arg Leu Tyr Leu Asp Val Gly Ser
 50 55 60

His Pro Glu Tyr Ala Thr Ala Glu Cys Asp Asn Leu Thr Gln Leu Ile
 65 70 75 80

Asn Phe Glu Lys Ala Gly Asp Val Ile Ala Asp Arg Met Ala Val Asp
 85 90 95

Ala Glu Glu Ser Leu Ala Lys Glu Asp Ile Ala Gly Gln Val Tyr Leu
 100 105 110

Phe Lys Asn Asn Val Asp Ser Val Gly Asn Ser Tyr Gly Cys His Glu
 115 120 125

Asn Tyr Leu Val Gly Arg Ser Met Pro Leu Lys Ala Leu Gly Lys Arg
 130 135 140

Leu Met Pro Phe Leu Ile Thr Arg Gln Leu Ile Cys Gly Ala Gly Arg
 145 150 155 160

Ile His His Pro Asn Pro Leu Asp Lys Gly Glu Ser Phe Pro Leu Gly
 165 170 175

Tyr Cys Ile Ser Gln Arg Ser Asp His Val Trp Glu Gly Val Ser Ser
 180 185 190

Ala Thr Thr Arg Ser Arg Pro Ile Ile Asn Thr Arg Asp Glu Pro His
 195 200 205

Ala Asp Ser His Ser Tyr Arg Arg Leu His Val Ile Val Gly Asp Ala
 210 215 220


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Asn Met Ala Glu Pro Ser Ile Ala Leu Lys Val Gly Ser Thr Leu Leu
225                      230                      235                      240

Val Leu Glu Met Ile Glu Ala Asp Phe Gly Leu Pro Ser Leu Glu Leu
                      245                      250                      255

Ala Asn Asp Ile Ala Ser Ile Arg Glu Ile Ser Arg Asp Ala Thr Gly
260                      265                      270

Ser Thr Leu Leu Ser Leu Lys Asp Gly Thr Thr Met Thr Ala Leu Gln
275                      280                      285

Ile Gln Gln Val Val Phe Glu His Ala Ser Lys Trp Leu Glu Gln Arg
290                      295                      300

Pro Glu Pro Glu Phe Ser Gly Thr Ser Asn Thr Glu Met Ala Arg Val
305                      310                      315                      320

Leu Asp Leu Trp Gly Arg Met Leu Lys Ala Ile Glu Ser Gly Asp Phe
325                      330                      335

Ser Glu Val Asp Thr Glu Ile Asp Trp Val Ile Lys Lys Lys Leu Ile
340                      345                      350

Asp Arg Phe Ile Gln Arg Gly Asn Leu Gly Leu Asp Asp Pro Lys Leu
355                      360                      365

Ala Gln Val Asp Leu Thr Tyr His Asp Ile Arg Pro Gly Arg Gly Leu
370                      375                      380

Phe Ser Val Leu Gln Ser Arg Gly Met Ile Lys Arg Trp Thr Thr Asp
385                      390                      395                      400

Glu Ala Ile Leu Ala Ala Val Asp Thr Ala Pro Asp Thr Thr Arg Ala
405                      410                      415

His Leu Arg Gly Arg Ile Leu Lys Ala Ala Asp Thr Leu Gly Val Pro
420                      425                      430

Val Thr Val Asp Trp Met Arg His Lys Val Asn Arg Pro Glu Pro Gln
435                      440                      445

Ser Val Glu Leu Gly Asp Pro
450                      455

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<210> 527

<211> 519

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(496)

<223> RXN01167

<400> 527

gtgtcgtttt atttgcacac tagcaggtaa actgtgtgag acgaattctt ttgcggcaac 60

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ttggaggccg cattctagta ggcaaaggac tgatacctag atg gca gat cgc gtt    115
                Met Ala Asp Arg Val

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1

5

ctt cgt ggc agc cgc atg ggc gcc gtg agc tat gag acg gat agg gac 163
 Leu Arg Gly Ser Arg Met Gly Ala Val Ser Tyr Glu Thr Asp Arg Asp
 10 15 20

cac gat ctg gct cct cgc cag ctc gtg aag tac aag acc gca gac ggg 211
 His Asp Leu Ala Pro Arg Gln Leu Val Lys Tyr Lys Thr Ala Asp Gly
 25 30 35

gaa atc tat gag gtt ccc ttc gct gat gat gcg gaa atc ccc gag gag 259
 Glu Ile Tyr Glu Val Pro Phe Ala Asp Asp Ala Glu Ile Pro Glu Glu
 40 45 50

tgg atg tgc aag aac ggt aag cta ggc atc ctc atg gaa ggt gag gga 307
 Trp Met Cys Lys Asn Gly Lys Leu Gly Ile Leu Met Glu Gly Glu Gly
 55 60 65

gtc gag tcc aag ccg gtc aag cct cca cgt act cac tgg gat atg ttg 355
 Val Glu Ser Lys Pro Val Lys Pro Pro Arg Thr His Trp Asp Met Leu
 70 75 80 85

cgt gag cgt cgc tca att gaa gag ctg gat gtg ctg ctg gaa gag cgc 403
 Arg Glu Arg Arg Ser Ile Glu Glu Leu Asp Val Leu Leu Glu Glu Arg
 90 95 100

atc gag gca ctt cgt aag cgt cgt cgc aat gca gcg aaa ctg ctg aag 451
 Ile Glu Ala Leu Arg Lys Arg Arg Arg Asn Ala Ala Lys Leu Leu Lys
 105 110 115

gct cag caa gag gct gaa gaa gca gaa aag gca gct gaa gag gtt 496
 Ala Gln Gln Glu Ala Glu Glu Ala Glu Lys Ala Ala Glu Glu Val
 120 125 130

taatcttctt gcttaagtta gaa 519

<210> 528

<211> 132

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 528

Met Ala Asp Arg Val Leu Arg Gly Ser Arg Met Gly Ala Val Ser Tyr
 1 5 10 15

Glu Thr Asp Arg Asp His Asp Leu Ala Pro Arg Gln Leu Val Lys Tyr
 20 25 30

Lys Thr Ala Asp Gly Glu Ile Tyr Glu Val Pro Phe Ala Asp Asp Ala
 35 40 45

Glu Ile Pro Glu Glu Trp Met Cys Lys Asn Gly Lys Leu Gly Ile Leu
 50 55 60

Met Glu Gly Glu Gly Val Glu Ser Lys Pro Val Lys Pro Pro Arg Thr
 65 70 75 80

His Trp Asp Met Leu Arg Glu Arg Arg Ser Ile Glu Glu Leu Asp Val
 85 90 95

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Leu Leu Glu Glu Arg Ile Glu Ala Leu Arg Lys Arg Arg Arg Asn Ala
    100                      105                      110

Ala Lys Leu Leu Lys Ala Gln Gln Glu Ala Glu Glu Ala Glu Lys Ala
    115                      120                      125

Ala Glu Glu Val
    130

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<210> 529
 <211> 344
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(321)
 <223> FRXA01167

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<400> 529
cct cgc cag ctc gtc aag tac aag acc gca gac ggg gaa atc tat gag    48
Pro Arg Gln Leu Val Lys Tyr Lys Thr Ala Asp Gly Glu Ile Tyr Glu
   1           5           10           15

gtt ccc ttc gct gat gat gcg gaa atc ccc gag gag tgg atg tgc aag    96
Val Pro Phe Ala Asp Asp Ala Glu Ile Pro Glu Glu Trp Met Cys Lys
           20           25           30

aac ggt aag cta ggc atc ctc atg gaa ggt gag gga gtc gag tcc aag    144
Asn Gly Lys Leu Gly Ile Leu Met Glu Gly Glu Gly Val Glu Ser Lys
           35           40           45

ccg gtc aag cct cca cgt act cac tgg gat atg ttg cgt gag cgt cgc    192
Pro Val Lys Pro Pro Arg Thr His Trp Asp Met Leu Arg Glu Arg Arg
           50           55           60

tca att gaa gag ctg gat gtg ctg ctg gaa gag cgc atc gag gca ctt    240
Ser Ile Glu Glu Leu Asp Val Leu Leu Glu Glu Arg Ile Glu Ala Leu
           65           70           75           80

cgt aag cgt cgt cgc aat gca gcg aaa ctg ctg aag gct cag caa gag    288
Arg Lys Arg Arg Arg Asn Ala Ala Lys Leu Leu Lys Ala Gln Gln Glu
           85           90           95

gct gaa gaa gca gaa aag gca gct gaa gag gtt taatcttcct gcctaagtta 341
Ala Glu Glu Ala Glu Lys Ala Ala Glu Glu Val
           100           105

gaa                                                                    344

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<210> 530
 <211> 107
 <212> PRT
 <213> Corynebacterium glutamicum

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<400> 530
Pro Arg Gln Leu Val Lys Tyr Lys Thr Ala Asp Gly Glu Ile Tyr Glu
   1           5           10           15

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Val Pro Phe Ala Asp Asp Ala Glu Ile Pro Glu Glu Trp Met Cys Lys
 20 25 30
 Asn Gly Lys Leu Gly Ile Leu Met Glu Gly Glu Gly Val Glu Ser Lys
 35 40 45
 Pro Val Lys Pro Pro Arg Thr His Trp Asp Met Leu Arg Glu Arg Arg
 50 55 60
 Ser Ile Glu Glu Leu Asp Val Leu Leu Glu Glu Arg Ile Glu Ala Leu
 65 70 75 80
 Arg Lys Arg Arg Arg Asn Ala Ala Lys Leu Leu Lys Ala Gln Gln Glu
 85 90 95
 Ala Glu Glu Ala Glu Lys Ala Ala Glu Glu Val
 100 105

<210> 531
 <211> 1119
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1096)
 <223> RXN01169

<400> 531
 tcttgatcgg aatcggcgca aacatcgtct acgaacacct cagcgcgtaa cctcggcgcc 60
 attatcctca gacagctttt agcgcgcaaca aggagcatca ttg aaa cgg gtc gtt 115
 Leu Lys Arg Val Val
 1 5
 gaa gcg tgg gat aga ttt caa atc cca ctg tat atc acg gct ctt atc 163
 Glu Ala Trp Asp Arg Phe Gln Ile Pro Leu Tyr Ile Thr Ala Leu Ile
 10 15 20
 gcc gga gca ctg gtg ggt ttg cag tgg cca ggc tct aca ggg ggt ttc 211
 Ala Gly Ala Leu Val Gly Leu Gln Trp Pro Gly Ser Thr Gly Gly Phe
 25 30 35
 gaa agc gcc att aac cca gcg tta atg gcg ctg ctt tat gcc act ttt 259
 Glu Ser Ala Ile Asn Pro Ala Leu Met Ala Leu Leu Tyr Ala Thr Phe
 40 45 50
 ctc ggt att ccg atc act cgg att ggt gca gcg ctg aaa gat ctg aga 307
 Leu Gly Ile Pro Ile Thr Arg Ile Gly Ala Ala Leu Lys Asp Leu Arg
 55 60 65
 ttt ctc ata gtg ctc atg tcc gtc aat ttt gtt gca gtg cct ctg gtg 355
 Phe Leu Ile Val Leu Met Ser Val Asn Phe Val Ala Val Pro Leu Val
 70 75 80 85
 gct ttt gcg ttg agc aga ttc att gcg ggt gat gag gcg ctt cta atc 403
 Ala Phe Ala Leu Ser Arg Phe Ile Ala Gly Asp Glu Ala Leu Leu Ile
 90 95 100
 gga ttt tta ctg gtg att ctc gcg ccg tgc att gat tac gtc att gtc 451

Gly Phe Leu	Leu Val	Ile Leu	Ala Pro	Cys Ile	Asp Tyr	Val Ile	Val	
	105			110		115		
ttt gct ggt	ttg gcc agg	gcc gcc	caa gac	aag ctc	ctt gcc	gcc acg	499	
Phe Ala Gly	Leu Ala Arg	Ala Ala	Gln Asp	Lys Leu	Leu Ala	Ala Thr		
	120		125		130			
cca ata tta	atg ctt	gtc caa	atc ctg	ctg atc	ccc gtc	ttc ctg	gct	547
Pro Ile Leu	Met Leu	Val Gln	Ile Leu	Leu Ile	Pro Val	Phe Leu	Ala	
	135		140		145			
gtt ttt gtg	ggt tca	gat gcc	ctt ggc	tca atc	tct ttc	ggc cca	ttt	595
Val Phe Val	Gly Ser	Asp Ala	Leu Gly	Ser Ile	Ser Phe	Gly Pro	Phe	
	150		155		160		165	
gta gaa gca	ttt ttc	ctc ctg	att ctc	att cca	ctt gtt	gct gct	gcg	643
Val Glu Ala	Phe Phe	Leu Leu	Ile Leu	Ile Pro	Leu Val	Ala Ala	Ala	
		170		175		180		
gga act cag	caa gtg	gca aga	aag tgg	cag gta	gga cgt	aca att	atg	691
Gly Thr Gln	Gln Val	Ala Arg	Lys Trp	Gln Val	Gly Arg	Thr Ile	Met	
	185		190		195			
gct gct gca	gaa gca	atc atg	gtg cct	tta atg	atg ctg	acg ttg	ttc	739
Ala Ala Ala	Glu Ala	Ile Met	Val Pro	Leu Met	Met Leu	Thr Leu	Phe	
	200		205		210			
gct gtc atc	gca tgc	caa gtg	gaa gct	gtg agt	ggt caa	ttc acc	gat	787
Ala Val Ile	Ala Ser	Gln Val	Glu Ala	Val Ser	Gly Gln	Phe Thr	Asp	
	215		220		225			
atc gcc aca	gta gtg	cca cta	tat gtc	gcc ttt	ttg atg	gtg atg	att	835
Ile Ala Thr	Val Val	Pro Leu	Tyr Val	Ala Phe	Leu Met	Val Met	Ile	
	230		235		240		245	
cca att ggt	ggc ggg	ata tcc	aaa ctc	ggt ggc	tta ggt	ttc aaa	gag	883
Pro Ile Gly	Gly Gly	Ile Ser	Lys Leu	Gly Gly	Leu Gly	Phe Lys	Glu	
	250		255		260			
caa cga gcc	atc gtt	ttt agc	gga gca	acc cgt	aac tct	ttg gtc	gtt	931
Gln Arg Ala	Ile Val	Phe Ser	Gly Ala	Thr Arg	Asn Ser	Leu Val	Val	
	265		270		275			
tta cct tta	gcg tta	gca ctt	ccc gca	ggc ctg	gaa ata	gcg gcc	gtc	979
Leu Pro Leu	Ala Leu	Ala Leu	Pro Ala	Gly Leu	Glu Ile	Ala Ala	Val	
	280		285		290			
gta gtt gtc	act caa	acc ctc	gtg gaa	ctg att	ggc atg	gtt gtc	tac	1027
Val Val Val	Thr Gln	Thr Leu	Val Glu	Leu Ile	Gly Met	Val Val	Tyr	
	295		300		305			
gtg cgc atc	atc cct	tta att	ttc cat	gaa aag	cag aca	tac agg	aaa	1075
Val Arg Ile	Ile Pro	Leu Ile	Phe His	Glu Lys	Gln Thr	Tyr Arg	Lys	
	310		315		320		325	
ctt tca ggc	ata ggg	gag tca	tgaaacagaa	cggaagcta	agg			1119
Leu Ser Gly	Ile Gly	Glu Ser						
	330							

<210> 532

<211> 332

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 532

Leu Lys Arg Val Val Glu Ala Trp Asp Arg Phe Gln Ile Pro Leu Tyr
 1 5 10 15

Ile Thr Ala Leu Ile Ala Gly Ala Leu Val Gly Leu Gln Trp Pro Gly
 20 25 30

Ser Thr Gly Gly Phe Glu Ser Ala Ile Asn Pro Ala Leu Met Ala Leu
 35 40 45

Leu Tyr Ala Thr Phe Leu Gly Ile Pro Ile Thr Arg Ile Gly Ala Ala
 50 55 60

Leu Lys Asp Leu Arg Phe Leu Ile Val Leu Met Ser Val Asn Phe Val
 65 70 75 80

Ala Val Pro Leu Val Ala Phe Ala Leu Ser Arg Phe Ile Ala Gly Asp
 85 90 95

Glu Ala Leu Leu Ile Gly Phe Leu Leu Val Ile Leu Ala Pro Cys Ile
 100 105 110

Asp Tyr Val Ile Val Phe Ala Gly Leu Ala Arg Ala Ala Gln Asp Lys
 115 120 125

Leu Leu Ala Ala Thr Pro Ile Leu Met Leu Val Gln Ile Leu Leu Ile
 130 135 140

Pro Val Phe Leu Ala Val Phe Val Gly Ser Asp Ala Leu Gly Ser Ile
 145 150 155 160

Ser Phe Gly Pro Phe Val Glu Ala Phe Phe Leu Leu Ile Leu Ile Pro
 165 170 175

Leu Val Ala Ala Ala Gly Thr Gln Gln Val Ala Arg Lys Trp Gln Val
 180 185 190

Gly Arg Thr Ile Met Ala Ala Ala Glu Ala Ile Met Val Pro Leu Met
 195 200 205

Met Leu Thr Leu Phe Ala Val Ile Ala Ser Gln Val Glu Ala Val Ser
 210 215 220

Gly Gln Phe Thr Asp Ile Ala Thr Val Val Pro Leu Tyr Val Ala Phe
 225 230 235 240

Leu Met Val Met Ile Pro Ile Gly Gly Gly Ile Ser Lys Leu Gly Gly
 245 250 255

Leu Gly Phe Lys Glu Gln Arg Ala Ile Val Phe Ser Gly Ala Thr Arg
 260 265 270

Asn Ser Leu Val Val Leu Pro Leu Ala Leu Ala Leu Pro Ala Gly Leu
 275 280 285

Glu Ile Ala Ala Val Val Val Val Thr Gln Thr Leu Val Glu Leu Ile
 290 295 300

Gly Met Val Val Tyr Val Arg Ile Ile Pro Leu Ile Phe His Glu Lys
305 310 315 320

Gln Thr Tyr Arg Lys Leu Ser Gly Ile Gly Glu Ser
325 330

<210> 533

<211> 590

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(567)

<223> FRXA01169

<400> 533

atc ccc gtc ttc ctg gct gtt ttt gtg ggt tca gat gcc ctt ggc tca 48
Ile Pro Val Phe Leu Ala Val Phe Val Gly Ser Asp Ala Leu Gly Ser
1 5 10 15

atc tct ttc ggc cca ttt gta gaa gca ttt ttc ctc ctg att ctc att 96
Ile Ser Phe Gly Pro Phe Val Glu Ala Phe Phe Leu Leu Ile Leu Ile
20 25 30

cca ctt gtt gct gct gcg gga act cag caa gtg gca aga aag tgg cag 144
Pro Leu Val Ala Ala Ala Gly Thr Gln Gln Val Ala Arg Lys Trp Gln
35 40 45

gta gga cgt aca att atg gct gct gca gaa gca atc atg gtg cct tta 192
Val Gly Arg Thr Ile Met Ala Ala Glu Ala Ile Met Val Pro Leu
50 55 60

atg atg ctg acg ttg ttc gct gtc atc gca tcg caa gtg gaa gct gtg 240
Met Met Leu Thr Leu Phe Ala Val Ile Ala Ser Gln Val Glu Ala Val
65 70 75 80

agt ggt caa ttc acc gat atc gcc aca gta gtg cca cta tat gtc gcc 288
Ser Gly Gln Phe Thr Asp Ile Ala Thr Val Val Pro Leu Tyr Val Ala
85 90 95

ttt ttg atg gtg atg att cca att ggt ggc ggg ata tcc aaa ctc ggt 336
Phe Leu Met Val Met Ile Pro Ile Gly Gly Gly Ile Ser Lys Leu Gly
100 105 110

ggc tta ggt ttc aaa gag caa cga gcc atc gtt ttt agc gga gca acc 384
Gly Leu Gly Phe Lys Glu Gln Arg Ala Ile Val Phe Ser Gly Ala Thr
115 120 125

cgt aac tct ttg gtc gtt tta cct tta gcg tta gca ctt ccc gca ggc 432
Arg Asn Ser Leu Val Val Leu Pro Leu Ala Leu Ala Leu Pro Ala Gly
130 135 140

ctg gaa ata gcg gcc gtc gta gtt gtc act caa acc ctc gtg gaa ctg 480
Leu Glu Ile Ala Ala Val Val Val Val Thr Gln Thr Leu Val Glu Leu
145 150 155 160

att ggc atg gtt gtc tac gtg cgc atc atc cct tta att ttc cat gaa 528
Ile Gly Met Val Val Tyr Val Arg Ile Ile Pro Leu Ile Phe His Glu

165 170 175
 aag cag aca tac agg aaa ctt tca ggc ata ggg gag tca tgaacagaa 577
 Lys Gln Thr Tyr Arg Lys Leu Ser Gly Ile Gly Glu Ser
 180 185
 cggaagcta agg 590

<210> 534
 <211> 189
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 534
 Ile Pro Val Phe Leu Ala Val Phe Val Gly Ser Asp Ala Leu Gly Ser
 1 5 10 15
 Ile Ser Phe Gly Pro Phe Val Glu Ala Phe Phe Leu Leu Ile Leu Ile
 20 25 30
 Pro Leu Val Ala Ala Ala Gly Thr Gln Gln Val Ala Arg Lys Trp Gln
 35 40 45
 Val Gly Arg Thr Ile Met Ala Ala Ala Glu Ala Ile Met Val Pro Leu
 50 55 60
 Met Met Leu Thr Leu Phe Ala Val Ile Ala Ser Gln Val Glu Ala Val
 65 70 75 80
 Ser Gly Gln Phe Thr Asp Ile Ala Thr Val Val Pro Leu Tyr Val Ala
 85 90 95
 Phe Leu Met Val Met Ile Pro Ile Gly Gly Gly Ile Ser Lys Leu Gly
 100 105 110
 Gly Leu Gly Phe Lys Glu Gln Arg Ala Ile Val Phe Ser Gly Ala Thr
 115 120 125
 Arg Asn Ser Leu Val Val Leu Pro Leu Ala Leu Ala Leu Pro Ala Gly
 130 135 140
 Leu Glu Ile Ala Ala Val Val Val Val Thr Gln Thr Leu Val Glu Leu
 145 150 155 160
 Ile Gly Met Val Val Tyr Val Arg Ile Ile Pro Leu Ile Phe His Glu
 165 170 175
 Lys Gln Thr Tyr Arg Lys Leu Ser Gly Ile Gly Glu Ser
 180 185

<210> 535
 <211> 738
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> {101}...(715)
 <223> RXN01173

<400> 535

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agatctgttt ctatgtatta aagatcacac cgagtgggtgg aatttctctca agtgatttac 60
ccacaatgga ctttgttgat acccaattcg agaaaggcca atg cac gtg agc act 115
                                         Met His Val Ser Thr
                                         1                               5

ctt cca aac aag aaa ctg cgt act cgc att ttc gca ggc acc gct gcc 163
Leu Pro Asn Lys Lys Leu Arg Thr Arg Ile Phe Ala Gly Thr Ala Ala
                               10                               20

gtc gca ctg tca ctt ggt gtt gcg tct tgc tca aac gca gaa gat gct 211
Val Ala Leu Ser Leu Gly Val Ala Ser Cys Ser Asn Ala Glu Asp Ala
                               25                               30                               35

gtg gat agc gca aca gat gct gcc aac tct gca acc tcc gcc gcg gga 259
Val Asp Ser Ala Thr Asp Ala Ala Asn Ser Ala Thr Ser Ala Ala Gly
                               40                               45                               50

tct gca att aac gat gcc acc ggc act tcc agc gca tcc acc aca gag 307
Ser Ala Ile Asn Asp Ala Thr Gly Thr Ser Ser Ala Ser Thr Thr Glu
                               55                               60                               65

cct tcc gga acc tct gga tcc gac tcc ggg tct gac tct gct gga gga 355
Pro Ser Gly Thr Ser Gly Ser Asp Ser Gly Ser Asp Ser Ala Gly Gly
                               70                               75                               80                               85

gac acc act gaa gta gaa agc gcc gat ggg tcc acc atc agc atc cca 403
Asp Thr Thr Glu Val Glu Ser Ala Asp Gly Ser Thr Ile Ser Ile Pro
                               90                               95                               100

act gcc gtc gtc acc gct gca aat gct gca gga ttc agt acc ccg gaa 451
Thr Ala Val Val Thr Ala Ala Asn Ala Ala Gly Phe Ser Thr Pro Glu
                               105                               110                               115

tcc gtg gaa gaa ggc ccg aat ggt gag tca ttg gtg acg ttc cct gaa 499
Ser Val Glu Glu Gly Pro Asn Gly Glu Ser Leu Val Thr Phe Pro Glu
                               120                               125                               130

ggc tac att gtt aac tct gca gaa ggt ggt gca caa gca ctg gtc gcc 547
Gly Tyr Ile Val Asn Ser Ala Glu Gly Gly Ala Gln Ala Leu Val Gly
                               135                               140                               145

atg atc ggt gaa acc tgg atc ggc gaa ggc gga cta tcc gcg gca gtg 595
Met Ile Gly Glu Thr Trp Ile Gly Glu Gly Leu Ser Ala Ala Val
                               150                               155                               160                               165

ggt ctc cca act ggg cct gaa gaa gca aca aca aat ggt tgg act caa 643
Gly Leu Pro Thr Gly Pro Glu Glu Ala Thr Thr Asn Gly Trp Thr Gln
                               170                               175                               180

cag ttc aca tct gga gta att agc tgg ctt gat gat gga tca gga cag 691
Gln Phe Thr Ser Gly Val Ile Ser Trp Leu Asp Asp Gly Ser Gly Gln
                               185                               190                               195

ttc gca gct tct gtt gaa cct gct taagggaatc tcacctggcc tcc 738
Phe Ala Ala Ser Val Glu Pro Ala
                               200                               205

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<210> 536
<211> 205
<212> PRT
<213> Corynebacterium glutamicum
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400> 536																	
Met	His	Val	Ser	Thr	Leu	Pro	Asn	Lys	Lys	Leu	Arg	Thr	Arg	Ile	Phe		
1				5					10					15			
Ala Gly Thr Ala Ala Val Ala Leu Ser Leu Gly Val Ala Ser Cys Ser																	
			20					25					30				
Asn Ala Glu Asp Ala Val Asp Ser Ala Thr Asp Ala Ala Asn Ser Ala																	
		35					40						45				
Thr Ser Ala Ala Gly Ser Ala Ile Asn Asp Ala Thr Gly Thr Ser Ser																	
		50				55						60					
Ala Ser Thr Thr Glu Pro Ser Gly Thr Ser Gly Ser Asp Ser Gly Ser																	
		65			70					75					80		
Asp Ser Ala Gly Gly Asp Thr Thr Glu Val Glu Ser Ala Asp Gly Ser																	
				85					90					95			
Thr Ile Ser Ile Pro Thr Ala Val Val Thr Ala Ala Asn Ala Ala Gly																	
		100						105					110				
Phe Ser Thr Pro Glu Ser Val Glu Glu Gly Pro Asn Gly Glu Ser Leu																	
		115					120					125					
Val Thr Phe Pro Glu Gly Tyr Ile Val Asn Ser Ala Glu Gly Gly Ala																	
		130				135						140					
Gln Ala Leu Val Gly Met Ile Gly Glu Thr Trp Ile Gly Glu Gly Gly																	
		145			150					155				160			
Leu Ser Ala Ala Val Gly Leu Pro Thr Gly Pro Glu Glu Ala Thr Thr																	
				165				170						175			
Asn Gly Trp Thr Gln Gln Phe Thr Ser Gly Val Ile Ser Trp Leu Asp																	
			180					185					190				
Asp Gly Ser Gly Gln Phe Ala Ala Ser Val Glu Pro Ala																	
		195				200						205					

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<210> 537
<211> 738
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(715)
<223> FRXA01173
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<400> 537
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 ccacaatgga ctttgttgat acccaattcg agaaaggcca atg cac gtg agc act 115
 Met His Val Ser Thr

1

5

ctt cca aac aag aaa ctg cgt act cgc att ttc gca ggc acc gct gcc 163
 Leu Pro Asn Lys Lys Leu Arg Thr Arg Ile Phe Ala Gly Thr Ala Ala
 10 15 20

gtc gca ctg tca ctt ggt gtt gcg tct tgc tca aac gca gaa gat gct 211
 Val Ala Leu Ser Leu Gly Val Ala Ser Cys Ser Asn Ala Glu Asp Ala
 25 30 35

gtg gat agc gca aca gat gct gcc aac tct gca acc tcc gcc gcg gga 259
 Val Asp Ser Ala Thr Asp Ala Ala Asn Ser Ala Thr Ser Ala Ala Gly
 40 45 50

tct gca att aac gat gcc acc ggc act tcc agc gca tcc acc aca gag 307
 Ser Ala Ile Asn Asp Ala Thr Gly Thr Ser Ser Ala Ser Thr Thr Glu
 55 60 65

cct tcc gga acc tct gga tcc gac tcc ggg tct gac tct gct gga gga 355
 Pro Ser Gly Thr Ser Gly Ser Asp Ser Gly Ser Asp Ser Ala Gly Gly
 70 75 80 85

gac acc act gaa gta gaa agc gcc gat ggg tcc acc atc agc atc cca 403
 Asp Thr Thr Glu Val Glu Ser Ala Asp Gly Ser Thr Ile Ser Ile Pro
 90 95 100

act gcc gtc gtc acc gct gca aat gct gca gga ttc agt acc ccg gaa 451
 Thr Ala Val Val Thr Ala Ala Asn Ala Ala Gly Phe Ser Thr Pro Glu
 105 110 115

tcc gtg gaa gaa ggc ccg aat ggt gag tca ttg gtg acg ttc cct gaa 499
 Ser Val Glu Glu Gly Pro Asn Gly Glu Ser Leu Val Thr Phe Pro Glu
 120 125 130

ggc tac att gtt aac tct gca gaa ggt ggt gca caa gca ctg gtc gcc 547
 Gly Tyr Ile Val Asn Ser Ala Glu Gly Gly Ala Gln Ala Leu Val Gly
 135 140 145

atg atc ggt gaa acc tgg atc ggc gaa ggc gga cta tcc gcg gca gtg 595
 Met Ile Gly Glu Thr Trp Ile Gly Glu Gly Gly Leu Ser Ala Ala Val
 150 155 160 165

ggt ctc cca act ggg cct gaa gaa gca aca aca aat ggt tgg act caa 643
 Gly Leu Pro Thr Gly Pro Glu Glu Ala Thr Thr Asn Gly Trp Thr Gln
 170 175 180

cag ttc aca tct gga gta att agc tgg ctt gat gat gga tca gga cag 691
 Gln Phe Thr Ser Gly Val Ile Ser Trp Leu Asp Asp Gly Ser Gly Gln
 185 190 195

ttc gca gct tct gtt gaa cct gct taagggaatc tcacctggcc tcc 738
 Phe Ala Ala Ser Val Glu Pro Ala
 200 205

<210> 538

<211> 205

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 538

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Met His Val Ser Thr Leu Pro Asn Lys Lys Leu Arg Thr Arg Ile Phe
 1          5          10          15

Ala Gly Thr Ala Ala Val Ala Leu Ser Leu Gly Val Ala Ser Cys Ser
          20          25          30

Asn Ala Glu Asp Ala Val Asp Ser Ala Thr Asp Ala Ala Asn Ser Ala
          35          40          45

Thr Ser Ala Ala Gly Ser Ala Ile Asn Asp Ala Thr Gly Thr Ser Ser
          50          55          60

Ala Ser Thr Thr Glu Pro Ser Gly Thr Ser Gly Ser Asp Ser Gly Ser
          65          70          75          80

Asp Ser Ala Gly Gly Asp Thr Thr Glu Val Glu Ser Ala Asp Gly Ser
          85          90          95

Thr Ile Ser Ile Pro Thr Ala Val Val Thr Ala Ala Asn Ala Ala Gly
          100          105          110

Phe Ser Thr Pro Glu Ser Val Glu Glu Gly Pro Asn Gly Glu Ser Leu
          115          120          125

Val Thr Phe Pro Glu Gly Tyr Ile Val Asn Ser Ala Glu Gly Gly Ala
          130          135          140

Gln Ala Leu Val Gly Met Ile Gly Glu Thr Trp Ile Gly Glu Gly Gly
          145          150          155          160

Leu Ser Ala Ala Val Gly Leu Pro Thr Gly Pro Glu Glu Ala Thr Thr
          165          170          175

Asn Gly Trp Thr Gln Gln Phe Thr Ser Gly Val Ile Ser Trp Leu Asp
          180          185          190

Asp Gly Ser Gly Gln Phe Ala Ala Ser Val Glu Pro Ala
          195          200          205

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<210> 539

<211> 873

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(850)

<223> RXN01174

<400> 539

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agatggtgga attagctcgg aatattgaga agttgaggta atg agc aac atg cag 115
                Met Ser Asn Met Gln
                1          5

```

```

gga aac gat tcc aag aaa tct agc ggc gcg agt cgt gcg gag agc cca 163
Gly Asn Asp Ser Lys Lys Ser Ser Gly Ala Ser Arg Ala Glu Ser Pro
          10          15          20

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ctg atc aag ttc cgg aca ttg att atc gtc atc ttt gtc atc ttg atc	211
Leu Ile Lys Phe Arg Thr Leu Ile Ile Val Ile Phe Val Ile Leu Ile	
25 30 35	
ggt ggt ttg gca tct att gca gtg gga cct gtc gtg tac cag ctc atc	259
Val Gly Leu Ala Ser Ile Ala Val Gly Pro Val Val Tyr Gln Leu Ile	
40 45 50	
atg gga cct ggt gtg aaa acc gaa gga atc cag gct gat ggc gca gca	307
Met Gly Pro Gly Val Lys Thr Glu Gly Ile Gln Ala Asp Gly Ala Ala	
55 60 65	
cct gcg tcc acc gac atg aac ggc acc tgg gat gtt gcc cca ggg agt	355
Pro Ala Ser Thr Asp Met Asn Gly Thr Trp Asp Val Ala Pro Gly Ser	
70 75 80 85	
att cca aac acc acc tca gct gga ttc acc ttc gct gag atc ctg cca	403
Ile Pro Asn Thr Thr Ser Ala Gly Phe Thr Phe Ala Glu Ile Leu Pro	
90 95 100	
ggc gaa gaa aag atc acc tcc ggc tca acc act ggt gtc act ggc gaa	451
Gly Glu Glu Lys Ile Thr Ser Gly Ser Thr Thr Thr Gly Glu Glu	
105 110 115	
gtg gtc atc gag gat aac tcc ctg atc tct ggt ctg att acc gtc aac	499
Val Val Ile Glu Asp Asn Ser Leu Ile Ser Gly Leu Ile Thr Val Asn	
120 125 130	
atg act cac atc acc acc gat cag gaa aag cgc gac atc aac gtg cgc	547
Met Thr His Ile Thr Thr Asp Gln Glu Lys Arg Asp Ile Asn Val Arg	
135 140 145	
act aag ctc ttc cac acc gat cag tac cca gaa gca acc ttt gag gtt	595
Thr Lys Leu Phe His Thr Asp Gln Tyr Pro Glu Ala Thr Phe Glu Val	
150 155 160 165	
acc gat tcc gtt gat ctt tct gcg ctc cca gac acc gga tcc att gct	643
Thr Asp Ser Val Asp Leu Ser Ala Leu Pro Asp Thr Gly Ser Ile Ala	
170 175 180	
cag gtt gtc atc cca ggc gag ttg acc atc cac ggt gaa acc aag gct	691
Gln Val Val Ile Pro Gly Glu Leu Thr Ile His Gly Glu Thr Lys Ala	
185 190 195	
gtg gag cct acc ttt gat gta ctt cgt act ggt gac caa gtt atc gtg	739
Val Glu Pro Thr Phe Asp Val Leu Arg Thr Gly Asp Gln Val Ile Val	
200 205 210	
gct tcc gat atc gaa atc aac cgc ctc gac ttc ggt gta gaa acc cca	787
Ala Ser Asp Ile Glu Ile Asn Arg Leu Asp Phe Gly Val Glu Thr Pro	
215 220 225	
gag ttc atc gcc gca aag atc aat gag acc ggc gag atc aac gtc cga	835
Glu Phe Ile Ala Ala Lys Ile Asn Glu Thr Gly Glu Ile Asn Val Arg	
230 235 240 245	
atc gta ttg gag aaa taaacctga tggcatcacg gat	873
Ile Val Leu Glu Lys	
250	

<210> 540
 <211> 250
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 540
 Met Ser Asn Met Gln Gly Asn Asp Ser Lys Lys Ser Ser Gly Ala Ser
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 Arg Ala Glu Ser Pro Leu Ile Lys Phe Arg Thr Leu Ile Ile Val Ile
 20 25 30
 Phe Val Ile Leu Ile Val Gly Leu Ala Ser Ile Ala Val Gly Pro Val
 35 40 45
 Val Tyr Gln Leu Ile Met Gly Pro Gly Val Lys Thr Glu Gly Ile Gln
 50 55 60
 Ala Asp Gly Ala Ala Pro Ala Ser Thr Asp Met Asn Gly Thr Trp Asp
 65 70 75 80
 Val Ala Pro Gly Ser Ile Pro Asn Thr Thr Ser Ala Gly Phe Thr Phe
 85 90 95
 Ala Glu Ile Leu Pro Gly Glu Glu Lys Ile Thr Ser Gly Ser Thr Thr
 100 105 110
 Gly Val Thr Gly Glu Val Val Ile Glu Asp Asn Ser Leu Ile Ser Gly
 115 120 125
 Leu Ile Thr Val Asn Met Thr His Ile Thr Thr Asp Gln Glu Lys Arg
 130 135 140
 Asp Ile Asn Val Arg Thr Lys Leu Phe His Thr Asp Gln Tyr Pro Glu
 145 150 155 160
 Ala Thr Phe Glu Val Thr Asp Ser Val Asp Leu Ser Ala Leu Pro Asp
 165 170 175
 Thr Gly Ser Ile Ala Gln Val Val Ile Pro Gly Glu Leu Thr Ile His
 180 185 190
 Gly Glu Thr Lys Ala Val Glu Pro Thr Phe Asp Val Leu Arg Thr Gly
 195 200 205
 Asp Gln Val Ile Val Ala Ser Asp Ile Glu Ile Asn Arg Leu Asp Phe
 210 215 220
 Gly Val Glu Thr Pro Glu Phe Ile Ala Ala Lys Ile Asn Glu Thr Gly
 225 230 235 240
 Glu Ile Asn Val Arg Ile Val Leu Glu Lys
 245 250

<210> 541
 <211> 873
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(850)

<223> FRXA01174

<400> 541

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agatggtgga attagctcgg aatattgaga agttgagga atg agc aac atg cag 115
                               Met Ser Asn Met Gln
                               1 5
gga aac gat tcc aag aaa tct agc ggc gcg agt cgt gcg gag agc cca 163
Gly Asn Asp Ser Lys Lys Ser Ser Gly Ala Ser Arg Ala Glu Ser Pro
                               10 15 20
ctg atc aag ttc cgg aca ttg att atc gtc atc ttt gtc atc ttg atc 211
Leu Ile Lys Phe Arg Thr Leu Ile Ile Val Ile Phe Val Ile Leu Ile
                               25 30 35
gtt ggt ttg gca tct att gca gtg gga cct gtc gtg tac cag ctc atc 259
Val Gly Leu Ala Ser Ile Ala Val Gly Pro Val Val Tyr Gln Leu Ile
                               40 45 50
atg gga cct ggt gtg aaa acc gaa gga atc cag gct gat ggc gca gca 307
Met Gly Pro Gly Val Lys Thr Glu Gly Ile Gln Ala Asp Gly Ala Ala
                               55 60 65
cct gcg tcc acc gac atg aac ggc acc tgg gat gtt gcc cca ggg agt 355
Pro Ala Ser Thr Asp Met Asn Gly Thr Trp Asp Val Ala Pro Gly Ser
                               70 75 80 85
att cca aac acc acc tca gct gga ttc acc ttc gct gag atc ctg cca 403
Ile Pro Asn Thr Thr Ser Ala Gly Phe Thr Phe Ala Glu Ile Leu Pro
                               90 95 100
ggc gaa gaa aag atc acc tcc ggc tca acc act ggt gtc act ggc gaa 451
Gly Glu Glu Lys Ile Thr Ser Gly Ser Thr Thr Gly Val Thr Gly Glu
                               105 110 115
gtg gtc atc gag gat aac tcc ctg atc tct ggt ctg att acc gtc aac 499
Val Val Ile Glu Asp Asn Ser Leu Ile Ser Gly Leu Ile Thr Val Asn
                               120 125 130
atg act cac atc acc acc gat cag gaa aag cgc gac atc aac gtg cgc 547
Met Thr His Ile Thr Thr Asp Gln Glu Lys Arg Asp Ile Asn Val Arg
                               135 140 145
act aag ctc ttc cac acc gat cag tac cca gaa gca acc ttt gag gtt 595
Thr Lys Leu Phe His Thr Asp Gln Tyr Pro Glu Ala Thr Phe Glu Val
                               150 155 160 165
acc gat tcc gtt gat ctt tct gcg ctc cca gac acc gga tcc att gct 643
Thr Asp Ser Val Asp Leu Ser Ala Leu Pro Asp Thr Gly Ser Ile Ala
                               170 175 180
cag gtt gtc atc cca ggc gag ttg acc atc cac ggt gaa acc aag gct 691
Gln Val Val Ile Pro Gly Glu Leu Thr Ile His Gly Glu Thr Lys Ala
                               185 190 195
gtg gag cct acc ttt gat gta ctt cgt act ggt gac caa gtt atc gtg 739
Val Glu Pro Thr Phe Asp Val Leu Arg Thr Gly Asp Gln Val Ile Val

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200	205	210	
gct tcc gat atc gaa atc aac cgc ctc gac ttc ggt gta gaa acc cca			787
Ala Ser Asp Ile Glu Ile Asn Arg Leu Asp Phe Gly Val Glu Thr Pro			
215	220	225	
gag ttc atc gcc gca aag atc aat gag acc ggc gag atc aac gtc cga			835
Glu Phe Ile Ala Ala Lys Ile Asn Glu Thr Gly Glu Ile Asn Val Arg			
230	235	240	245
atc gta ttg gag aaa taaacctga tggcatcacg gat			873
Ile Val Leu Glu Lys			
250			

<210> 542

<211> 250

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 542

Met Ser Asn Met Gln Gly Asn Asp Ser Lys Lys Ser Ser Gly Ala Ser			
1	5	10	15
Arg Ala Glu Ser Pro Leu Ile Lys Phe Arg Thr Leu Ile Ile Val Ile			
20	25	30	
Phe Val Ile Leu Ile Val Gly Leu Ala Ser Ile Ala Val Gly Pro Val			
35	40	45	
Val Tyr Gln Leu Ile Met Gly Pro Gly Val Lys Thr Glu Gly Ile Gln			
50	55	60	
Ala Asp Gly Ala Ala Pro Ala Ser Thr Asp Met Asn Gly Thr Trp Asp			
65	70	75	80
Val Ala Pro Gly Ser Ile Pro Asn Thr Thr Ser Ala Gly Phe Thr Phe			
85	90	95	
Ala Glu Ile Leu Pro Gly Glu Glu Lys Ile Thr Ser Gly Ser Thr Thr			
100	105	110	
Gly Val Thr Gly Glu Val Val Ile Glu Asp Asn Ser Leu Ile Ser Gly			
115	120	125	
Leu Ile Thr Val Asn Met Thr His Ile Thr Thr Asp Gln Glu Lys Arg			
130	135	140	
Asp Ile Asn Val Arg Thr Lys Leu Phe His Thr Asp Gln Tyr Pro Glu			
145	150	155	160
Ala Thr Phe Glu Val Thr Asp Ser Val Asp Leu Ser Ala Leu Pro Asp			
165	170	175	
Thr Gly Ser Ile Ala Gln Val Val Ile Pro Gly Glu Leu Thr Ile His			
180	185	190	
Gly Glu Thr Lys Ala Val Glu Pro Thr Phe Asp Val Leu Arg Thr Gly			
195	200	205	
Asp Gln Val Ile Val Ala Ser Asp Ile Glu Ile Asn Arg Leu Asp Phe			

210

215

220

Gly Val Glu Thr Pro Glu Phe Ile Ala Ala Lys Ile Asn Glu Thr Gly
 225 230 235 240

Glu Ile Asn Val Arg Ile Val Leu Glu Lys
 245 250

<210> 543

<211> 1401

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1378)

<223> RXN01229

<400> 543

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aagctgtgct tatagggctt cctgcaccga taaaggactg atg atc atc tcc act 115
 Met Ile Ile Ser Thr 5

aac acc gct cac ccc ctg cac gaa ccg cac gta ccc agc cac cac aat 163
 Asn Thr Ala His Pro Leu His Glu Pro His Val Pro Ser His His Asn 10 15 20

cgt atg aat act ctg cgt gcc ggt gtg ctg ggt gct aat gac ggt atc 211
 Arg Met Asn Thr Leu Arg Ala Gly Val Leu Gly Ala Asn Asp Gly Ile 25 30 35

gtc tcc att gct gcg cta ctg ctc ggt gtg atc gcc acc gcc gcc agt 259
 Val Ser Ile Ala Ala Leu Leu Leu Gly Val Ile Ala Thr Gly Ala Ser 40 45 50

gac acc gtc gtg ttc ggc gct ggt ttg gcc tca acg atc gcg ggg gcg 307
 Asp Thr Val Val Phe Gly Ala Gly Leu Ala Ser Thr Ile Ala Gly Ala 55 60 65

gta tct atg gct ctc ggt gag tac gtc tct gtc tcc tca cag cgt gat 355
 Val Ser Met Ala Leu Gly Glu Tyr Val Ser Val Ser Ser Gln Arg Asp 70 75 80 85

acc gaa ccg gtg ctc atc gca aaa gaa gcg aag gag ctg gcc gaa gac 403
 Thr Glu Arg Val Leu Ile Ala Lys Glu Ala Lys Glu Leu Ala Glu Asp 90 95 100

ccg acg gcc gag cac gtc gag ctg tcg gag atc cta cac tcc tac gcc 451
 Pro Thr Ala Glu His Val Leu Ser Ser Glu Ile Leu His Ser Tyr Gly 105 110 115

atc tmc mmt gwg amt smr ras sms gcs rmm ayc grg awm ggg mas gcc 499
 Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Gly 120 125 130

gac gcc ttg gcc gcc cac ctt cag ctc gag ctc ggt att gat aat gag 547
 Asp Ala Leu Gly Ala His Leu Gln Leu Glu Leu Gly Ile Asp Asn Glu 135 140 145

caa ctg acc agc ccc ttg gcc gcc gcc ttc tcc tcg gcc gtg gct ttc	595
Gln Leu Thr Ser Pro Leu Ala Ala Ala Phe Ser Ser Ala Val Ala Phe	
150 155 160 165	
ctg ctc gga gca ctg ctg ccg atg gtg tyg gta ttc mtg gcc ccy kca	643
Leu Leu Gly Ala Leu Leu Pro Met Val Xaa Val Phe Xaa Ala Xaa Xaa	
170 175 180	
ggc tgg gac gcc ggc gtc gkc ttc gta gtc acg stg ctg gtc ctg gcg	691
Gly Trp Asp Ala Gly Xaa Xaa Phe Val Val Thr Xaa Leu Val Leu Ala	
185 190 195	
gkk acc ggg ttc atc tca rcc cmg rtc ycg ggt acc tyc ccm atg cgc	739
Xaa Thr Gly Phe Ile Ser Xaa Xaa Xaa Gly Thr Xaa Xaa Met Arg	
200 205 210	
gsg tgc sgg sgc ttk gkg rtc ggk ggt kcc ctc sgs cyg gcc ctg acc	787
Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Leu Xaa Xaa Ala Leu Thr	
215 220 225	
mta ccg tct tgg aaw cwa tts kks gss gcm gyw ktm kgw gsy kcs ksr	835
Xaa Pro Ser Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	
230 235 240 245	
rra mar arr rgg rrk rmk gsk kkt ktk gtg gyk gsk sgk ykt tkt cgw	883
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Xaa Xaa Xaa Xaa	
250 255 260	
cgm cks sws ram gwr rts rkc gsc gmc swc cty syw gmm say cmk ssg	931
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	
265 270 275	
ssk scw kqr wss rcy gcy scm ssm ggs ksk csm swk wtr kks yss sks	979
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	
280 285 290	
wsu mtw cky ktt tyy cyy csg smr gkw amc mmm myk gkk syw wkr rrw	1027
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	
295 300 305	
tkt tty ykr rra rrm srm ywm csr rkw rgg cca cca ctg tca ggc gag	1075
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Pro Leu Ser Gly Glu	
310 315 320 325	
att ctg ctt gct ggc ctc ggc ggt gag ata ggc atg ggg gaa ccg agg	1123
Ile Leu Leu Ala Gly Leu Gly Gly Glu Ile Gly Met Gly Glu Pro Arg	
330 335 340	
atc cca gtg act act ggt gac ctg gaa acc cgc ggt ctc cag tgc ctg	1171
Ile Pro Val Thr Thr Gly Asp Leu Glu Thr Arg Gly Leu Gln Cys Leu	
345 350 355	
ggc aag ctc ggg cag tgg coa ccg gta ggc ggt ggc cac ggg atg ata	1219
Gly Lys Leu Gly Gln Trp Pro Pro Val Gly Gly Gly His Gly Met Ile	
360 365 370	
cat cgg ttc cag aga agg ccc gga gaa aaa gga cat cag cag gcc acc	1267
His Arg Phe Gln Arg Arg Pro Gly Glu Lys Gly His Gln Gln Ala Thr	
375 380 385	

acc atc ctc cac cgc cat ccg cag tgc gac cag ggc gtc ggg cag ctc 1315
 Thr Ile Leu His Arg His Pro Gln Cys Asp Gln Gly Val Gly Gln Leu
 390 395 400 405

gcc cgg gcc cat gtg gat cag gga gta cca ggc caa cag gcc tgc cca 1363
 Ala Arg Ala His Val Asp Gln Gly Val Pro Gly Gln Gln Ala Cys Pro
 410 415 420

gcg ctt cgg cga gtc tgagaggtcg gtaatagtgc cgt 1401
 Ala Leu Arg Arg Val
 425

<210> 544

<211> 426

<212> PRT

<213> Corynebacterium glutamicum

<400> 544

Met Ile Ile Ser Thr Asn Thr Ala His Pro Leu His Glu Pro His Val
 1 5 10 15

Pro Ser His His Asn Arg Met Asn Thr Leu Arg Ala Gly Val Leu Gly
 20 25 30

Ala Asn Asp Gly Ile Val Ser Ile Ala Ala Leu Leu Leu Gly Val Ile
 35 40 45

Ala Thr Gly Ala Ser Asp Thr Val Val Phe Gly Ala Gly Leu Ala Ser
 50 55 60

Thr Ile Ala Gly Ala Val Ser Met Ala Leu Gly Glu Tyr Val Ser Val
 65 70 75 80

Ser Ser Gln Arg Asp Thr Glu Arg Val Leu Ile Ala Lys Glu Ala Lys
 85 90 95

Glu Leu Ala Glu Asp Pro Thr Ala Glu His Val Glu Leu Ser Glu Ile
 100 105 110

Leu His Ser Tyr Gly Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 115 120 125

Xaa Xaa Gly Xaa Gly Asp Ala Leu Gly Ala His Leu Gln Leu Glu Leu
 130 135 140

Gly Ile Asp Asn Glu Gln Leu Thr Ser Pro Leu Ala Ala Ala Phe Ser
 145 150 155 160

Ser Ala Val Ala Phe Leu Leu Gly Ala Leu Leu Pro Met Val Xaa Val
 165 170 175

Phe Xaa Ala Xaa Xaa Gly Trp Asp Ala Gly Xaa Xaa Phe Val Val Thr
 180 185 190

Xaa Leu Val Leu Ala Xaa Thr Gly Phe Ile Ser Xaa Xaa Xaa Xaa Gly
 195 200 205

Thr Xaa Xaa Met Arg Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Leu
 210 215 220

Xaa Xaa Ala Leu Thr Xaa Pro Ser Trp Xaa Xaa Xaa Xaa Xaa Xaa
 225 230 235 240
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa
 245 250 255
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 260 265 270
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 275 280 285
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 290 295 300
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro
 305 310 315 320
 Pro Leu Ser Gly Glu Ile Leu Leu Ala Gly Leu Gly Gly Glu Ile Gly
 325 330 335
 Met Gly Glu Pro Arg Ile Pro Val Thr Thr Gly Asp Leu Glu Thr Arg
 340 345 350
 Gly Leu Gln Cys Leu Gly Lys Leu Gly Gln Trp Pro Pro Val Gly Gly
 355 360 365
 Gly His Gly Met Ile His Arg Phe Gln Arg Arg Pro Gly Glu Lys Gly
 370 375 380
 His Gln Gln Ala Thr Thr Ile Leu His Arg His Pro Gln Cys Asp Gln
 385 390 395 400
 Gly Val Gly Gln Leu Ala Arg Ala His Val Asp Gln Gly Val Pro Gly
 405 410 415
 Gln Gln Ala Cys Pro Ala Leu Arg Arg Val
 420 425

<210> 545

<211> 793

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(793)

<223> FRXA01229

<400> 545

tagcccgaa agacggcgag ggttggtct gcttcgttgt gggaaaacta ggcccttaat 60

aagctgtgct tatagggtct cctgcaccga taaaggactg atg atc atc tcc act 115
 Met Ile Ile Ser Thr
 1 5

aac acc gct cac ccc ctg cac gaa ccg cac gta ccc agc cac cac aat 163
 Asn Thr Ala His Pro Leu His Glu Pro His Val Pro Ser His His Asn
 10 15 20

cgt atg aat act ctg cgt gcc ggt gtg ctg ggt gct aat gac ggt atc 211
 Arg Met Asn Thr Leu Arg Ala Gly Val Leu Gly Ala Asn Asp Gly Ile
 25 30 35
 gtc tcc att gct gcg cta ctg ctc ggt gtg atc gcc acc ggc gcc agt 259
 Val Ser Ile Ala Ala Leu Leu Gly Val Ile Ala Thr Gly Ala Ser
 40 45 50
 gac acc gtc gtg ttc ggc gct ggt ttg gcc tca acg atc gcg ggg gcg 307
 Asp Thr Val Val Phe Gly Ala Gly Leu Ala Ser Thr Ile Ala Gly Ala
 55 60 65
 gta tct atg gct ctc ggt gag tac gtc tct gtc tcc tca cag cgt gat 355
 Val Ser Met Ala Leu Gly Glu Tyr Val Ser Val Ser Ser Gln Arg Asp
 70 75 80 85
 acc gaa cgg gtg ctc atc gca aaa gaa gcg aag gag ctg gcc gaa gac 403
 Thr Glu Arg Val Leu Ile Ala Lys Glu Ala Lys Glu Leu Ala Glu Asp
 90 95 100
 ccg acg gcc gag cac gtc gag ctg tcg gag atc cta cac tcc tac ggc 451
 Pro Thr Ala Glu His Val Leu Ser Glu Ile Leu His Ser Tyr Gly
 105 110 115
 atc tcc cct gag act gcg aac cag gcg gcc acc gag atc ggg cag gcc 499
 Ile Ser Pro Glu Thr Ala Asn Gln Ala Ala Thr Glu Ile Gly Gln Gly
 120 125 130
 gac gcc ttg ggc gcc cac ctt cag ctc gag ctc ggt att gat aat gag 547
 Asp Ala Leu Gly Ala His Leu Gln Leu Glu Leu Gly Ile Asp Asn Glu
 135 140 145
 caa ctg acc agc ccc ttg gcc gcc gcc ttc tcc tcg gcc gtg gct ttc 595
 Gln Leu Thr Ser Pro Leu Ala Ala Ala Phe Ser Ser Ala Val Ala Phe
 150 155 160 165
 ctg ctc gga gca ctg ctg ccg atg gtg tcg gta ttc atc gcc cct gca 643
 Leu Leu Gly Ala Leu Leu Pro Met Val Ser Val Phe Ile Ala Pro Ala
 170 175 180
 ggc tgg gac gcc ggc gtg gtc ttc gta gtc acg ctg ctg gtc ctg gcg 691
 Gly Trp Asp Ala Gly Val Val Phe Val Val Thr Leu Leu Val Leu Ala
 185 190 195
 gtg acc ggg ttc atc tca gcc cag atc tcg ggt acc tcc cca atg cgc 739
 Val Thr Gly Phe Ile Ser Ala Gln Ile Ser Gly Thr Ser Pro Met Arg
 200 205 210
 gcg tgc ggg cgc ttg gtg atc ggt ggt gcc ctc ggc ctg gcc cta acc 787
 Ala Cys Gly Arg Leu Val Ile Gly Gly Ala Leu Gly Leu Ala Leu Thr
 215 220 225
 tac ggt 793
 Tyr Gly
 230

<210> 546

<211> 231

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 546

Met Ile Ile Ser Thr Asn Thr Ala His Pro Leu His Glu Pro His Val
 1 5 10 15

Pro Ser His His Asn Arg Met Asn Thr Leu Arg Ala Gly Val Leu Gly
 20 25 30

Ala Asn Asp Gly Ile Val Ser Ile Ala Ala Leu Leu Leu Gly Val Ile
 35 40 45

Ala Thr Gly Ala Ser Asp Thr Val Val Phe Gly Ala Gly Leu Ala Ser
 50 55 60

Thr Ile Ala Gly Ala Val Ser Met Ala Leu Gly Glu Tyr Val Ser Val
 65 70 75 80

Ser Ser Gln Arg Asp Thr Glu Arg Val Leu Ile Ala Lys Glu Ala Lys
 85 90 95

Glu Leu Ala Glu Asp Pro Thr Ala Glu His Val Glu Leu Ser Glu Ile
 100 105 110

Leu His Ser Tyr Gly Ile Ser Pro Glu Thr Ala Asn Gln Ala Ala Thr
 115 120 125

Glu Ile Gly Gln Gly Asp Ala Leu Gly Ala His Leu Gln Leu Glu Leu
 130 135 140

Gly Ile Asp Asn Glu Gln Leu Thr Ser Pro Leu Ala Ala Phe Ser
 145 150 155 160

Ser Ala Val Ala Phe Leu Leu Gly Ala Leu Leu Pro Met Val Ser Val
 165 170 175

Phe Ile Ala Pro Ala Gly Trp Asp Ala Gly Val Val Phe Val Val Thr
 180 185 190

Leu Leu Val Leu Ala Val Thr Gly Phe Ile Ser Ala Gln Ile Ser Gly
 195 200 205

Thr Ser Pro Met Arg Ala Cys Gly Arg Leu Val Ile Gly Gly Ala Leu
 210 215 220

Gly Leu Ala Leu Thr Tyr Gly
 225 230

<210> 547

<211> 630

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(607)

<223> RXN01246

<400> 547

gggaaggagg agaaggctgc tgtgagctct gcagcccccg tccgctgact ttcaatgctt 60

catggactcc cagatacaca acctcogaaa gggaaccccc atg aag cgc act atc 115
Met Lys Arg Thr Ile
1 5

acc atc gcc gct ctc gcc ttg acc tcc acc ctg gtt ttg tcc gcc tgc 163
Thr Ile Ala Ala Leu Ala Leu Thr Ser Thr Leu Val Leu Ser Ala Cys
10 15 20

gca gat aac act gag gga gaa aac acc gac acc acg acc atc gcc act 211
Ala Asp Asn Thr Glu Gly Glu Asn Thr Asp Thr Thr Thr Ile Ala Thr
25 30 35

acg tcc gcc ccc gac acc acc gaa acg acc ggg gcc acc acg gat cct 259
Thr Ser Ala Pro Asp Thr Thr Glu Thr Thr Gly Ala Thr Thr Asp Pro
40 45 50

gag aca gag acg ggg gcg gcc gga gag gtc tcc gcc gag cac aat gat 307
Glu Thr Glu Thr Gly Ala Ala Gly Glu Val Ser Ala Glu His Asn Asp
55 60 65

gcg gac atc atg ttc gcg cag atg atg atc cgc cat cac caa cag gcc 355
Ala Asp Ile Met Phe Ala Gln Met Met Ile Pro His His Gln Gln Ala
70 75 80 85

gtg gag atg agt gaa atc ctc ctg gcc aag gac gat atc cgc gcc gag 403
Val Glu Met Ser Glu Ile Leu Leu Ala Lys Asp Asp Ile Pro Ala Glu
90 95 100

gtc atc gag ttc acc cag ggt gtt atc gat gcc cag ggc cgc gag atc 451
Val Ile Glu Phe Thr Gln Gly Val Ile Asp Ala Gln Gly Pro Glu Ile
105 110 115

gac cgg atg aat acc atg ctc gag acc tgg gaa gaa gat cgc gtc acc 499
Asp Arg Met Asn Thr Met Leu Glu Thr Trp Glu Glu Asp Pro Val Thr
120 125 130

ggt gat atg ggt gag atg gac cat ggc ggg atg agt gga atg atg agc 547
Gly Asp Met Gly Glu Met Asp His Gly Gly Met Ser Gly Met Met Ser
135 140 145

gag gag gac atg aca gcc ctc gag gac gcc cag ggc acc cga ggc tgc 595
Glu Glu Asp Met Thr Ala Leu Glu Asp Ala Gln Gly Thr Arg Gly Cys
150 155 160 165

ccg gct cta cct tgagcagatg accgcccacc atg 630
Pro Ala Leu Pro

<210> 548

<211> 169

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 548

Met Lys Arg Thr Ile Thr Ile Ala Ala Leu Ala Leu Thr Ser Thr Leu
1 5 10 15

Val Leu Ser Ala Cys Ala Asp Asn Thr Glu Gly Glu Asn Thr Asp Thr
20 25 30

Thr Thr Ile Ala Thr Thr Ser Ala Pro Asp Thr Thr Glu Thr Thr Gly
 35 40 45
 Ala Thr Thr Asp Pro Glu Thr Glu Thr Gly Ala Ala Gly Glu Val Ser
 50 55 60
 Ala Glu His Asn Asp Ala Asp Ile Met Phe Ala Gln Met Met Ile Pro
 65 70 75 80
 His His Gln Gln Ala Val Glu Met Ser Glu Ile Leu Leu Ala Lys Asp
 85 90 95
 Asp Ile Pro Ala Glu Val Ile Glu Phe Thr Gln Gly Val Ile Asp Ala
 100 105 110
 Gln Gly Pro Glu Ile Asp Arg Met Asn Thr Met Leu Glu Thr Trp Glu
 115 120 125
 Glu Asp Pro Val Thr Gly Asp Met Gly Glu Met Asp His Gly Gly Met
 130 135 140
 Ser Gly Met Met Ser Glu Glu Asp Met Thr Ala Leu Glu Asp Ala Gln
 145 150 155 160
 Gly Thr Arg Gly Cys Pro Ala Leu Pro
 165

<210> 549

<211> 739

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(739)

<223> FRXA01246

<400> 549

gggaaggagg agaaggtgc tgtgagctct gcagcccccg tccgctgact ttcaatgctt 60

catggactcc ccgatacaca acctccgaaa gggaaccccc atg aag cgc act atc 115
 Met Lys Arg Thr Ile
 1 5

acc atc gcc gct ctc gcc ttg acc tcc acc ctg gtt ttg tcc gcc tgc 163
 Thr Ile Ala Ala Leu Ala Leu Thr Ser Thr Leu Val Leu Ser Ala Cys
 10 15 20

gca gat aac act gag gga gaa aac acc gac acc acg acc atc gcc act 211
 Ala Asp Asn Thr Glu Gly Glu Asn Thr Asp Thr Thr Thr Ile Ala Thr
 25 30 35

acg tcc gcc ccc gac acc acc gaa acg acc ggg gcc acc acg gat cct 259
 Thr Ser Ala Pro Asp Thr Thr Thr Thr Gly Ala Thr Thr Asp Pro
 40 45 50

gag aca gag acg ggg gcg gcc gga gag gtc tcc gcc gag cac aat gat 307
 Glu Thr Glu Thr Gly Ala Ala Gly Glu Val Ser Ala Glu His Asn Asp
 55 60 65

gcg gac atc atg ttc gcg cag atg atg atc ccg cat cac caa cag gcc 355
 Ala Asp Ile Met Phe Ala Gln Met Met Ile Pro His His Gln Gln Ala
 70 75 80 85

gtg gag atg agt gaa atc ctc ctg gcc aag gac gat atc ccg gcc gag 403
 Val Glu Met Ser Glu Ile Leu Leu Ala Lys Asp Asp Ile Pro Ala Glu
 90 95 100

gtc atc gag ttc acc cag ggt gtt atc gat gcc cag ggc ccg gag atc 451
 Val Ile Glu Phe Thr Gln Gly Val Ile Asp Ala Gln Gly Pro Glu Ile
 105 110 115

gac cgg atg aat acc atg ctc gag acc tgg gaa gaa gat ccg gtc acc 499
 Asp Arg Met Asn Thr Met Leu Glu Thr Trp Glu Glu Asp Pro Val Thr
 120 125 130

ggt gat atg ggt gag atg gac cat ggc ggg atg agt gga atg atg agc 547
 Gly Asp Met Gly Glu Met Asp His Gly Gly Met Ser Gly Met Met Ser
 135 140 145

gag gag gac atg aca gcc ctc gag gac gcc cag ggc acc gag gct gcc 595
 Glu Glu Asp Met Thr Ala Leu Glu Asp Ala Gln Gly Thr Glu Ala Ala
 150 155 160 165

cgg ctc tac ctt gag cag atg acc gcc cac cat gag ggc gcg gtc gat 643
 Arg Leu Tyr Leu Glu Gln Met Thr Ala His His Glu Gly Ala Val Asp
 170 175 180

atg gcc cgc gat gag gtc act gat ggc cag aac ccg cag gcc atc gct 691
 Met Ala Arg Asp Glu Val Thr Asp Gly Gln Asn Pro Gln Ala Ile Ala
 185 190 195

ctg gct gag cag gtc att gaa gat cag gag gcc gag atc gcc gag att 739
 Leu Ala Glu Gln Val Ile Glu Asp Gln Glu Ala Glu Ile Ala Glu Ile
 200 205 210

<210> 550

<211> 213

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 550

Met Lys Arg Thr Ile Thr Ile Ala Ala Leu Ala Leu Thr Ser Thr Leu
 1 5 10 15

Val Leu Ser Ala Cys Ala Asp Asn Thr Glu Gly Glu Asn Thr Asp Thr
 20 25 30

Thr Thr Ile Ala Thr Thr Ser Ala Pro Asp Thr Thr Glu Thr Thr Gly
 35 40 45

Ala Thr Thr Asp Pro Glu Thr Glu Thr Gly Ala Ala Gly Glu Val Ser
 50 55 60

Ala Glu His Asn Asp Ala Asp Ile Met Phe Ala Gln Met Met Ile Pro
 65 70 75 80

His His Gln Gln Ala Val Glu Met Ser Glu Ile Leu Leu Ala Lys Asp
 85 90 95

```

Asp Ile Pro Ala Glu Val Ile Glu Phe Thr Gln Gly Val Ile Asp Ala
      100                      105                      110

Gln Gly Pro Glu Ile Asp Arg Met Asn Thr Met Leu Glu Thr Trp Glu
      115                      120                      125

Glu Asp Pro Val Thr Gly Asp Met Gly Glu Met Asp His Gly Gly Met
      130                      135                      140

Ser Gly Met Met Ser Glu Glu Asp Met Thr Ala Leu Glu Asp Ala Gln
      145                      150                      155                      160

Gly Thr Glu Ala Ala Arg Leu Tyr Leu Glu Gln Met Thr Ala His His
      165                      170                      175

Glu Gly Ala Val Asp Met Ala Arg Asp Glu Val Thr Asp Gly Gln Asn
      180                      185                      190

Pro Gln Ala Ile Ala Leu Ala Glu Gln Val Ile Glu Asp Gln Glu Ala
      195                      200                      205

Glu Ile Ala Glu Ile
      210

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<210> 551

<211> 471

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(471)

<223> RXN01249

<400> 551

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tct cag att gtg gcg gtg tct tct cac ggt ctt acc acg atc cag gag      48
Ser Gln Ile Val Ala Val Ser Ser His Gly Leu Thr Thr Ile Gln Glu
      1                      5                      10                      15

```

```

att gac gtg aaa cga gca gcg atc gca gcc gcc gcc ctt acc ctc gcc      96
Ile Asp Val Lys Arg Ala Ala Ile Ala Ala Ala Leu Thr Leu Ala
      20                      25                      30

```

```

ctc acg ggg tgt tcg gcc gcc gac ccg gaa ccc acc gcc gac ggg acg      144
Leu Thr Gly Cys Ser Ala Ala Asp Pro Glu Pro Thr Ala Asp Gly Thr
      35                      40                      45

```

```

gtg tcc cag gat aca ttc ctg act acc cat ggc ctg gcc gcc atg gac      192
Val Ser Gln Asp Thr Phe Leu Thr Thr His Gly Leu Ala Ala Met Asp
      50                      55                      60

```

```

gcg gtg gag atc att gat cac ctc gac cgg cag aag gtc act gag cgt      240
Ala Val Glu Ile Ile Asp His Leu Asp Arg Gln Lys Val Thr Glu Arg
      65                      70                      75                      80

```

```

ccc acg gat ctg atc gcc tca gtg cgt gcc gat gaa ctg ctg ctc tcg      288
Pro Thr Asp Leu Ile Ala Ser Val Arg Ala Asp Glu Leu Leu Leu Ser
      85                      90                      95

```

```

agc gat gac cag gaa gtc gtg gtc gat ctt ccc gac aat cag acg tat      336

```

```

Ser Asp Asp Gln Glu Val Val Val Asp Leu Pro Asp Asn Gln Thr Tyr
      100      105      110
gtc tgc atc gca ccc tac ctc aac tcc acc cac gac tgc ttc tac cac 384
Val Ser Ile Ala Pro Tyr Leu Asn Ser Thr His Asp Cys Phe Tyr His
      115      120      125
agc ctc acg acc tgc ctg ggg gat ctc gac aat gag gat atc cat gtc 432
Ser Leu Thr Thr Cys Leu Gly Asp Leu Asp Asn Glu Asp Ile His Val
      130      135      140
atg atc acc gat gaa ggc acc ggc gag gtc ctg ttc gat 471
Met Ile Thr Asp Glu Ala Thr Gly Glu Val Leu Phe Asp
      145      150      155

```

<210> 552

<211> 157

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 552

```

Ser Gln Ile Val Ala Val Ser Ser His Gly Leu Thr Thr Ile Gln Glu
      1      5      10      15
Ile Asp Val Lys Arg Ala Ala Ile Ala Ala Ala Leu Thr Leu Ala
      20      25      30
Leu Thr Gly Cys Ser Ala Ala Asp Pro Glu Pro Thr Ala Asp Gly Thr
      35      40      45
Val Ser Gln Asp Thr Phe Leu Thr Thr His Gly Leu Ala Ala Met Asp
      50      55      60
Ala Val Glu Ile Ile Asp His Leu Asp Arg Gln Lys Val Thr Glu Arg
      65      70      75      80
Pro Thr Asp Leu Ile Ala Ser Val Arg Ala Asp Glu Leu Leu Leu Ser
      85      90      95
Ser Asp Asp Gln Glu Val Val Val Asp Leu Pro Asp Asn Gln Thr Tyr
      100      105      110
Val Ser Ile Ala Pro Tyr Leu Asn Ser Thr His Asp Cys Phe Tyr His
      115      120      125
Ser Leu Thr Thr Cys Leu Gly Asp Leu Asp Asn Glu Asp Ile His Val
      130      135      140
Met Ile Thr Asp Glu Ala Thr Gly Glu Val Leu Phe Asp
      145      150      155

```

<210> 553

<211> 400

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(400)

<223> FRXA01249

<400> 553

gaattgacgt ggaaccgagc agcgatcgca gcccgccgcc cttaccctcg cccctcacggg 60
 gtgttcggcc gccgaccggg aaccaccgcg cgacgggacg gtg tcc cag gat aca 115
 Val Ser Gln Asp Thr
 1 5

ttc ctg act acc cat ggc ctg gcc gcc atg gac gcg gtg gag atc att 163
 Phe Leu Thr Thr His Gly Leu Ala Ala Met Asp Ala Val Glu Ile Ile
 10 15 20

gat cac ctg gac cgg cag aag gtc act gag cgt ccc acg gat ctg atc 211
 Asp His Leu Asp Arg Gln Lys Val Thr Glu Arg Pro Thr Asp Leu Ile
 25 30 35

gcc tca gtg cgt gcc gat gaa ctg ctg ctc tcg agc gat gac cag gaa 259
 Ala Ser Val Arg Ala Asp Glu Leu Leu Ser Ser Asp Asp Gln Glu
 40 45 50

gtc gtg gtc gat ctt ccc gac aat cag acg tat gtc tcg atc gca ccc 307
 Val Val Val Asp Leu Pro Asp Asn Gln Thr Tyr Val Ser Ile Ala Pro
 55 60 65

tac ctc aac tcc acc cac gac tgc ttc tac cac agc ctc acg acc tgc 355
 Tyr Leu Asn Ser Thr His Asp Cys Phe Tyr His Ser Leu Thr Thr Cys
 70 75 80 85

ctg ggg gat ctc gac aat gag gat atc cat gtc atg atc acc gat 400
 Leu Gly Asp Leu Asp Asn Glu Asp Ile His Val Met Ile Thr Asp
 90 95 100

<210> 554

<211> 100

<212> PRT

<213> Corynebacterium glutamicum

<400> 554

Val Ser Gln Asp Thr Phe Leu Thr Thr His Gly Leu Ala Ala Met Asp
 1 5 10 15

Ala Val Glu Ile Ile Asp His Leu Asp Arg Gln Lys Val Thr Glu Arg
 20 25 30

Pro Thr Asp Leu Ile Ala Ser Val Arg Ala Asp Glu Leu Leu Leu Ser
 35 40 45

Ser Asp Asp Gln Glu Val Val Val Asp Leu Pro Asp Asn Gln Thr Tyr
 50 55 60

Val Ser Ile Ala Pro Tyr Leu Asn Ser Thr His Asp Cys Phe Tyr His
 65 70 75 80

Ser Leu Thr Thr Cys Leu Gly Asp Leu Asp Asn Glu Asp Ile His Val
 85 90 95

Met Ile Thr Asp
 100

Gly Glu Val Ser Ala Val Thr Val Asp Pro Lys Val Val Asp Pro Glu
50 55 60

Asp Val Glu Thr Leu Gln Asp Leu Leu Leu Gly Ala Phe Lys Asp Ala
65 70 75 80

His Asn Lys Val Ala Asn Val Ala Glu Glu Met Gly Pro Leu Ser
85 90 95

Gln Gly Met Gly Gly Leu Phe
100

<210> 557

<211> 432

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(409)

<223> FRXA01251

<400> 557

tgtaagccga gagcgaacct gccaaaagta aggggagggt tcgcggtgac gtcggttagga 60

tcgagcggaag aaaccaacaa acttcttagg agccattctc atg acc cag cca gat 115
Met Thr Gln Pro Asp
1 5

atg tcc cag atc ctc gcc caa gct cag cag atg cag gct caa cta cag 163
Met Ser Gln Ile Leu Ala Gln Ala Gln Gln Met Gln Ala Gln Leu Gln
10 15 20

gcc gct cag cag gaa atc ctg gca acc acc gtt gtc gga aat gca gga 211
Ala Ala Gln Gln Glu Ile Leu Ala Thr Thr Val Val Gly Asn Ala Gly
25 30 35

aac ggg ctg gtt acc gtc act atg gcc ggc aac ggc gag gtc ttc gca 259
Asn Gly Leu Val Thr Val Thr Met Ala Gly Asn Gly Glu Val Phe Ala
40 45 50

gtg acc gtt gac cca aag gtc gtt gac cct gaa gat gtc gaa acc cta 307
Val Thr Val Asp Pro Lys Val Val Asp Pro Glu Asp Val Glu Thr Leu
55 60 65

cag gac ctt ctg ctc ggt gca ttc aag gat gcc cat aac aag gtc gca 355
Gln Asp Leu Leu Leu Gly Ala Phe Lys Asp Ala His Asn Lys Val Ala
70 75 80 85

aac gtt gct gaa gag aag atg ggc cca cta tcc cag ggc atg ggt ggc 403
Asn Val Ala Glu Glu Lys Met Gly Pro Leu Ser Gln Gly Met Gly Gly
90 95 100

ctc ttc taattagttg ctaaagcgag ggc 432
Leu Phe

<210> 558

<211> 103
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 558
 Met Thr Gln Pro Asp Met Ser Gln Ile Leu Ala Gln Ala Gln Gln Met
 1 5 10 15
 Gln Ala Gln Leu Gln Ala Ala Gln Gln Glu Ile Leu Ala Thr Thr Val
 20 25 30
 Val Gly Asn Ala Gly Asn Gly Leu Val Thr Val Thr Met Ala Gly Asn
 35 40 45
 Gly Glu Val Phe Ala Val Thr Val Asp Pro Lys Val Val Asp Pro Glu
 50 55 60
 Asp Val Glu Thr Leu Gln Asp Leu Leu Leu Gly Ala Phe Lys Asp Ala
 65 70 75 80
 His Asn Lys Val Ala Asn Val Ala Glu Glu Lys Met Gly Pro Leu Ser
 85 90 95

Gln Gly Met Gly Gly Leu Phe
 100

<210> 559
 <211> 1035
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1012)
 <223> RXN01263

<400> 559
 agtggccttt ggagttattt tgatgacggt atcggcgact gctgggatcc tctcttttt 60
 atctccaaat agaagccaag ctgcgccacc ccaatttagt ttg acc ccg tat gat 115
 Leu Thr Pro Tyr Asp
 1 5
 cca acc gct gta aat aag gag tcg gaa aaa gaa gca gca aag aat ctg 163
 Pro Thr Ala Val Asn Lys Glu Ser Glu Lys Glu Ala Ala Lys Asn Leu
 10 15 20
 ttt ggc gct gag gcg ttg aca gtg gat ccg gat gcc ggt gag gtt gtt 211
 Phe Gly Ala Glu Ala Leu Thr Val Asp Pro Asp Ala Gly Glu Val Val
 25 30 35
 gat cga gta gat aat ttt tat ccg acg act gct aag gca aaa cga gat 259
 Asp Arg Val Asp Asn Phe Tyr Pro Thr Thr Ala Lys Ala Lys Arg Asp
 40 45 50
 tac cca agt aac tat gca gcg ggt tgt cac caa gaa gtc aat gag act 307
 Tyr Pro Ser Asn Tyr Ala Ala Gly Cys His Gln Glu Val Asn Glu Thr
 55 60 65
 agt cct gag tca tgt gtt tat ggt gat aaa aat tct gat ttt tct gta 355

Ser	Pro	Glu	Ser	Cys	Val	Tyr	Gly	Asp	Lys	Asn	Ser	Asp	Phe	Ser	Val	
70					75					80					85	
gca	ctt	gtc	ggc	gac	tcc	cac	gct	ggc	cat	tgg	ctt	cct	gcc	ttg	gaa	403
Ala	Leu	Val	Gly	Asp	Ser	His	Ala	Gly	His	Trp	Leu	Pro	Ala	Leu	Glu	
			90						95					100		
cca	att	gct	gaa	gca	cag	ggg	tgg	aga	ttg	gaa	gtt	tat	aca	aag	tca	451
Pro	Ile	Ala	Glu	Ala	Gln	Gly	Trp	Arg	Leu	Glu	Val	Tyr	Thr	Lys	Ser	
			105					110					115			
cag	tgt	cca	ctc	ata	agc	act	gcg	atc	aaa	ctt	ggc	gaa	act	ttt	tat	499
Gln	Cys	Pro	Leu	Ile	Ser	Thr	Ala	Ile	Lys	Leu	Gly	Glu	Thr	Phe	Tyr	
			120				125						130			
gca	gaa	tgc	tat	gag	tgg	aat	gaa	aaa	tta	ctt	gct	aag	cta	act	gga	547
Ala	Glu	Cys	Tyr	Glu	Trp	Asn	Glu	Lys	Leu	Leu	Ala	Lys	Leu	Thr	Gly	
			135				140				145					
cct	tct	gca	cca	aat	cat	gtg	att	gta	agt	agc	caa	cgt	tac	gct	tct	595
Pro	Ser	Ala	Pro	Asn	Val	Ile	Val	Val	Ser	Ser	Gln	Arg	Tyr	Ala	Ser	
					155					160					165	
gca	aat	ccg	tta	atc	gat	agt	gtc	gcg	acg	gga	acc	gtt	tcc	gaa	gga	643
Ala	Asn	Pro	Leu	Ile	Asp	Ser	Val	Ala	Thr	Gly	Thr	Val	Ser	Glu	Gly	
			170					175						180		
tat	gaa	atg	gca	tgg	aat	tca	tta	aaa	gat	gca	ggc	gtt	tct	att	tct	691
Tyr	Glu	Met	Ala	Trp	Asn	Ser	Leu	Lys	Asp	Ala	Gly	Val	Ser	Ile	Ser	
			185					190					195			
gta	ctt	ctt	gat	act	cct	cgg	ccg	caa	att	gat	atc	cca	gaa	tgt	gta	739
Val	Leu	Leu	Asp	Thr	Pro	Arg	Pro	Gln	Ile	Asp	Ile	Pro	Glu	Cys	Val	
			200				205					210				
gca	tca	aac	cgc	gat	aat	ctc	tca	gaa	tgt	tca	gtt	cac	cgg	agc	gtt	787
Ala	Ser	Asn	Arg	Asp	Asn	Leu	Ser	Glu	Cys	Ser	Val	His	Arg	Ser	Val	
			215			220					225					
gcg	ctt	ggg	act	gaa	gct	cat	cct	cag	caa	aaa	act	gca	gct	caa	aat	835
Ala	Leu	Gly	Thr	Glu	Ala	His	Pro	Gln	Gln	Lys	Thr	Ala	Ala	Gln	Asn	
			230			235				240					245	
ata	gac	gtg	cct	gta	ttg	gat	ttg	agt	aat	tgg	att	tgt	ccg	gaa	gaa	883
Ile	Asp	Val	Pro	Val	Leu	Asp	Leu	Ser	Asn	Trp	Ile	Cys	Pro	Glu	Glu	
				250					255					260		
tat	tgc	tcc	gct	gtt	atc	gga	aat	gtt	ttg	gta	tac	agg	gat	tca	cat	931
Tyr	Cys	Ser	Ala	Val	Ile	Gly	Asn	Val	Leu	Val	Tyr	Arg	Asp	Ser	His	
			265				270						275			
cat	ttg	acc	gct	acg	tat	gct	cgt	agt	ctc	tct	agc	gca	tta	tgg	aat	979
His	Leu	Thr	Ala	Thr	Tyr	Arg	Ser	Leu	Ser	Ser	Ser	Ala	Leu	Trp	Asn	
			280				285					290				
gag	ttg	gtt	gcc	tca	aat	ggc	gag	cct	ttt	aag	taagaggtag	ttgttcaagt	1032			
Glu	Leu	Val	Ala	Ser	Asn	Gly	Glu	Pro	Phe	Lys						
			295			300										

agc

1035

<210> 560

<211> 304

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 560

Leu Thr Pro Tyr Asp Pro Thr Ala Val Asn Lys Glu Ser Glu Lys Glu
 1 5 10 15

Ala Ala Lys Asn Leu Phe Gly Ala Glu Ala Leu Thr Val Asp Pro Asp
 20 25 30

Ala Gly Glu Val Val Asp Arg Val Asp Asn Phe Tyr Pro Thr Thr Ala
 35 40 45

Lys Ala Lys Arg Asp Tyr Pro Ser Asn Tyr Ala Ala Gly Cys His Gln
 50 55 60

Glu Val Asn Glu Thr Ser Pro Glu Ser Cys Val Tyr Gly Asp Lys Asn
 65 70 75 80

Ser Asp Phe Ser Val Ala Leu Val Gly Asp Ser His Ala Gly His Trp
 85 90 95

Leu Pro Ala Leu Glu Pro Ile Ala Glu Ala Gln Gly Trp Arg Leu Glu
 100 105 110

Val Tyr Thr Lys Ser Gln Cys Pro Leu Ile Ser Thr Ala Ile Lys Leu
 115 120 125

Gly Glu Thr Phe Tyr Ala Glu Cys Tyr Glu Trp Asn Glu Lys Leu Leu
 130 135 140

Ala Lys Leu Thr Gly Pro Ser Ala Pro Asn His Val Ile Val Ser Ser
 145 150 155 160

Gln Arg Tyr Ala Ser Ala Asn Pro Leu Ile Asp Ser Val Ala Thr Gly
 165 170 175

Thr Val Ser Glu Gly Tyr Glu Met Ala Trp Asn Ser Leu Lys Asp Ala
 180 185 190

Gly Val Ser Ile Ser Val Leu Leu Asp Thr Pro Arg Pro Gln Ile Asp
 195 200 205

Ile Pro Glu Cys Val Ala Ser Asn Arg Asp Asn Leu Ser Glu Cys Ser
 210 215 220

Val His Arg Ser Val Ala Leu Gly Thr Glu Ala His Pro Gln Gln Lys
 225 230 235 240

Thr Ala Ala Gln Asn Ile Asp Val Pro Val Leu Asp Leu Ser Asn Trp
 245 250 255

Ile Cys Pro Glu Glu Tyr Cys Ser Ala Val Ile Gly Asn Val Leu Val
 260 265 270

Tyr Arg Asp Ser His His Leu Thr Ala Thr Tyr Ala Arg Ser Leu Ser
 275 280 285

Ser Ala Leu Trp Asn Glu Leu Val Ala Ser Asn Gly Glu Pro Phe Lys
 290 295 300

<210> 561
 <211> 1035
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1012)
 <223> FRXA01263

<400> 561
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 atctccaat agaagccaag ctgcgccacc ccaatttagt ttg acc ccg tat gat 115
 Leu Thr Pro Tyr Asp
 1 5
 cca acc gct gta aat aag gag tcg gaa aaa gaa gca gca aag aat ctg 163
 Pro Thr Ala Val Asn Lys Glu Ser Glu Lys Glu Ala Ala Lys Asn Leu
 10 15 20
 ttt ggc gct gag gcg ttg aca gtg gat ccg gat gcc ggt gag gtt gtt 211
 Phe Gly Ala Glu Ala Leu Thr Val Asp Pro Asp Ala Gly Glu Val Val
 25 30 35
 gat cga gta gat aat ttt tat ccg acg act gct aag gca aaa cga gat 259
 Asp Arg Val Asp Asn Phe Tyr Pro Thr Thr Ala Lys Ala Lys Arg Asp
 40 45 50
 tac cca agt aac tat gca gcg ggt tgt cac caa gaa gtc aat gag act 307
 Tyr Pro Ser Asn Tyr Ala Ala Gly Cys His Gln Glu Val Asn Glu Thr
 55 60 65
 agt cct gag tca tgt gtt tat ggt gat aaa aat tct gat ttt tct gta 355
 Ser Pro Glu Ser Cys Val Tyr Gly Asp Lys Asn Ser Asp Phe Ser Val
 70 75 80 85
 gca ctt gtc ggt gac tcc cac gct ggt cat tgg ctt cct gcc ttg gaa 403
 Ala Leu Val Gly Asp Ser His Ala Gly His Trp Leu Pro Ala Leu Glu
 90 95 100
 cca att gct gaa gca cag ggg tgg aga ttg gaa gtt tat aca aag tca 451
 Pro Ile Ala Glu Ala Gln Gly Trp Arg Leu Glu Val Tyr Thr Lys Ser
 105 110 115
 cag tgt cca ctc ata agc act gcg atc aaa ctt ggt gaa act ttt tat 499
 Gln Cys Pro Leu Ile Ser Thr Ala Ile Lys Leu Gly Glu Thr Phe Tyr
 120 125 130
 gca gaa tgc tat gag tgg aat gaa aaa tta ctt gct aag cta act gga 547
 Ala Glu Cys Tyr Glu Trp Asn Glu Lys Leu Leu Ala Lys Leu Thr Gly
 135 140 145
 cct tct gca cca aat cat gtg att gta agt agc caa cgt tac gct tct 595

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Pro Ser Ala Pro Asn His Val Ile Val Ser Ser Gln Arg Tyr Ala Ser
150                      155                      160                      165

gca aat ccg tta atc gat agt gtc gcg acg gga acc gtt tcc gaa gga      643
Ala Asn Pro Leu Ile Asp Ser Val Ala Thr Gly Thr Val Ser Glu Gly
                      170                      175                      180

tat gaa atg gca tgg aat tca tta aaa gat gca ggt gtt tct att tct      691
Tyr Glu Met Ala Trp Asn Ser Leu Lys Asp Ala Gly Val Ser Ile Ser
                      185                      190                      195

gta ctt ctt gat act cct cgg ccg caa att gat atc cca gaa tgt gta      739
Val Leu Leu Asp Thr Pro Arg Pro Gln Ile Asp Ile Pro Glu Cys Val
                      200                      205                      210

gca tca aac cgc gat aat ctc tca gaa tgt tca gtt cac cgg agc gtt      787
Ala Ser Asn Arg Asp Asn Leu Ser Glu Cys Ser Val His Arg Ser Val
                      215                      220                      225

gcg ctt ggg act gaa gct cat cct cag caa aaa act gca gct caa aat      835
Ala Leu Gly Thr Glu Ala His Pro Gln Gln Lys Thr Ala Ala Gln Asn
                      230                      235                      240                      245

ata gac gtg cct gta ttg gat ttg agt aat tgg att tgt ccg gaa gaa      883
Ile Asp Val Pro Val Leu Asp Leu Ser Asn Trp Ile Cys Pro Glu Glu
                      250                      255                      260

tat tgc tcc gct gtt atc gga aat gct ttg gta tac agg gat tca cat      931
Tyr Cys Ser Ala Val Ile Gly Asn Val Leu Val Tyr Arg Asp Ser His
                      265                      270                      275

cat ttg acc gct acg tat gct cgt agt ctc tct agc gca tta tgg aat      979
His Leu Thr Ala Thr Tyr Ala Arg Ser Leu Ser Ser Ala Leu Trp Asn
                      280                      285                      290

gag ttg gtt gcc tca aat ggt gag cct ttt aag taagaggttag ttgttcaagt 1032
Glu Leu Val Ala Ser Asn Gly Glu Pro Phe Lys
                      295                      300

agc                                                                1035

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<210> 562

<211> 304

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 562

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Leu Thr Pro Tyr Asp Pro Thr Ala Val Asn Lys Glu Ser Glu Lys Glu
 1                      5                      10                      15

Ala Ala Lys Asn Leu Phe Gly Ala Glu Ala Leu Thr Val Asp Pro Asp
                20                      25                      30

Ala Gly Glu Val Val Asp Arg Val Asp Asn Phe Tyr Pro Thr Thr Ala
 35                      40                      45

Lys Ala Lys Arg Asp Tyr Pro Ser Asn Tyr Ala Ala Gly Cys His Gln
 50                      55                      60

Glu Val Asn Glu Thr Ser Pro Glu Ser Cys Val Tyr Gly Asp Lys Asn

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65	70	75	80
Ser Asp Phe	Ser Val Ala Leu Val Gly Asp	Ser Ser His Ala Gly His Trp	
	85	90	95
Leu Pro Ala	Leu Glu Pro Ile Ala Glu Ala Gln Gly Trp Arg Leu Glu		
	100	105	110
Val Tyr Thr	Lys Ser Gln Cys Pro Leu Ile Ser Thr Ala Ile Lys Leu		
	115	120	125
Gly Glu Thr	Phe Tyr Ala Glu Cys Tyr Glu Trp Asn Glu Lys Leu Leu		
	130	135	140
Ala Lys Leu	Thr Gly Pro Ser Ala Pro Asn His Val Ile Val Ser Ser		
	145	150	155
Gln Arg Tyr	Ala Ser Ala Asn Pro Leu Ile Asp Ser Val Ala Thr Gly		
	165	170	175
Thr Val Ser	Glu Gly Tyr Glu Met Ala Trp Asn Ser Leu Lys Asp Ala		
	180	185	190
Gly Val Ser	Ile Ser Val Leu Leu Asp Thr Pro Arg Pro Gln Ile Asp		
	195	200	205
Ile Pro Glu	Cys Val Ala Ser Asn Arg Asp Asn Leu Ser Glu Cys Ser		
	210	215	220
Val His Arg	Ser Val Ala Leu Gly Thr Glu Ala His Pro Gln Gln Lys		
	225	230	235
Thr Ala Ala	Gln Asn Ile Asp Val Pro Val Leu Asp Leu Ser Asn Trp		
	245	250	255
Ile Cys Pro	Glu Glu Tyr Cys Ser Ala Val Ile Gly Asn Val Leu Val		
	260	265	270
Tyr Arg Asp	Ser His His Leu Thr Ala Thr Tyr Ala Arg Ser Leu Ser		
	275	280	285
Ser Ala Leu	Trp Asn Glu Leu Val Ala Ser Asn Gly Glu Pro Phe Lys		
	290	295	300

<210> 563

<211> 1158

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1135)

<223> RXN01266

<400> 563

gattgtgaag ttttatact gtcataattct ggtgattttc gccctgctca tgaagtggcg 60

gacgagcaat ggcccgatat agatttagta aggaactaaa atg cca aaa gta agt 115
Met Pro Lys Val Ser 5

gtg gtt act ggt ttt tat aac cgc tgt gag cat tta gaa cga acc att 163
Val Val Thr Gly Phe Tyr Asn Arg Cys Glu His Leu Glu Arg Thr Ile 10 15 20

gag tct att ctt aac caa act tat agc gat ttt gaa tta att gtt ttt 211
Glu Ser Ile Leu Asn Gln Thr Tyr Ser Asp Phe Glu Leu Ile Val Phe 25 30 35

gat gat gca tcg aca gat gga aca gct tca cga ttg tta gag tta aaa 259
Asp Asp Ala Ser Thr Asp Gly Thr Ala Ser Arg Leu Leu Glu Leu Lys 40 45 50

gaa aaa tat gat gat ccg cgt ttc cga ttt atc att cat gaa gag aat 307
Glu Lys Tyr Asp Asp Pro Arg Phe Arg Phe Ile Ile His Glu Glu Asn 55 60 65

aaa ggt ttc gta aaa ggg tta tca gaa gca att tct gga gct aaa ggg 355
Lys Gly Phe Val Lys Gly Leu Ser Glu Ala Ile Ser Gly Ala Lys Gly 70 75 80 85

cag tat att gca gtc cag gga tca ggc gat gta tct ctt cct cgc cgt 403
Gln Tyr Ile Ala Val Gln Gly Ser Gly Asp Val Ser Leu Pro Arg 90 95 100

tta gag ctt cag gta gag ttt cta gac gcg aat cct tcg gta ggt gct 451
Leu Glu Leu Gln Val Glu Phe Leu Asp Ala Asn Pro Ser Val Gly Ala 105 110 115

gtg ggt ggt gct atc tat aat att caa gaa gat acg gga aca cgc aac 499
Val Gly Gly Ala Ile Tyr Asn Ile Gln Glu Asp Thr Gly Thr Arg Asn 120 125 130

cca cag aga ttt gaa aag cca att gct aca ttc gat gat tta ttg aca 547
Pro Gln Arg Phe Glu Lys Pro Ile Ala Thr Phe Asp Asp Leu Leu Thr 135 140 145

tct aat ccg ttc act cac gga gaa gtg atg tat cgc tta gac ctt tat 595
Ser Asn Pro Phe Thr His Gly Glu Val Met Tyr Arg Leu Asp Leu Tyr 150 155 160 165

aag agt ata ggt ggg tat cga agt ggc ttt act ttt gct caa gat cgt 643
Lys Ser Ile Gly Gly Tyr Arg Ser Gly Phe Thr Phe Ala Gln Asp Arg 170 175 180

gat tta tgg ttg agg atg gcg aaa aaa gca gat ctg ggt atc att cca 691
Asp Leu Trp Leu Arg Met Ala Lys Lys Ala Asp Leu Gly Ile Ile Pro 185 190 195

gat ttt ctt tat cac cgt tac aca ctt tta gat ggt gtc tct ttc gtc 739
Asp Phe Leu Tyr His Arg Tyr Thr Leu Leu Asp Gly Val Ser Phe Val 200 205 210

ccg gat aaa act ata cgt cag cga tgc ttt tca gaa gct gcg gtg cga 787
Pro Asp Lys Thr Ile Arg Gln Arg Cys Phe Ser Glu Ala Ala Val Arg 215 220 225

ctg gca tta atg cca gaa gag gaa gga gct tta gcc tac tct agg ctg 835

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Leu Ala Leu Met Pro Glu Glu Glu Gly Ala Leu Ala Tyr Ser Arg Leu
230                235                240                245

gaa gct gaa ggg cct act gcc gta gtt cct atc gct gat aga gct gtt    883
Glu Ala Glu Gly Pro Thr Ala Val Val Pro Ile Ala Asp Arg Ala Val
                250                255                260

cag aaa ttt gtc cct aaa gcg gct att cgc tta tgt cta tat ggt gct    931
Gln Lys Phe Val Pro Lys Ala Ala Ile Arg Leu Cys Leu Tyr Gly Ala
                265                270                275

ccg gaa act ggt tta cac atg gct cga gac tat atc cag aac cct ctg    979
Pro Glu Thr Gly Leu His Met Ala Arg Asp Tyr Ile Gln Asn Pro Leu
                280                285                290

cgc cgt acc ata gtt gta gtt ttg atc agc atc tat tcg tct aga tta    1027
Arg Arg Thr Ile Val Val Val Leu Ile Ser Ile Tyr Ser Ser Arg Leu
                295                300                305

att aag cct ctt caa gat att cta tat aag tct att ttt aag ggg gtc    1075
Ile Lys Pro Leu Gln Asp Ile Leu Tyr Lys Ser Ile Phe Lys Gly Val
310                315                320                325

tcg att tct aaa cct att aag agt tca ctc gtg aag ttt aca aga aga    1123
Ser Ile Ser Lys Pro Ile Lys Ser Ser Leu Val Lys Phe Thr Arg Arg
                330                335                340

att caa ggg aag tagcgaaaaa ccgcatctac caa    1158
Ile Gln Gly Lys
                345

<210> 564
<211> 345
<212> PRT
<213> Corynebacterium glutamicum

<400> 564
Met Pro Lys Val Ser Val Val Thr Gly Phe Tyr Asn Arg Cys Glu His
1                5                10                15

Leu Glu Arg Thr Ile Glu Ser Ile Leu Asn Gln Thr Tyr Ser Asp Phe
20                25                30

Glu Leu Ile Val Phe Asp Asp Ala Ser Thr Asp Gly Thr Ala Ser Arg
35                40                45

Leu Leu Glu Leu Lys Glu Lys Tyr Asp Asp Pro Arg Phe Arg Phe Ile
50                55                60

Ile His Glu Glu Asn Lys Gly Phe Val Lys Gly Leu Ser Glu Ala Ile
65                70                75                80

Ser Gly Ala Lys Gly Gln Tyr Ile Ala Val Gln Gly Ser Gly Asp Val
85                90                95

Ser Leu Pro Arg Arg Leu Glu Leu Gln Val Glu Phe Leu Asp Ala Asn
100                105                110

Pro Ser Val Gly Ala Val Gly Gly Ala Ile Tyr Asn Ile Gln Glu Asp
115                120                125

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Thr Gly Thr Arg Asn Pro Gln Arg Phe Glu Lys Pro Ile Ala Thr Phe
  130                      135                      140

Asp Asp Leu Leu Thr Ser Asn Pro Phe Thr His Gly Glu Val Met Tyr
  145                      150                      155                      160

Arg Leu Asp Leu Tyr Lys Ser Ile Gly Gly Tyr Arg Ser Gly Phe Thr
                      165                      170                      175

Phe Ala Gln Asp Arg Asp Leu Trp Leu Arg Met Ala Lys Lys Ala Asp
                      180                      185                      190

Leu Gly Ile Ile Pro Asp Phe Leu Tyr His Arg Tyr Thr Leu Leu Asp
  195                      200                      205

Gly Val Ser Phe Val Pro Asp Lys Thr Ile Arg Gln Arg Cys Phe Ser
  210                      215                      220

Glu Ala Ala Val Arg Leu Ala Leu Met Pro Glu Glu Glu Gly Ala Leu
  225                      230                      235                      240

Ala Tyr Ser Arg Leu Glu Ala Glu Gly Pro Thr Ala Val Val Pro Ile
  245                      250                      255

Ala Asp Arg Ala Val Gln Lys Phe Val Pro Lys Ala Ala Ile Arg Leu
  260                      265                      270

Cys Leu Tyr Gly Ala Pro Glu Thr Gly Leu His Met Ala Arg Asp Tyr
  275                      280                      285

Ile Gln Asn Pro Leu Arg Arg Thr Ile Val Val Val Leu Ile Ser Ile
  290                      295                      300

Tyr Ser Ser Arg Leu Ile Lys Pro Leu Gln Asp Ile Leu Tyr Lys Ser
  305                      310                      315                      320

Ile Phe Lys Gly Val Ser Ile Ser Lys Pro Ile Lys Ser Ser Leu Val
  325                      330                      335

Lys Phe Thr Arg Arg Ile Gln Gly Lys
  340                      345

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<210> 565

<211> 1158

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1135)

<223> FRXA01266

<400> 565

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gacgagcaat ggcccgatat agatttagta aggaactaaa atg cca aaa gta agt 115

Met Pro Lys Val Ser

1

5

gtg gtt act ggt ttt tat aac cgc tgt gag cat tta gaa cga acc att	163
Val Val Thr Gly Phe Tyr Asn Arg Cys Glu His Leu Glu Arg Thr Ile	
10 15 20	
gag tct att ctt aac caa act tat agc gat ttt gaa tta att gtt ttt	211
Glu Ser Ile Leu Asn Gln Thr Tyr Ser Asp Phe Glu Leu Ile Val Phe	
25 30 35	
gat gat gca tcg aca gat gga aca gct tca cga ttg tta gag tta aaa	259
Asp Asp Ala Ser Thr Asp Gly Thr Ala Ser Arg Leu Leu Glu Leu Lys	
40 45 50	
gaa aaa tat gat gat ccg cgt ttc cga ttt atc att cat gaa gag aat	307
Glu Lys Tyr Asp Asp Pro Arg Phe Arg Phe Ile Ile His Glu Glu Asn	
55 60 65	
aaa ggt ttc gta aaa ggg tta tca gaa gca att tct gga gct aaa ggg	355
Lys Gly Phe Val Lys Gly Leu Ser Glu Ala Ile Ser Gly Ala Lys Gly	
70 75 80 85	
cag tat att gca gtc cag gga tca ggc gat gta tct ctt cct cgc cgt	403
Gln Tyr Ile Ala Val Gln Gly Ser Gly Asp Val Ser Leu Pro Arg Arg	
90 95 100	
tta gag ctt cag gta gag ttt cta gac gcg aat cct tcg gta ggt gct	451
Leu Glu Leu Gln Val Glu Phe Leu Asp Ala Asn Pro Ser Val Gly Ala	
105 110 115	
gtg ggt ggt gct atc tat aat att caa gaa gat acg gga aca cgc aac	499
Val Gly Gly Ala Ile Tyr Asn Ile Gln Glu Asp Thr Gly Thr Arg Asn	
120 125 130	
cca cag aga ttt gaa aag cca att gct aca ttc gat gat tta ttg aca	547
Pro Gln Arg Phe Glu Lys Pro Ile Ala Thr Phe Asp Asp Leu Leu Thr	
135 140 145	
tct aat ccg ttc act cac gga gaa gtg atg tat cgc tta gac ctt tat	595
Ser Asn Pro Phe Thr His Gly Glu Val Met Tyr Arg Leu Asp Leu Tyr	
150 155 160 165	
aag agt ata ggt ggg tat cga agt ggc ttt act ttt gct caa gat cgt	643
Lys Ser Ile Gly Gly Tyr Arg Ser Gly Phe Thr Phe Ala Gln Asp Arg	
170 175 180	
gat tta tgg ttg agg atg gcg aaa aaa gca gat ctg ggt atc att cca	691
Asp Leu Trp Leu Arg Met Ala Lys Lys Ala Asp Leu Gly Ile Ile Pro	
185 190 195	
gat ttt ctt tat cac cgt tac aca ctt tta gat ggt gtc tct ttc gtc	739
Asp Phe Leu Tyr His Arg Tyr Thr Leu Leu Asp Gly Val Ser Phe Val	
200 205 210	
ccg gat aaa act ata cgt cag cga tgc ttt tca gaa gct gcg gtg cga	787
Pro Asp Lys Thr Ile Arg Gln Arg Cys Phe Ser Glu Ala Ala Val Arg	
215 220 225	
ctg gca tta atg cca gaa gag gaa gga gct tta gcc tac tct agg ctg	835
Leu Ala Leu Met Pro Glu Glu Glu Gly Ala Leu Ala Tyr Ser Arg Leu	
230 235 240 245	
gaa gct gaa ggg cct act gcc gta gtt cct atc gct gat aga gct gtt	883

Glu Ala Glu Gly Pro Thr Ala Val Val Pro Ile Ala Asp Arg Ala Val
 250 255 260

cag aaa ttt gtc cct aaa gcg gct att cgc tta tgt cta tat ggt gct 931
 Gln Lys Phe Val Pro Lys Ala Ala Ile Arg Leu Cys Leu Tyr Gly Ala
 265 270 275

cgc gaa act ggt tta cac atg gct cga gac tat atc cag aac cct ctg 979
 Pro Glu Thr Gly Leu His Met Ala Arg Asp Tyr Ile Gln Asn Pro Leu
 280 285 290

cgc cgt acc ata gtt gta gtt ttg atc agc atc tat tgc tct aga tta 1027
 Arg Arg Thr Ile Val Val Val Leu Ile Ser Ile Tyr Ser Ser Arg Leu
 295 300 305

att aag cct ctt caa gat att cta tat aag tct att ttt aag ggg gtc 1075
 Ile Lys Pro Leu Gln Asp Ile Leu Tyr Lys Ser Ile Phe Lys Gly Val
 310 315 320 325

tgc att tct aaa cct att aag agt tca ctc gtg aag ttt aca aga aga 1123
 Ser Ile Ser Lys Pro Ile Lys Ser Ser Leu Val Lys Phe Thr Arg Arg
 330 335 340

att caa ggg aag tagcgaaaaa ccgcattctac caa 1158
 Ile Gln Gly Lys
 345

<210> 566
 <211> 345
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 566
 Met Pro Lys Val Ser Val Val Thr Gly Phe Tyr Asn Arg Cys Glu His
 1 5 10 15

Leu Glu Arg Thr Ile Glu Ser Ile Leu Asn Gln Thr Tyr Ser Asp Phe
 20 25 30

Glu Leu Ile Val Phe Asp Asp Ala Ser Thr Asp Gly Thr Ala Ser Arg
 35 40 45

Leu Leu Glu Leu Lys Glu Lys Tyr Asp Asp Pro Arg Phe Arg Phe Ile
 50 55 60

Ile His Glu Glu Asn Lys Gly Phe Val Lys Gly Leu Ser Glu Ala Ile
 65 70 75 80

Ser Gly Ala Lys Gly Gln Tyr Ile Ala Val Gln Gly Ser Gly Asp Val
 85 90 95

Ser Leu Pro Arg Arg Leu Glu Leu Gln Val Glu Phe Leu Asp Ala Asn
 100 105 110

Pro Ser Val Gly Ala Val Gly Gly Ala Ile Tyr Asn Ile Gln Glu Asp
 115 120 125

Thr Gly Thr Arg Asn Pro Gln Arg Phe Glu Lys Pro Ile Ala Thr Phe
 130 135 140

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Asp Asp Leu Leu Thr Ser Asn Pro Phe Thr His Gly Glu Val Met Tyr
145                      150                      155                      160

Arg Leu Asp Leu Tyr Lys Ser Ile Gly Gly Tyr Arg Ser Gly Phe Thr
                      165                      170                      175

Phe Ala Gln Asp Arg Asp Leu Trp Leu Arg Met Ala Lys Lys Ala Asp
                      180                      185                      190

Leu Gly Ile Ile Pro Asp Phe Leu Tyr His Arg Tyr Thr Leu Leu Asp
                      195                      200                      205

Gly Val Ser Phe Val Pro Asp Lys Thr Ile Arg Gln Arg Cys Phe Ser
210                      215                      220

Glu Ala Ala Val Arg Leu Ala Leu Met Pro Glu Glu Glu Gly Ala Leu
225                      230                      235                      240

Ala Tyr Ser Arg Leu Glu Ala Glu Gly Pro Thr Ala Val Val Pro Ile
                      245                      250                      255

Ala Asp Arg Ala Val Gln Lys Phe Val Pro Lys Ala Ala Ile Arg Leu
260                      265                      270

Cys Leu Tyr Gly Ala Pro Glu Thr Gly Leu His Met Ala Arg Asp Tyr
275                      280                      285

Ile Gln Asn Pro Leu Arg Arg Thr Ile Val Val Val Leu Ile Ser Ile
290                      295                      300

Tyr Ser Ser Arg Leu Ile Lys Pro Leu Gln Asp Ile Leu Tyr Lys Ser
305                      310                      315                      320

Ile Phe Lys Gly Val Ser Ile Ser Lys Pro Ile Lys Ser Ser Leu Val
325                      330                      335

Lys Phe Thr Arg Arg Ile Gln Gly Lys
340                      345

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<210> 567

<211> 1041

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1018)

<223> RXN01275

<400> 567

cgccatacta ggctcgccct ttctgacggg aactcggata ggcttctgta aaaccatccc 60

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cggtgaagag agactcgtgg ctgaaataac caccocatta atg gaa aaa att cgc 115
Met Glu Lys Ile Arg
1 5

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tca ccc gca gtc caa tca gat gca ctg cag gtt ttt aaa tca gca ctt 163
Ser Pro Ala Val Gln Ser Asp Ala Leu Gln Val Phe Lys Ser Ala Leu
10 15 20

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gct gcg aca gtc acg tgg tgg att tcg gtt aac ctc ctt aac tcc caa 211
 Ala Ala Thr Val Thr Trp Trp Ile Ser Val Asn Leu Leu Asn Ser Gln
 25 30 35

cta ccc ttt tta gct ccc tgg gta gcg tta atg acg atg caa ttc acc 259
 Leu Pro Phe Leu Ala Pro Trp Val Ala Leu Met Thr Met Gln Phe Thr
 40 45 50

gtc tac cac acc ttt atc agt gga att cag act gca att gct tct gtc 307
 Val Tyr His Thr Phe Ile Ser Gly Ile Gln Thr Ala Ile Ala Ser Val
 55 60 65

atc gga gtt gga ctt tcc ttt gtc ata ggc act tac tta gac gta agt 355
 Ile Gly Val Gly Leu Ser Phe Val Ile Gly Thr Tyr Leu Asp Val Ser
 70 75 80 85

gtg tgg act ttt ggc ctt gca atg gtc ata gga tta ata ggt gca cga 403
 Val Trp Thr Phe Gly Leu Ala Met Val Ile Gly Leu Ile Gly Ala Arg
 90 95 100

gta cca aag ctc cgc gcg gaa gga ata ggt att gct act aca tcc att 451
 Val Pro Lys Leu Arg Ala Glu Gly Ile Gly Ile Ala Thr Ser Ile
 105 110 115

ttt ctt ctt gcc tcc ggg ttt gat gat caa caa ccc ctt cta tac gac 499
 Phe Leu Leu Ala Ser Gly Phe Asp Asp Gln Gln Pro Leu Leu Tyr Asp
 120 125 130

cgt att tta gag atc ctg ctc ggc gtg gct gtt gcc ata gcc atc aac 547
 Arg Ile Leu Glu Ile Leu Leu Gly Val Ala Val Ala Ile Ala Ile Asn
 135 140 145

ctc atc atc ttt cct ccc tta cgc gac cag gag gca aac atg gtg gta 595
 Leu Ile Ile Phe Pro Pro Leu Arg Asp Gln Glu Ala Asn Met Val Val
 150 155 160 165

gga aac tta gat cgg agg atg ggt gag gtt tta caa aaa atg gcc gat 643
 Gly Asn Leu Asp Arg Arg Met Gly Glu Val Leu Gln Lys Met Ala Asp
 170 175 180

gag ctt gca gaa aag tgg aat atc gac aat gca gat gag tgg ctg gaa 691
 Glu Leu Ala Glu Lys Trp Asn Ile Asp Asn Ala Asp Glu Trp Leu Glu
 185 190 195

gaa att aat tct att aac aat gac cta gaa aaa gcg tgg cac tcc gtg 739
 Glu Ile Asn Ser Ile Asn Asn Asp Leu Glu Lys Ala Trp His Ser Val
 200 205 210

cgg ttc gtt cgc gaa agc cgt cga gtt aat cct cgt aaa atc cgc atc 787
 Arg Phe Val Arg Glu Ser Arg Arg Val Asn Pro Arg Lys Ile Arg Ile
 215 220 225

caa gag ggc cgc ccc cag cct acg gaa aca agt tat gaa tca aac ctc 835
 Gln Glu Gly Arg Pro Gln Pro Thr Glu Thr Ser Tyr Glu Ser Asn Leu
 230 235 240 245

acc agc att gat gaa ggg atc gct cat tta cgc cac ctt gcc cgt act 883
 Thr Ser Ile Asp Glu Gly Ile Ala His Leu Arg His Leu Ala Arg Thr
 250 255 260

ctt cgt gat acc ccg att ata gat tcc gac tgg gga tcc agt att cca 931

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Leu Arg Asp Thr Pro Ile Ile Asp Ser Asp Trp Gly Ser Ser Ile Pro
      265                      270                      275

gca aca gtg ggt atc cct tat gca cga tgc cgg agc ttt gct cgc aga 979
Ala Thr Val Gly Ile Pro Tyr Ala Arg Cys Arg Ser Phe Ala Arg Arg
      280                      285                      290

tcc gaa tca gga aat aga tcc tat ccg cga ccg gct etc taaactttca 1028
Ser Glu Ser Gly Asn Arg Ser Tyr Pro Arg Pro Ala Leu
      295                      300                      305

agtgagatga gtg 1041

<210> 568
<211> 306
<212> PRT
<213> Corynebacterium glutamicum

<400> 568
Met Glu Lys Ile Arg Ser Pro Ala Val Gln Ser Asp Ala Leu Gln Val
  1          5          10          15

Phe Lys Ser Ala Leu Ala Ala Thr Val Thr Trp Trp Ile Ser Val Asn
      20          25          30

Leu Leu Asn Ser Gln Leu Pro Phe Leu Ala Pro Trp Val Ala Leu Met
      35          40          45

Thr Met Gln Phe Thr Val Tyr His Thr Phe Ile Ser Gly Ile Gln Thr
      50          55          60

Ala Ile Ala Ser Val Ile Gly Val Gly Leu Ser Phe Val Ile Gly Thr
      65          70          75          80

Tyr Leu Asp Val Ser Val Trp Thr Phe Gly Leu Ala Met Val Ile Gly
      85          90          95

Leu Ile Gly Ala Arg Val Pro Lys Leu Arg Ala Glu Gly Ile Gly Ile
      100          105          110

Ala Thr Thr Ser Ile Phe Leu Leu Ala Ser Gly Phe Asp Asp Gln Gln
      115          120          125

Pro Leu Leu Tyr Asp Arg Ile Leu Glu Ile Leu Leu Gly Val Ala Val
      130          135          140

Ala Ile Ala Ile Asn Leu Ile Ile Phe Pro Pro Leu Arg Asp Gln Glu
      145          150          155          160

Ala Asn Met Val Val Gly Asn Leu Asp Arg Arg Met Gly Glu Val Leu
      165          170          175

Gln Lys Met Ala Asp Glu Leu Ala Glu Lys Trp Asn Ile Asp Asn Ala
      180          185          190

Asp Glu Trp Leu Glu Glu Ile Asn Ser Ile Asn Asn Asp Leu Glu Lys
      195          200          205

Ala Trp His Ser Val Arg Phe Val Arg Glu Ser Arg Arg Val Asn Pro
      210          215          220

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Arg Lys Ile Arg Ile Gln Glu Gly Arg Pro Gln Pro Thr Glu Thr Ser
 225 230 235 240

Tyr Glu Ser Asn Leu Thr Ser Ile Asp Glu Gly Ile Ala His Leu Arg
 245 250 255

His Leu Ala Arg Thr Leu Arg Asp Thr Pro Ile Ile Asp Ser Asp Trp
 260 265 270

Gly Ser Ser Ile Pro Ala Thr Val Gly Ile Pro Tyr Ala Arg Cys Arg
 275 280 285

Ser Phe Ala Arg Arg Ser Glu Ser Gly Asn Arg Ser Tyr Pro Arg Pro
 290 295 300

Ala Leu
 305

<210> 569

<211> 1041

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1018)

<223> FRXA01275

<400> 569

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cggtgaagag agactcgtgg ctgaaataac caccocatta atg gaa aaa att cgc 115
 Met Glu Lys Ile Arg
 1 5

tca ccc gca gtc caa tca gat gca ctg cag gtt ttt aaa tca gca ctt 163
 Ser Pro Ala Val Gln Ser Asp Ala Leu Gln Val Phe Lys Ser Ala Leu
 10 15 20

gct gcg aca gtc acg tgg tgg att tcg gtt aac ctc ctt aac tcc caa 211
 Ala Ala Thr Val Thr Trp Trp Ile Ser Val Asn Leu Leu Asn Ser Gln
 25 30 35

cta ccc ttt tta gct ccc tgg gta gcg tta atg acg atg caa ttc acc 259
 Leu Pro Phe Leu Ala Pro Trp Val Ala Leu Met Thr Met Gln Phe Thr
 40 45 50

gtc tac cac acc ttt atc agt gga att cag act gca att gct tct gtc 307
 Val Tyr His Thr Phe Ile Ser Gly Ile Gln Thr Ala Ile Ala Ser Val
 55 60 65

atc gga gtt gga ctt tcc ttt gtc ata ggc act tac tta gac gta agt 355
 Ile Gly Val Gly Leu Ser Phe Val Ile Gly Thr Tyr Leu Asp Val Ser
 70 75 80 85

gtg tgg act ttt ggc ctt gca atg gtc ata gga tta ata ggt gca cga 403
 Val Trp Thr Phe Gly Leu Ala Met Val Ile Gly Leu Ile Gly Ala Arg
 90 95 100

gta cca aag ctc cgc gcg gaa gga ata ggt att gct act aca tcc att 451
 Val Pro Lys Leu Arg Ala Glu Gly Ile Gly Ile Ala Thr Thr Ser Ile
 105 110 115
 ttt ctt ctt gcc tcc ggg ttt gat gat caa caa ccc ctt cta tac gac 499
 Phe Leu Leu Ala Ser Gly Phe Asp Asp Gln Gln Pro Leu Leu Tyr Asp
 120 125 130
 cgt att tta gag atc ctg ctc ggc gtg gct gtt gcc ata gcc atc aac 547
 Arg Ile Leu Glu Ile Leu Leu Gly Val Ala Val Ala Ile Ala Ile Asn
 135 140 145
 ctc atc atc ttt cct ccc tta cgc gac cag gag gca aac atg gtg gta 595
 Leu Ile Ile Phe Pro Pro Leu Arg Asp Gln Glu Ala Asn Met Val Val
 150 155 160 165
 gga aac tta gat cgg agg atg ggt gag gtt tta caa aaa atg gcc gat 643
 Gly Asn Leu Asp Arg Arg Met Gly Glu Val Leu Gln Lys Met Ala Asp
 170 175 180
 gag ctt gca gaa aag tgg aat atc gac aat gca gat gag tgg ctg gaa 691
 Glu Leu Ala Glu Lys Trp Asn Ile Asp Asn Ala Asp Glu Trp Leu Glu
 185 190 195
 gaa att aat tct att aac aat gac cta gaa aaa gcg tgg cac tcc gtg 739
 Glu Ile Asn Ser Ile Asn Asn Asp Leu Glu Lys Ala Trp His Ser Val
 200 205 210
 cgg ttc gtt cgc gaa agc cgt cga gtt aat cct cgt aaa atc cgc atc 787
 Arg Phe Val Arg Glu Ser Arg Arg Val Asn Pro Arg Lys Ile Arg Ile
 215 220 225
 caa gag ggc cgc ccc cag cct acg gaa aca agt tat gaa tca aac ctc 835
 Gln Glu Gly Arg Pro Gln Pro Thr Glu Thr Ser Tyr Glu Ser Asn Leu
 230 235 240 245
 acc agc att gat gaa ggg atc gct cat tta cgc cac ctt gcc cgt act 883
 Thr Ser Ile Asp Glu Gly Ile Ala His Leu Arg His Leu Ala Arg Thr
 250 255 260
 ctt cgt gat acc ccg att ata gat tcc gac tgg gga tcc agt att cca 931
 Leu Arg Asp Thr Pro Ile Ile Asp Ser Asp Trp Gly Ser Ser Ile Pro
 265 270 275
 gca aca gtg ggt atc cct tat gca cga tgc cgg agc ttt gct cgc aga 979
 Ala Thr Val Gly Ile Pro Tyr Ala Arg Cys Arg Ser Phe Ala Arg Arg
 280 285 290
 tcc gaa tca gga aat aga tcc tat ccg cga ccg gct etc taaactttca 1028
 Ser Glu Ser Gly Asn Arg Ser Tyr Pro Arg Pro Ala Leu
 295 300 305
 agtgagatga gtg 1041

<210> 570

<211> 306

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 570

Met Glu Lys Ile Arg Ser Pro Ala Val Gln Ser Asp Ala Leu Gln Val
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 Phe Lys Ser Ala Leu Ala Ala Thr Val Thr Trp Trp Ile Ser Val Asn
 20 25 30
 Leu Leu Asn Ser Gln Leu Pro Phe Leu Ala Pro Trp Val Ala Leu Met
 35 40 45
 Thr Met Gln Phe Thr Val Tyr His Thr Phe Ile Ser Gly Ile Gln Thr
 50 55 60
 Ala Ile Ala Ser Val Ile Gly Val Gly Leu Ser Phe Val Ile Gly Thr
 65 70 75 80
 Tyr Leu Asp Val Ser Val Trp Thr Phe Gly Leu Ala Met Val Ile Gly
 85 90 95
 Leu Ile Gly Ala Arg Val Pro Lys Leu Arg Ala Glu Gly Ile Gly Ile
 100 105 110
 Ala Thr Thr Ser Ile Phe Leu Leu Ala Ser Gly Phe Asp Asp Gln Gln
 115 120 125
 Pro Leu Leu Tyr Asp Arg Ile Leu Glu Ile Leu Leu Gly Val Ala Val
 130 135 140
 Ala Ile Ala Ile Asn Leu Ile Ile Phe Pro Pro Leu Arg Asp Gln Glu
 145 150 155 160
 Ala Asn Met Val Val Gly Asn Leu Asp Arg Arg Met Gly Glu Val Leu
 165 170 175
 Gln Lys Met Ala Asp Glu Leu Ala Glu Lys Trp Asn Ile Asp Asn Ala
 180 185 190
 Asp Glu Trp Leu Glu Glu Ile Asn Ser Ile Asn Asn Asp Leu Glu Lys
 195 200 205
 Ala Trp His Ser Val Arg Phe Val Arg Glu Ser Arg Arg Val Asn Pro
 210 215 220
 Arg Lys Ile Arg Ile Gln Glu Gly Arg Pro Gln Pro Thr Glu Thr Ser
 225 230 235 240
 Tyr Glu Ser Asn Leu Thr Ser Ile Asp Glu Gly Ile Ala His Leu Arg
 245 250 255
 His Leu Ala Arg Thr Leu Arg Asp Thr Pro Ile Ile Asp Ser Asp Trp
 260 265 270
 Gly Ser Ser Ile Pro Ala Thr Val Gly Ile Pro Tyr Ala Arg Cys Arg
 275 280 285
 Ser Phe Ala Arg Arg Ser Glu Ser Gly Asn Arg Ser Tyr Pro Arg Pro
 290 295 300
 Ala Leu
 305

<210> 571
 <211> 885
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(862)
 <223> RXN01281

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 Val Gly Leu Ser Arg
 1 5
 tca cat tat cag cta gcc gca gaa aac acc aaa tcc ctt gtt aga atg 163
 Ser His Tyr Gln Leu Ala Ala Glu Asn Thr Lys Ser Leu Val Arg Met
 10 15 20
 gtt ccc atg act gtt cct caa gga aac gaa cca gca aag aag ctc gcc 211
 Val Pro Met Thr Val Pro Gln Gly Asn Glu Pro Ala Lys Lys Leu Ala
 25 30 35
 act gac ctt aac cga aac caa gtc gtg gat gaa ctt tct gca gct gtt 259
 Thr Asp Leu Asn Arg Asn Gln Val Val Asp Glu Leu Ser Ala Ala Val
 40 45 50
 tcc cga ggt caa ctc act ttg gag gaa ttt gaa gat cgc tcc tcc aaa 307
 Ser Arg Gly Gln Leu Thr Leu Glu Glu Phe Glu Asp Arg Ser Ser Lys
 55 60 65
 gca tgg aat gcc cgc cac tta gac act ctt gta gag ctg atc tct gat 355
 Ala Trp Asn Ala Arg His Leu Asp Thr Leu Val Glu Leu Ile Ser Asp
 70 75 80 85
 gtg aac gac aat ccc tac act ctg ctt ggt cag caa ttt ccc ggc gcc 403
 Val Asn Asp Asn Pro Tyr Thr Leu Leu Gly Gln Gln Phe Pro Gly Ala
 90 95 100
 tcc tat gcg ccg gcg gcc tac gag acc act ccc cca gcg atg ccc aat 451
 Ser Tyr Ala Pro Ala Ala Tyr Glu Thr Thr Pro Pro Ala Met Pro Asn
 105 110 115
 gtg tca gat cct gta aat att gtc cgc aac agg att acc ggc aac ccg 499
 Val Ser Asp Pro Val Asn Ile Val Arg Asn Arg Ile Thr Gly Asn Pro
 120 125 130
 aat ggc tcc aaa atg tcg gtc tcg ttt atg ggt ggc acc gtg cgc aaa 547
 Asn Gly Ser Lys Met Ser Val Ser Phe Met Gly Thr Val Arg Lys
 135 140 145
 ggt gga tgg cat gtg cct aat gtt cac aca tcc ttc gcc atg atg ggc 595
 Gly Gly Trp His Val Pro Asn Val His Thr Ser Phe Ala Met Met Gly
 150 155 160 165
 ggc aat cag atc gat ttg cgc gac gcc ttc ctg gaa agc gac cgc att 643
 Gly Asn Gln Ile Asp Leu Arg Asp Ala Phe Leu Glu Ser Asp Arg Ile
 170 175 180

cag atc aac gcc tac aca ttc atg ggt ggc atc gag att att gtt ccc 691
 Gln Ile Asn Ala Tyr Thr Phe Met Gly Gly Ile Glu Ile Ile Val Pro
 185 190 195
 gag ggt gtt ttt gtc att tgt gat ggc atg ggc att ttc ggc ggc ttc 739
 Glu Gly Val Phe Val Ile Cys Asp Gly Met Gly Ile Phe Gly Gly Phe
 200 205 210
 gaa cag tct gtg gac aag gcc ggt gca ctc aat ccc gcg cgc ctg cca 787
 Glu Gln Ser Val Asp Lys Ala Gly Ala Leu Asn Pro Ala Arg Leu Pro
 215 220 225
 agc aac gcg ccc acg gtc cac atc aaa ggc ctg gcg ttc atg ggc gga 835
 Ser Asn Ala Pro Thr Val His Ile Lys Gly Leu Ala Phe Met Gly Gly
 230 235 240 245
 gtc agc gta gtc acc aag aaa aac att taaaaagctt gtgcagcgc 882
 Val Ser Val Val Thr Lys Lys Asn Ile
 250
 ccc 885

<210> 572
 <211> 254
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 572
 Val Gly Leu Ser Arg Ser His Tyr Gln Leu Ala Ala Glu Asn Thr Lys
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 Ser Leu Val Arg Met Val Pro Met Thr Val Pro Gln Gly Asn Glu Pro
 20 25 30
 Ala Lys Lys Leu Ala Thr Asp Leu Asn Arg Asn Gln Val Val Asp Glu
 35 40 45
 Leu Ser Ala Ala Val Ser Arg Gly Gln Leu Thr Leu Glu Glu Phe Glu
 50 55 60
 Asp Arg Ser Ser Lys Ala Trp Asn Ala Arg His Leu Asp Thr Leu Val
 65 70 75 80
 Glu Leu Ile Ser Asp Val Asn Asp Asn Pro Tyr Thr Leu Leu Gly Gln
 85 90 95
 Gln Phe Pro Gly Ala Ser Tyr Ala Pro Ala Ala Tyr Glu Thr Thr Pro
 100 105 110
 Pro Ala Met Pro Asn Val Ser Asp Pro Val Asn Ile Val Arg Asn Arg
 115 120 125
 Ile Thr Gly Asn Pro Asn Gly Ser Lys Met Ser Val Ser Phe Met Gly
 130 135 140
 Gly Thr Val Arg Lys Gly Gly Trp His Val Pro Asn Val His Thr Ser
 145 150 155 160
 Phe Ala Met Met Gly Gly Asn Gln Ile Asp Leu Arg Asp Ala Phe Leu
 165 170 175

Glu Ser Asp Arg Ile Gln Ile Asn Ala Tyr Thr Phe Met Gly Gly Ile
180 185 190

Glu Ile Ile Val Pro Glu Gly Val Phe Val Ile Cys Asp Gly Met Gly
195 200 205

Ile Phe Gly Gly Phe Glu Gln Ser Val Asp Lys Ala Gly Ala Leu Asn
210 215 220

Pro Ala Arg Leu Pro Ser Asn Ala Pro Thr Val His Ile Lys Gly Leu
225 230 235 240

Ala Phe Met Gly Gly Val Ser Val Val Thr Lys Lys Asn Ile
245 250

<210> 573

<211> 885

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(862)

<223> FRXA01281

<400> 573

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gcgcttgagt gcgaggtgcc gtcaattccc aactacaaga gtg gga ctc agc cgt 115
Val Gly Leu Ser Arg
1 5

tca cat tat cag cta gcc gca gaa aac acc aaa tcc ctt gtt aga atg 163
Ser His Tyr Gln Leu Ala Ala Glu Asn Thr Lys Ser Leu Val Arg Met
10 15 20

gtt ccc atg act gtt cct caa gga aac gaa cca gca aag aag ctc gcc 211
Val Pro Met Thr Val Pro Gln Gly Asn Glu Pro Ala Lys Lys Leu Ala
25 30 35

act gac ctt aac cga aac caa gtc gtg gat gaa ctt tct gca gct gtt 259
Thr Asp Leu Asn Arg Asn Gln Val Val Asp Glu Leu Ser Ala Ala Val
40 45 50

tcc cga ggt caa ctc act ttg gag gaa ttt gaa gat cgc tcc tcc aaa 307
Ser Arg Gly Gln Leu Thr Leu Glu Glu Phe Glu Asp Arg Ser Ser Lys
55 60 65

gca tgg aat gcc cgc cac tta gac act ctt gta gag ctg atc tct gat 355
Ala Trp Asn Ala Arg His Leu Asp Thr Leu Val Glu Leu Ile Ser Asp
70 75 80 85

gtg aac gac aat ccc tac act ctg ctt ggt cag caa ttt ccc ggc gcc 403
Val Asn Asp Asn Pro Tyr Thr Leu Leu Gly Gln Gln Phe Pro Gly Ala
90 95 100

tcc tat gcg ccg gcg gcc tac gag acc act ccc cca gcg atg ccc aat 451
Ser Tyr Ala Pro Ala Ala Tyr Glu Thr Thr Pro Pro Ala Met Pro Asn
105 110 115

gtg tca gat cct gta aat att gtc cgc aac agg att acc ggc aac ccg 499
Val Ser Asp Pro Val Asn Ile Val Arg Asn Arg Ile Thr Gly Asn Pro
120 125 130

aat ggc tcc aaa atg tcg gtc tcg ttt atg ggt ggc acc gtg cgc aaa 547
Asn Gly Ser Lys Met Ser Val Ser Phe Met Gly Gly Thr Val Arg Lys
135 140 145

ggt gga tgg cat gtg cct aat gtt cac aca tcc ttc gcc atg atg ggc 595
Gly Gly Trp His Val Pro Asn Val His Thr Ser Phe Ala Met Met Gly
150 155 160 165

ggc aat cag atc gat ttg cgc gac gcc ttc ctg gaa agc gac cgc att 643
Gly Asn Gln Ile Asp Leu Arg Asp Ala Phe Leu Glu Ser Asp Arg Ile
170 175 180

cag atc aac gcc tac aca ttc atg ggt ggc atc gag att att gtt ccc 691
Gln Ile Asn Ala Tyr Thr Phe Met Gly Gly Ile Glu Ile Val Pro
185 190 195

gag ggt gtt ttt gtc att tgt gat ggc atg ggc att ttc ggc gcc ttc 739
Glu Gly Val Phe Val Ile Cys Asp Gly Met Gly Ile Phe Gly Gly Phe
200 205 210

gaa cag tct gtg gac aag gcc ggt gca ctc aat ccc gcg cgc ctg cca 787
Glu Gln Ser Val Asp Lys Ala Gly Ala Leu Asn Pro Ala Arg Leu Pro
215 220 225

agc aac gcg ccc acg gtc cac atc aaa ggc ctg gcg ttc atg ggc gga 835
Ser Asn Ala Pro Thr Val His Ile Lys Gly Leu Ala Phe Met Gly Gly
230 235 240 245

gtc agc gta gtc acc aag aaa aac att taaaaagcgtt gtcgacgcgc 882
Val Ser Val Val Thr Lys Lys Asn Ile
250

ccc 885

<210> 574

<211> 254

<212> FRT

<213> *Corynebacterium glutamicum*

<400> 574

Val Gly Leu Ser Arg Ser His Tyr Gln Leu Ala Ala Glu Asn Thr Lys
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Ser Leu Val Arg Met Val Pro Met Thr Val Pro Gln Gly Asn Glu Pro
20 25 30

Ala Lys Lys Leu Ala Thr Asp Leu Asn Arg Asn Gln Val Val Asp Glu
35 40 45

Leu Ser Ala Ala Val Ser Arg Gly Gln Leu Thr Leu Glu Glu Phe Glu
50 55 60

Asp Arg Ser Ser Lys Ala Trp Asn Ala Arg His Leu Asp Thr Leu Val
65 70 75 80

[illegible]

<211> 1206

<212> DNA

<213> *Corynebacterium glutamicum*

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<221> CDS

<222> {101} . . (1183)

<223> RXN01296

<400> 575

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agatccagaa tcgatcactc tacgaccagg aaaaactttc atg tcc atc gag caa    115
                Met Ser Ile Glu Gln
                1                5

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gca atc act tca ctc tcc gca aga gtg cgg gaa cta aag ccc atc atc 163
Ala Ile Thr Ser Leu Ser Ala Arg Val Arg Glu Leu Lys Pro Ile Ile
10 15 20

gag act gaa gaa gcc acc aaa acc gca ctg atc atc ccc ttt atc agc 211
Glu Thr Glu Glu Ala Thr Lys Thr Ala Leu Ile Ile Pro Phe Ile Ser
25 30 35

aac gtt ctc ggc tac gac gtc act gat cct cgt gaa gtc att ccg gaa 259
Asn Val Leu Gly Tyr Asp Val Thr Asp Pro Arg Glu Val Ile Pro Glu

	40					45					50						
	tac	act	gct	gat	gtt	ggc	gtc	aaa	aag	ggt	gag	aag	gtc	gac	ttc	gct	307
	Tyr	Thr	Ala	Asp	Val	Gly	Val	Lys	Lys	Gly	Glu	Lys	Val	Asp	Phe	Ala	
	55						60					65					
	atc	aaa	acc	ggc	gat	gat	ttc	cac	ttc	ctc	atc	gaa	tgc	aaa	aag	gtc	355
	Ile	Lys	Thr	Gly	Asp	Asp	Phe	His	Phe	Leu	Ile	Glu	Cys	Lys	Lys	Val	
	70						75				80					85	
	ggc	tcc	cca	ctc	agc	ctc	gat	cac	gct	aac	cag	ctc	gtc	cgc	tat	ttc	403
	Gly	Ser	Pro	Leu	Ser	Leu	Asp	His	Ala	Asn	Gln	Leu	Val	Arg	Tyr	Phe	
					90					95					100		
	aat	gtc	aca	gac	acc	gaa	ttt	gcc	att	ctc	acc	aac	ggc	gaa	atc	tac	451
	Asn	Val	Thr	Asp	Thr	Glu	Phe	Ala	Ile	Leu	Thr	Asn	Gly	Glu	Ile	Tyr	
				105					110					115			
	caa	ttc	tat	gga	caa	ctc	gat	gca	gcc	aac	cgc	atg	gat	gca	aaa	cca	499
	Gln	Phe	Tyr	Gly	Gln	Leu	Asp	Ala	Ala	Asn	Arg	Met	Asp	Ala	Lys	Pro	
				120				125					130				
	ttc	atg	acc	ttg	gat	ttg	aac	aat	att	gat	gcc	cgt	cag	ttc	cct	cat	547
	Phe	Met	Thr	Leu	Asp	Leu	Asn	Asn	Ile	Asp	Ala	Arg	Gln	Phe	Pro	His	
							140					145					
	ttg	gaa	atg	tgt	acc	cgc	aag	cat	ttc	aac	cca	caa	gcg	cta	gcc	gcc	595
	Leu	Glu	Met	Cys	Thr	Arg	Lys	His	Phe	Asn	Pro	Gln	Ala	Leu	Ala	Ala	
	150						155				160					165	
	aac	gct	gaa	gaa	ctg	aag	tac	att	gct	gaa	ttg	aag	aaa	gtc	atc	gcg	643
	Asn	Ala	Glu	Glu	Leu	Lys	Tyr	Ile	Ala	Glu	Leu	Lys	Lys	Val	Ile	Ala	
					170					175					180		
	aat	caa	ttc	caa	gaa	cct	gac	gta	gaa	atc	gtc	aag	atg	ctt	gcg	gcg	691
	Asn	Gln	Phe	Gln	Glu	Pro	Asp	Val	Glu	Ile	Val	Lys	Met	Leu	Ala	Ala	
				185					190					195			
	aca	gtc	acc	aca	aag	cgt	atg	act	gca	caa	aat	ctg	gaa	ttc	ttc	acc	739
	Thr	Val	Thr	Thr	Lys	Arg	Met	Thr	Ala	Gln	Asn	Leu	Glu	Phe	Phe	Thr	
				200				205					210				
	cgc	ttg	gtt	aat	act	gcg	tct	tcc	cag	ttc	ctc	aaa	gac	gag	gtc	aat	787
	Arg	Leu	Val	Asn	Thr	Ala	Ser	Ser	Gln	Phe	Leu	Lys	Asp	Glu	Val	Asn	
				215			220					225					
	cgt	aga	ttg	cgc	tcc	gcc	caa	gtc	ttt	gag	gat	cct	gtc	caa	aca	caa	835
	Arg	Arg	Leu	Arg	Ser	Ala	Gln	Val	Phe	Glu	Asp	Pro	Val	Gln	Thr	Gln	
	230					235					240					245	
	ggt	gct	gat	gca	gaa	aca	cca	gca	gag	gac	gaa	gca	gta	atc	gaa	gaa	883
	Gly	Ala	Asp	Ala	Glu	Thr	Pro	Ala	Glu	Asp	Glu	Ala	Val	Ile	Glu	Glu	
					250				255						260		
	gtg	gtt	tca	gaa	atc	gtg	acg	aca	gaa	gag	gaa	atc	cac	ggt	cat	tca	931
	Val	Val	Ser	Glu	Ile	Val	Thr	Thr	Glu	Glu	Glu	Ile	His	Gly	His	Ser	
				265					270					275			
	att	gtc	cgt	gca	att	tgc	tgc	tca	gag	gta	tcg	gca	caa	gaa	atc	acc	979
	Ile	Val	Arg	Ala	Ile	Cys	Cys	Ser	Glu	Val	Ser	Ala	Gln	Glu	Ile	Thr	
				280				285					290				

atg cgt gac gca aaa tcc tac tgc gct att ctc ttc caa gac aac aac 1027
Met Arg Asp Ala Lys Ser Tyr Cys Ala Ile Leu Phe Gln Asp Asn Asn
295 300 305

cga aag cca atc gcc cgt ttc tac ttt gat cgc aag att cca cgc atc 1075
Arg Lys Pro Ile Ala Arg Phe Tyr Phe Asp Arg Lys Ile Pro Arg Ile
310 315 320 325

ggc atc ttc aat gct gaa ggc gag cag gaa cac ttt gat ttg gaa tcc 1123
Gly Ile Phe Asn Ala Glu Gly Glu Gln Glu His Phe Asp Leu Glu Ser
330 335 340

atc gaa gat atc tac aac cac gct gat ctt ctg cat tcc cgc gtc gta 1171
Ile Glu Asp Ile Tyr Asn His Ala Asp Leu Leu His Ser Arg Val Val
345 350 355

gca ttg aac gct taagttctgc ctttagttct gca 1206
Ala Leu Asn Ala
360

<210> 576
<211> 361
<212> PRT
<213> Corynebacterium glutamicum

<400> 576
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Leu Lys Pro Ile Ile Glu Thr Glu Glu Ala Thr Lys Thr Ala Leu Ile
20 25 30

Ile Pro Phe Ile Ser Asn Val Leu Gly Tyr Asp Val Thr Asp Pro Arg
35 40 45

Glu Val Ile Pro Glu Tyr Thr Ala Asp Val Gly Val Lys Lys Gly Glu
50 55 60

Lys Val Asp Phe Ala Ile Lys Thr Gly Asp Asp Phe His Phe Leu Ile
65 70 75 80

Glu Cys Lys Lys Val Gly Ser Pro Leu Ser Leu Asp His Ala Asn Gln
85 90 95

Leu Val Arg Tyr Phe Asn Val Thr Asp Thr Glu Phe Ala Ile Leu Thr
100 105 110

Asn Gly Glu Ile Tyr Gln Phe Tyr Gly Gln Leu Asp Ala Ala Asn Arg
115 120 125

Met Asp Ala Lys Pro Phe Met Thr Leu Asp Leu Asn Asn Ile Asp Ala
130 135 140

Arg Gln Phe Pro His Leu Glu Met Cys Thr Arg Lys His Phe Asn Pro
145 150 155 160

Gln Ala Leu Ala Ala Asn Ala Glu Glu Leu Lys Tyr Ile Ala Glu Leu
165 170 175

Lys Lys Val Ile Ala Asn Gln Phe Gln Glu Pro Asp Val Glu Ile Val
 180 185 190
 Lys Met Leu Ala Ala Thr Val Thr Thr Lys Arg Met Thr Ala Gln Asn
 195 200 205
 Leu Glu Phe Phe Thr Arg Leu Val Asn Thr Ala Ser Ser Gln Phe Leu
 210 215 220
 Lys Asp Glu Val Asn Arg Arg Leu Arg Ser Ala Gln Val Phe Glu Asp
 225 230 235 240
 Pro Val Gln Thr Gln Gly Ala Asp Ala Glu Thr Pro Ala Glu Asp Glu
 245 250 255
 Ala Val Ile Glu Glu Val Val Ser Glu Ile Val Thr Thr Glu Glu Glu
 260 265 270
 Ile His Gly His Ser Ile Val Arg Ala Ile Cys Cys Ser Glu Val Ser
 275 280 285
 Ala Gln Glu Ile Thr Met Arg Asp Ala Lys Ser Tyr Cys Ala Ile Leu
 290 295 300
 Phe Gln Asp Asn Asn Arg Lys Pro Ile Ala Arg Phe Tyr Phe Asp Arg
 305 310 315 320
 Lys Ile Pro Arg Ile Gly Ile Phe Asn Ala Glu Gly Glu Gln Glu His
 325 330 335
 Phe Asp Leu Glu Ser Ile Glu Asp Ile Tyr Asn His Ala Asp Leu Leu
 340 345 350
 His Ser Arg Val Val Ala Leu Asn Ala
 355 360

<210> 577

<211> 1206

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> {101}..(1183)

<223> FRXA01296

<400> 577

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 agatccagaa tcgatcactc tacgaccagg aaaaactttc atg tcc atc gag caa 115
 Met Ser Ile Glu Gln
 1 5

 gca atc act tca ctc tcc gca aga gtg cgg gaa cta aag ccc atc atc 163
 Ala Ile Thr Ser Leu Ser Ala Arg Val Arg Glu Leu Lys Pro Ile Ile
 10 15 20

 gag act gaa gaa gcc acc aaa acc gca ctg atc atc ccc ttt atc agc 211
 Glu Thr Glu Glu Ala Thr Lys Thr Ala Leu Ile Ile Pro Phe Ile Ser
 25 30 35

aac gtt ctc ggc tac gac gtc act gat cct cgt gaa gtc att ccg gaa 259
 Asn Val Leu Gly Tyr Asp Val Thr Asp Pro Arg Glu Val Ile Pro Glu
 40 45 50

tac act gct gat gtt ggc gtc aaa aag ggt gag aag gtc gac ttc gct 307
 Tyr Thr Ala Asp Val Gly Val Lys Lys Gly Glu Lys Val Asp Phe Ala
 55 60 65

atc aaa acc ggc gat gat ttc cac ttc ctc atc gaa tgc aaa aag gtc 355
 Ile Lys Thr Gly Asp Phe His Phe Leu Ile Glu Cys Lys Lys Val
 70 75 80 85

ggc tcc cca ctc agc ctc gat cac gct aac cag ctc gtc cgc tat ttc 403
 Gly Ser Pro Leu Ser Leu Asp His Ala Asn Gln Leu Val Arg Tyr Phe
 90 95 100

aat gtc aca gac acc gaa ttt gcc att ctc acc aac ggc gaa atc tac 451
 Asn Val Thr Asp Thr Glu Phe Ala Ile Leu Thr Asn Gly Glu Ile Tyr
 105 110 115

caa ttc tat gga caa ctc gat gca gcc aac cgc atg gat gca aaa cca 499
 Gln Phe Tyr Gly Gln Leu Asp Ala Ala Asn Arg Met Asp Ala Lys Pro
 120 125 130

ttc atg acc ttg gat ttg aac aat att gat gcc cgt cag ttc cct cat 547
 Phe Met Thr Leu Asp Leu Asn Asn Ile Asp Ala Arg Gln Phe Pro His
 135 140 145

ttg gaa atg tgt acc cgc aag cat ttc aac cca caa gcg cta gcc gcc 595
 Leu Glu Met Cys Thr Arg Lys His Phe Asn Pro Gln Ala Leu Ala Ala
 150 155 160 165

aac gct gaa gaa ctg aag tac att gct gaa ttg aag aaa gtc atc gcg 643
 Asn Ala Glu Glu Leu Lys Tyr Ile Ala Glu Leu Lys Lys Val Ile Ala
 170 175 180

aat caa ttc caa gaa cct gac gta gaa atc gtc aag atg ctt gcg gcg 691
 Asn Gln Phe Gln Glu Pro Asp Val Glu Ile Val Lys Met Leu Ala Ala
 185 190 195

aca gtc acc aca aag cgt atg act gca caa aat ctg gaa ttc ttc acc 739
 Thr Val Thr Thr Lys Arg Met Thr Ala Gln Asn Leu Glu Phe Phe Thr
 200 205 210

cgc ttg gtt aat act gcg tct tcc cag ttc ctc aaa gac gag gtc aat 787
 Arg Leu Val Asn Thr Ala Ser Ser Gln Phe Leu Lys Asp Glu Val Asn
 215 220 225

cgt aga ttg cgc tcc gcc caa gtc ttt gag gat cct gtc caa aca caa 835
 Arg Arg Leu Arg Ser Ala Gln Val Phe Glu Asp Pro Val Gln Thr Gln
 230 235 240 245

ggt gct gat gca gaa aca cca gca gag gac gaa gca gta atc gaa gaa 883
 Gly Ala Asp Ala Glu Thr Pro Ala Glu Asp Glu Ala Val Ile Glu Glu
 250 255 260

gtg gtt tca gaa atc gtg acg aca gaa gag gaa atc cac ggt cat tca 931
 Val Val Ser Glu Ile Val Thr Thr Glu Glu Glu Ile His Gly His Ser
 265 270 275

att gtc cgt gca att tgc tgc tca gag gta tgc gca caa gaa atc acc 979
 Ile Val Arg Ala Ile Cys Cys Ser Glu Val Ser Ala Gln Glu Ile Thr
 280 285 290

atg cgt gac gca aaa tcc tac tgc gct att ctc ttc caa gac aac aac 1027
 Met Arg Asp Ala Lys Ser Tyr Cys Ala Ile Leu Phe Gln Asp Asn Asn
 295 300 305

cga aag cca atc gcc cgt ttc tac ttt gat cgc aag att cca cgc atc 1075
 Arg Lys Pro Ile Ala Arg Phe Tyr Phe Asp Arg Lys Ile Pro Arg Ile
 310 315 320 325

ggc atc ttc aat gct gaa ggc gag cag gaa cac ttt gat ttg gaa tcc 1123
 Gly Ile Phe Asn Ala Glu Gly Glu Gln Glu His Phe Asp Leu Glu Ser
 330 335 340

atc gaa gat atc tac aac cac gct gat ctt ctg cat tcc cgc gtc gta 1171
 Ile Glu Asp Ile Tyr Asn His Ala Asp Leu Leu His Ser Arg Val Val
 345 350 355

gca ttg aac gct taagtctgc ctttagttct gca 1206
 Ala Leu Asn Ala
 360

<210> 578
 <211> 361
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 578
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 1 5 10 15
 Leu Lys Pro Ile Ile Glu Thr Glu Glu Ala Thr Lys Thr Ala Leu Ile
 20 25 30
 Ile Pro Phe Ile Ser Asn Val Leu Gly Tyr Asp Val Thr Asp Pro Arg
 35 40 45
 Glu Val Ile Pro Glu Tyr Thr Ala Asp Val Gly Val Lys Lys Gly Glu
 50 55 60
 Lys Val Asp Phe Ala Ile Lys Thr Gly Asp Asp Phe His Phe Leu Ile
 65 70 75 80
 Glu Cys Lys Lys Val Gly Ser Pro Leu Ser Leu Asp His Ala Asn Gln
 85 90 95
 Leu Val Arg Tyr Phe Asn Val Thr Asp Thr Glu Phe Ala Ile Leu Thr
 100 105 110
 Asn Gly Glu Ile Tyr Gln Phe Tyr Gly Gln Leu Asp Ala Ala Asn Arg
 115 120 125
 Met Asp Ala Lys Pro Phe Met Thr Leu Asp Leu Asn Asn Ile Asp Ala
 130 135 140
 Arg Gln Phe Pro His Leu Glu Met Cys Thr Arg Lys His Phe Asn Pro
 145 150 155 160

Gln Ala Leu Ala Ala Asn Ala Glu Glu Leu Lys Tyr Ile Ala Glu Leu
 165 170 175
 Lys Lys Val Ile Ala Asn Gln Phe Gln Glu Pro Asp Val Glu Ile Val
 180 185 190
 Lys Met Leu Ala Ala Thr Val Thr Thr Lys Arg Met Thr Ala Gln Asn
 195 200 205
 Leu Glu Phe Phe Thr Arg Leu Val Asn Thr Ala Ser Ser Gln Phe Leu
 210 215 220
 Lys Asp Glu Val Asn Arg Arg Leu Arg Ser Ala Gln Val Phe Glu Asp
 225 230 235 240
 Pro Val Gln Thr Gln Gly Ala Asp Ala Glu Thr Pro Ala Glu Asp Glu
 245 250 255
 Ala Val Ile Glu Glu Val Val Ser Glu Ile Val Thr Thr Glu Glu Glu
 260 265 270
 Ile His Gly His Ser Ile Val Arg Ala Ile Cys Cys Ser Glu Val Ser
 275 280 285
 Ala Gln Glu Ile Thr Met Arg Asp Ala Lys Ser Tyr Cys Ala Ile Leu
 290 295 300
 Phe Gln Asp Asn Asn Arg Lys Pro Ile Ala Arg Phe Tyr Phe Asp Arg
 305 310 315 320
 Lys Ile Pro Arg Ile Gly Ile Phe Asn Ala Glu Gly Glu Gln Glu His
 325 330 335
 Phe Asp Leu Glu Ser Ile Glu Asp Ile Tyr Asn His Ala Asp Leu Leu
 340 345 350
 His Ser Arg Val Val Ala Leu Asn Ala
 355 360

<210> 579
 <211> 1131
 <212> DNA
 <213> *Corynebacterium glutamicum*
 <220>
 <221> CDS
 <222> (101)..(1108)
 <223> RXN01306
 <400> 579
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 cccagacaat caccgccgctc cgaaggagaa tcgctaagcc atg act gaa tgg tat 115
 Met Thr Glu Trp Tyr 5
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 gtc gtt tta ccc gcc act att cta ctc atc gcg ctg tct gcg ttt ttc 163
 Val Val Leu Pro Ala Thr Ile Leu Leu Ile Ala Leu Ser Ala Phe Phe
 10 15 20

gtc atc att gag ttc gct ttg ctt gca gct agg cgg aac cgg tta gag 211
 Val Ile Ile Glu Phe Ala Leu Leu Ala Ala Arg Arg Asn Arg Leu Glu
 25 30 35

gag act gtg gaa acc tcg cgg tct tcc cgc gct gcg ttg cga agc ctc 259
 Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala Ala Leu Arg Ser Leu
 40 45 50

aat gaa ctt act ctc atg ctc gcg gcc gcg cag ttg gga atc acc atg 307
 Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln Leu Gly Ile Thr Met
 55 60 65

gtg act ttc gcg ttg ggt gct atc acg aag cgg tgg gtt cat tat gct 355
 Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro Trp Val His Tyr Ala
 70 75 80 85

ttg atg cgg ctc ttc gaa tgg gcg cgt ata cgg ctg gtt atg gca gat 403
 Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro Leu Val Met Ala Asp
 90 95 100

gtc att gcg ttt att ttg tcg ctg ttt atc gta acg ttt ctg cac ttg 451
 Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val Thr Phe Leu His Leu
 105 110 115

gtc atc gcc gaa atg gct cgg aaa tcc tgg gca atc gcg cat cgg gag 499
 Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala Ile Ala His Pro Glu
 120 125 130

acg gca ctt cga act atc gcg att ccc gca cgg gcc ttc att aac ctg 547
 Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg Gly Phe Ile Asn Leu
 135 140 145

ttt cgt cca ttg ctg cag tgg atc aac aaa atg gcg aac gat ttg gtc 595
 Phe Arg Pro Leu Leu Gln Trp Ile Asn Lys Met Ala Asn Asp Leu Val
 150 155 160 165

cgc aaa gtt ggt gaa act ccc gtt gat cga gct gca gct ggt gcc tat 643
 Arg Lys Val Gly Glu Thr Pro Val Asp Arg Ala Ala Ala Gly Gly Tyr
 170 175 180

gac acc gat acc ctc cat gcc ctc att gag cat tcc cga gaa act gcc 691
 Asp Thr Asp Thr Leu His Ala Leu Ile Glu His Ser Arg Glu Thr Gly
 185 190 195

gct ctg gat cag caa tcc gcc gcc caa atc agc gga att atc aag ctg 739
 Ala Leu Asp Gln Gln Ser Ala Ala Gln Ile Ser Gly Ile Ile Lys Leu
 200 205 210

gat aaa atc acg gtc ggt caa acc ctg acc gca tct cca ttt acg cac 787
 Asp Lys Ile Thr Val Gly Gln Thr Leu Thr Ala Ser Pro Phe Thr His
 215 220 225

agc gcc agc gcc acg gtt gct gag gtg caa gcc gca gct cag cgc agt 835
 Ser Ala Ser Ala Thr Val Ala Glu Val Gln Ala Ala Ala Gln Arg Ser
 230 235 240 245

gcc agc ttg cgt gtg ctt atc gac gcc ccc tcc cac ctt ttc cca cac 883
 Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser His Leu Phe Pro His
 250 255 260

gtc att cat gtg cga gac acc ctt ggt gcc tcg cca gac gag aag gct 931

Val Ile His Val Arg Asp Thr Leu Gly Ala Ser Pro Asp Glu Lys Ala
 265 270 275

tgc aag tgg tct cgc cca atc ctc acc gtt gct gag acc gac acg tta 979
 Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala Glu Thr Asp Thr Leu
 280 285 290

cac caa gcg ctg gaa tac atg cgg gag cat aac gag cag atc agt gcg 1027
 His Gln Ala Leu Glu Tyr Met Arg Glu His Asn Glu Gln Ile Ser Ala
 295 300 305

gtg ctt tcc gct gat ggg aaa acg gtg ctt ggt gta ata act tgg gat 1075
 Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly Val Ile Thr Trp Asp
 310 315 320 325

cac atc ttg aaa tac ctg tgg cct gca tcg gtg tagctaattt gaggtgcgct 1128
 His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val
 330 335

gaa 1131

<210> 580

<211> 336

<212> PRT

<213> Corynebacterium glutamicum

<400> 580

Met Thr Glu Trp Tyr Val Val Leu Pro Ala Thr Ile Leu Leu Ile Ala
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Leu Ser Ala Phe Phe Val Ile Ile Glu Phe Ala Leu Leu Ala Ala Arg
 20 25 30

Arg Asn Arg Leu Glu Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala
 35 40 45

Ala Leu Arg Ser Leu Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln
 50 55 60

Leu Gly Ile Thr Met Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro
 65 70 75 80

Trp Val His Tyr Ala Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro
 85 90 95

Leu Val Met Ala Asp Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val
 100 105 110

Thr Phe Leu His Leu Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala
 115 120 125

Ile Ala His Pro Glu Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg
 130 135 140

Gly Phe Ile Asn Leu Phe Arg Pro Leu Leu Gln Trp Ile Asn Lys Met
 145 150 155 160

Ala Asn Asp Leu Val Arg Lys Val Gly Glu Thr Pro Val Asp Arg Ala
 165 170 175

Ala Ala Gly Gly Tyr Asp Thr Asp Thr Leu His Ala Leu Ile Glu His
180 185 190

Ser Arg Glu Thr Gly Ala Leu Asp Gln Gln Ser Ala Ala Gln Ile Ser
195 200 205

Gly Ile Ile Lys Leu Asp Lys Ile Thr Val Gly Gln Thr Leu Thr Ala
210 215 220

Ser Pro Phe Thr His Ser Ala Ser Ala Thr Val Ala Glu Val Gln Ala
225 230 235 240

Ala Ala Gln Arg Ser Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser
245 250 255

His Leu Phe Pro His Val Ile His Val Arg Asp Thr Leu Gly Ala Ser
260 265 270

Pro Asp Glu Lys Ala Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala
275 280 285

Glu Thr Asp Thr Leu His Gln Ala Leu Glu Tyr Met Arg Glu His Asn
290 295 300

Glu Gln Ile Ser Ala Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly
305 310 315 320

Val Ile Thr Trp Asp His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val
325 330 335

<210> 581
<211> 1107
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (77)..(1084)
<223> FRXA01306

<400> 581
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ggagaatcga taagccatg act gaa tgg tat gtc gtt tta ccc gcc act att 112
Met Thr Glu Trp Tyr Val Val Leu Pro Ala Thr Ile
1 5 10

cta ctc atc gcg ctg tct gcg ttt ttc gtc atc att gag ttc gct ttg 160
Leu Leu Ile Ala Leu Ser Ala Phe Phe Val Ile Ile Glu Phe Ala Leu
15 20 25

ctt gca gct agg cgg aac cgg tta gag gag act gtg gaa acc tcg cgg 208
Leu Ala Ala Arg Arg Asn Arg Leu Glu Glu Thr Val Glu Thr Ser Arg
30 35 40

tct tcc cgc gct gcg ttg cga agc ctc aat gaa ctt act ctc atg ctc 256
Ser Ser Arg Ala Ala Leu Arg Ser Leu Asn Glu Leu Thr Leu Met Leu

45	50	55	60	
gcg ggc gcg cag ttg gga atc acc atg gtg act ttc gcg ttg ggt gct	304			
Ala Gly Ala Gln Leu Gly Ile Thr Met Val Thr Phe Ala Leu Gly Ala	65	70	75	
atc acg aag ccg tgg gtt cat tat gct ttg atg ccg ctc ttc gaa tgg	352			
Ile Thr Lys Pro Trp Val His Tyr Ala Leu Met Pro Leu Phe Glu Trp	80	85	90	
gcg cgt ata ccg ctg gtt atg gca gat gtc att gcg ttt att ttg tcg	400			
Ala Arg Ile Pro Leu Val Met Ala Asp Val Ile Ala Phe Ile Leu Ser	95	100	105	
ctg ttt atc gta acg ttt ctg cac ttg gtc atc gcc gaa atg gct ccg	448			
Leu Phe Ile Val Thr Phe Leu His Leu Val Ile Gly Glu Met Ala Pro	110	115	120	
aaa tcc tgg gca atc gcg cat ccg gag acg gca ctt cga act atc gcg	496			
Lys Ser Trp Ala Ile Ala His Pro Glu Thr Ala Leu Arg Thr Ile Ala	125	130	135	140
att ccc gca ccg ggc ttc att aac ctg ttt cgt cca ttg ctg cag tgg	544			
Ile Pro Ala Arg Gly Phe Ile Asn Leu Phe Arg Pro Leu Leu Gln Trp	145	150	155	
atc aac aaa atg gcg aac gat ttg gtc cgc aaa gtt ggt gaa act ccc	592			
Ile Asn Lys Met Ala Asn Asp Leu Val Arg Lys Val Gly Glu Thr Pro	160	165	170	
gtt gat cga gct gca gct ggt gcc tat gac acc gat acc ctc cat gcc	640			
Val Asp Arg Ala Ala Ala Gly Gly Tyr Asp Thr Asp Thr Leu His Ala	175	180	185	
ctc att gag cat tcc cga gaa act gcc gct ctg gat cag caa tcc gcc	688			
Leu Ile Glu His Ser Arg Glu Thr Gly Ala Leu Asp Gln Gln Ser Ala	190	195	200	
gcc caa atc agc gga att atc aag ctg gat aaa atc acg gtc ggt caa	736			
Ala Gln Ile Ser Gly Ile Ile Lys Leu Asp Lys Ile Thr Val Gly Gln	205	210	215	220
acc ctg acc gca tct cca ttt acg cac agc gcc agc gcc acg gtt gct	784			
Thr Leu Thr Ala Ser Pro Phe Thr His Ser Ala Ser Ala Thr Val Ala	225	230	235	
gag gtg caa gcc gca gct cag cgc agt gcc agc ttg cgt gtg ctt atc	832			
Glu Val Gln Ala Ala Ala Gln Arg Ser Gly Ser Leu Arg Val Leu Ile	240	245	250	
gac gcc ccc tcc cac ctt ttc cca cac gtc att cat gtg cga gac acc	880			
Asp Ala Pro Ser His Leu Phe Pro His Val Ile His Val Arg Asp Thr	255	260	265	
ctt ggt gcc tcg cca gac gag aag gct tcg aag tgg tct cgc cca atc	928			
Leu Gly Ala Ser Pro Asp Glu Lys Ala Ser Lys Trp Ser Arg Pro Ile	270	275	280	
ctc acc gtt gct gag acc gac acg tta cac caa gcg ctg gaa tac atg	976			
Leu Thr Val Ala Glu Thr Asp Thr Leu His Gln Ala Leu Glu Tyr Met	285	290	295	300

cgg gag cat aac gag cag atc agt gcg gtg ctt tcc gct gat ggg aaa 1024
 Arg Glu His Asn Glu Gln Ile Ser Ala Val Leu Ser Ala Asp Gly Lys
 305 310 315

acg gtg ctt ggt gta ata act tgg gat cac atc ttg aaa tac ctg tgg 1072
 Thr Val Leu Gly Val Ile Thr Trp Asp His Ile Leu Lys Tyr Leu Trp
 320 325 330

cct gca tcg gtg tagctaattt gaggtgcgct gaa 1107
 Pro Ala Ser Val
 335

<210> 582

<211> 336

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 582

Met Thr Glu Trp Tyr Val Val Leu Pro Ala Thr Ile Leu Leu Ile Ala
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Leu Ser Ala Phe Phe Val Ile Ile Glu Phe Ala Leu Leu Ala Ala Arg
 20 25 30

Arg Asn Arg Leu Glu Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala
 35 40 45

Ala Leu Arg Ser Leu Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln
 50 55 60

Leu Gly Ile Thr Met Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro
 65 70 75 80

Trp Val His Tyr Ala Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro
 85 90 95

Leu Val Met Ala Asp Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val
 100 105 110

Thr Phe Leu His Leu Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala
 115 120 125

Ile Ala His Pro Glu Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg
 130 135 140

Gly Phe Ile Asn Leu Phe Arg Pro Leu Leu Trp Ile Asn Lys Met
 145 150 155 160

Ala Asn Asp Leu Val Arg Lys Val Gly Glu Thr Pro Val Asp Arg Ala
 165 170 175

Ala Ala Gly Gly Tyr Asp Thr Asp Thr Leu His Ala Leu Ile Glu His
 180 185 190

Ser Arg Glu Thr Gly Ala Leu Asp Gln Gln Ser Ala Ala Gln Ile Ser
 195 200 205

Gly Ile Ile Lys Leu Asp Lys Ile Thr Val Gly Gln Thr Leu Thr Ala
 210 215 220

Ser Pro Phe Thr His Ser Ala Ser Ala Thr Val Ala Glu Val Gln Ala
 225 230 235 240

Ala Ala Gln Arg Ser Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser
 245 250 255

His Leu Phe Pro His Val Ile His Val Arg Asp Thr Leu Gly Ala Ser
 260 265 270

Pro Asp Glu Lys Ala Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala
 275 280 285

Glu Thr Asp Thr Leu His Gln Ala Leu Glu Tyr Met Arg Glu His Asn
 290 295 300

Glu Gln Ile Ser Ala Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly
 305 310 315 320

Val Ile Thr Trp Asp His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val
 325 330 335

<210> 583

<211> 423

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(400)

<223> RXN01324

<400> 583

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attccttgcg tctgcgagga ttcaaagcaa ggagcaacta atg tcc aac agc gaa 115
 Met Ser Asn Ser Glu
 1 5

tgc cac acc cac ggt tac atc gaa gaa aag cag cgt tac ctc gca cgc 163
 Cys His Thr His Gly Tyr Ile Glu Glu Lys Gln Arg Tyr Leu Ala Arg
 10 15 20

ctc aaa aga atc gaa ggc caa acc cga ggc att cac cgc atg atc gac 211
 Leu Lys Arg Ile Glu Gly Gln Thr Arg Gly Ile His Arg Met Ile Asp
 25 30 35

gag gaa caa tac tgc atc gac atc ctc acg cag atc tcc gca gtg aac 259
 Glu Glu Gln Tyr Cys Ile Asp Ile Leu Thr Gln Ile Ser Ala Val Asn
 40 45 50

tcc gca ctc aaa aac gtg gcg ttc ggc ctc ctc gac gat cac ctc gct 307
 Ser Ala Leu Lys Asn Val Ala Phe Gly Leu Leu Asp Asp His Leu Ala
 55 60 65

cac tgt gtc aaa gaa gca gct gac ctc ggc ggc gac gaa ctc gac gca 355
 His Cys Val Lys Glu Ala Ala Asp Leu Gly Gly Asp Glu Leu Asp Ala


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70              75              80              85
aaa ctc aaa gaa gtt tcc gac gcc atc gcc cgc ttc agt aag gcc      400
Lys Leu Lys Glu Val Ser Asp Ala Ile Ala Arg Phe Ser Lys Ala
          90              95              100

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<211> 100
<212> PRT
<213> Corynebacterium glutamicum

<400> 584
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Arg Tyr Leu Ala Arg Leu Lys Arg Ile Glu Gly Gln Thr Arg Gly Ile
          20              25              30
His Arg Met Ile Asp Glu Glu Gln Tyr Cys Ile Asp Ile Leu Thr Gln
          35              40              45
Ile Ser Ala Val Asn Ser Ala Leu Lys Asn Val Ala Phe Gly Leu Leu
          50              55              60
Asp Asp His Leu Ala His Cys Val Lys Glu Ala Ala Asp Leu Gly Gly
          65              70              75              80
Asp Glu Leu Asp Ala Lys Leu Lys Glu Val Ser Asp Ala Ile Ala Arg
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Phe Ser Lys Ala
          100

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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> {101}..(2497)
<223> RXN01331

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          Met Leu Thr Thr Leu
          1              5
tgg att gcg gtg ttg gta ttt acc gtt cca gga ttg gtc gtc tgg tgg 163
Trp Ile Ala Val Leu Val Phe Thr Val Pro Gly Leu Val Val Ser Trp
          10              15              20
gtt tct ggc ctt aaa gtg ccc tgg gct atc gca gcc tcc atc cca gcc 211
Val Ser Gly Leu Lys Val Pro Trp Ala Ile Ala Ala Ser Ile Pro Ala
          25              30              35

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acc ttc ggt att tac ggc ctg tcc gcc tgg ttg ctg ggc ttg tgg gag 259
 Thr Phe Gly Ile Tyr Gly Leu Ser Ala Trp Leu Leu Gly Leu Trp Glu
 40 45 50

atg cgt ttt gat ctc cat tct gta gtt att tcc aca ttg gtt ttc gct 307
 Met Arg Phe Asp Leu His Ser Val Val Ile Ser Thr Leu Val Phe Ala
 55 60 65

gog gtt gct ttg gta tgg cgc ttg ttt ttt gtc ggt ggt tgg ctt gta 355
 Ala Val Ala Leu Val Trp Arg Leu Phe Phe Val Gly Gly Trp Leu Val
 70 75 80 85

cgt cgg cgt aaa gca cgt atc cgc agg cag acg ctc cgc gat gaa gag 403
 Arg Arg Arg Lys Ala Arg Ile Arg Arg Gln Thr Leu Ala Asp Glu Glu
 90 95 100

cgg gca gaa aat gct gag gta tct gca ggg gag cct gcc gaa tog agc 451
 Arg Ala Glu Asn Ala Glu Val Ser Ala Gly Glu Pro Ala Glu Ser Ser
 105 110 115

aca aac gaa gca gcc gaa tct gaa tct gaa acc tcg gag cgt cgc gga 499
 Thr Asn Glu Ala Ala Glu Ser Glu Ser Glu Thr Ser Glu Arg Arg Gly
 120 125 130

atc tgg cgc gtg atc ttt gat tac atg cgc gac ggt ggc atc ttg gat 547
 Ile Trp Arg Val Ile Phe Asp Tyr Met Arg Asp Gly Gly Ile Leu Asp
 135 140 145

cac cgt tgg ctg ctg cct gcc gca ggt gct atc act ggt cgc tgg ctg 595
 His Arg Trp Leu Leu Pro Ala Ala Gly Ala Ile Thr Gly Ala Trp Leu
 150 155 160 165

atc att gat cgt gcc gtt gat ctg ctc ttg agc acc gag cat ggt ttg 643
 Ile Ile Asp Arg Ala Val Asp Leu Leu Ser Thr Glu His Gly Leu
 170 175 180

ggc gat atc gtc caa ggc tgg gat gtc cat tgg cat gct tcg act gtc 691
 Gly Asp Ile Val Gln Gly Trp Asp Val His Trp His Ala Ser Thr Val
 185 190 195

cgt ttt ata gat gag acc ggc att gcg tca tcc acg atg atg ggg cag 739
 Arg Phe Ile Asp Glu Thr Gly Ile Ala Ser Ser Thr Met Met Gly Gln
 200 205 210

ctg cgc aat att gaa acg cag caa gat ctg ttc tac cca agc gca tgg 787
 Leu Arg Asn Ile Glu Thr Gln Gln Asp Leu Phe Tyr Pro Ser Ala Trp
 215 220 225

cat gct ggt gca tgg gtg ctg tcg gat gtc gga aat ctg acg att gtt 835
 His Ala Gly Ala Trp Val Leu Ser Asp Val Gly Asn Leu Thr Ile Val
 230 235 240 245

gaa gcc acc aac ctc act ggc att gtg ctg tcc gga ttg ttg ctg cgc 883
 Glu Ala Thr Asn Leu Thr Gly Ile Val Leu Ser Gly Leu Leu Leu Pro
 250 255 260

tta gct gtt gca ctg att gca tgg cgg atg atc aac aat cgt gga ctg 931
 Leu Ala Val Ala Leu Ile Ala Trp Arg Met Ile Asn Asn Arg Gly Leu
 265 270 275

acc gcg cag att ggt gcg ggc ttt gct gga ctg atc acc att gcc tct 979
 Thr Ala Gln Ile Gly Ala Gly Phe Ala Gly Leu Ile Thr Ile Ala Ser
 280 285 290

ccg gta ctg ttc tgg gtt ggt aac tac gtg ggt gcg tgg cct tat gtt 1027
 Pro Val Leu Phe Trp Val Gly Asn Tyr Val Gly Ala Trp Pro Tyr Val
 295 300 305

gct gcg atc ggt gct tca ggt gtg gtg ctt gcg ctg ttt atg tcc act 1075
 Ala Ala Ile Gly Ala Ser Gly Val Val Leu Ala Leu Phe Met Ser Thr
 310 315 320 325

ccg tct gtg ccg gta aga atc ttt gcc gca gca ttg gcg ttc atg ggt 1123
 Pro Ser Val Pro Val Arg Ile Phe Ala Ala Ala Leu Ala Phe Met Gly
 330 335 340

atg ttc cag ctg cat cca gcc cca tcc acc atc gtg atc atg gtg ttg 1171
 Met Phe Gln Leu His Pro Ala Pro Ser Thr Ile Val Ile Met Val Leu
 345 350 355

ctg ctg tgg tgg ctg ctc aaa ctc gtg gtg gtt cca agc cag aaa gtg 1219
 Leu Leu Trp Trp Leu Leu Lys Leu Val Val Val Pro Ser Gln Lys Val
 360 365 370

aag ggc tgg aag gcg ggc atc ggt atc cgt ttg aag gat gtc ggc atc 1267
 Lys Gly Trp Lys Ala Gly Ile Gly Ile Arg Leu Lys Asp Val Gly Ile
 375 380 385

ctg gcc atc acg ggc atc atc ggt gtg ctc ttc atg ctg cct cag gtg 1315
 Leu Ala Ile Thr Gly Ile Ile Gly Val Leu Phe Met Leu Pro Gln Val
 390 395 400 405

att tca ggt tcc gaa caa acc gaa gat gtg ctg tca tat tct gct gag 1363
 Ile Ser Gly Ser Glu Gln Thr Glu Asp Val Leu Ser Tyr Ser Ala Glu
 410 415 420

gaa caa gtc acc cgc agc gag tcc tgg ttg gtg tct att ttc atg gag 1411
 Glu Gln Val Thr Arg Ser Glu Ser Trp Leu Val Ser Ile Phe Met Glu
 425 430 435

acc cgc cat gtt gat ttc ttc gga aat att gac atc gtc cca gtg ctg 1459
 Thr Arg His Val Asp Phe Phe Gly Asn Ile Asp Ile Val Pro Val Leu
 440 445 450

gta ttc gca gca atc ggt ggc gtg gtt gct ttg gtg tgg cgc gga aac 1507
 Val Phe Ala Ala Ile Gly Gly Val Val Ala Leu Val Trp Arg Gly Asn
 455 460 465

ttg tgg gcg ccg gtg ttt tac ttc gcc agc gtt gcg ttg acc gct aac 1555
 Leu Trp Ala Pro Val Phe Tyr Phe Ala Ser Val Ala Leu Thr Ala Asn
 470 475 480 485

tgc ctg aag cct ttt gaa gag ccg tgg ggt gat tgg ctc aac atc gtg 1603
 Ser Leu Lys Pro Phe Glu Glu Pro Trp Gly Asp Trp Leu Asn Ile Val
 490 495 500

ggc ggt ctg cat tac tcc aca gga cac cgt ttg atc atg cct gtc gcc 1651
 Gly Gly Leu His Tyr Ser Thr Gly His Arg Leu Ile Met Pro Val Ala
 505 510 515

atg ttc act ttt gct gcc gca ggt atc ggc gct gcc gca gtg atc cgt 1699

Met	Phe	Thr	Phe	Ala	Ala	Ala	Gly	Ile	Gly	Ala	Ala	Ala	Val	Ile	Arg	
		520					525						530			
ttg	atc	tgc	ttg	gga	cca	ata	aag	aag	ttc	acc	act	gtt	tcc	ggg	gtt	1747
Leu	Ile	Cys	Leu	Gly	Pro	Ile	Lys	Lys	Phe	Thr	Thr	Val	Ser	Gly	Val	
		535					540					545				
gtt	tct	gtg	gtg	atg	gct	ctt	gtt	gtg	gct	gtg	cca	ttg	cag	act	tgg	1795
Val	Ser	Val	Val	Met	Ala	Leu	Val	Val	Ala	Val	Pro	Leu	Gln	Thr	Trp	
		550			555					560					565	
gcg	aag	gat	ttt	gta	gag	gaa	gga	tcc	gaa	acc	aca	atc	ctt	gcg	cca	1843
Ala	Lys	Asp	Phe	Val	Glu	Glu	Gly	Ser	Glu	Thr	Thr	Ile	Leu	Ala	Pro	
				570					575					580		
cac	aat	gat	gaa	cgt	atg	gtg	agc	aac	aac	gac	ttg	gct	gcc	tgg	gac	1891
His	Asn	Asp	Phe	Arg	Met	Val	Ser	Asn	Asn	Asp	Leu	Ala	Ala	Trp	Asp	
			585					590					595			
tgg	tta	atc	caa	cag	cca	ggg	gga	gct	gac	atg	aac	atc	atg	ggg	gac	1939
Trp	Leu	Ile	Gln	Gln	Pro	Gly	Gly	Ala	Asp	Met	Asn	Ile	Met	Gly	Asp	
		600					605						610			
ccc	gca	gat	ggg	aac	ggc	tgg	atg	tat	gcc	tac	aac	ggc	ttg	cac	tcc	1987
Pro	Ala	Asp	Gly	Asn	Gly	Trp	Met	Tyr	Ala	Tyr	Asn	Gly	Leu	His	Ser	
		615				620					625					
gtg	gcc	cgc	cac	tat	gca	tgg	cca	gca	gca	ggc	gaa	ggc	tct	gcc	acc	2035
Val	Ala	Arg	His	Tyr	Ala	Trp	Pro	Ala	Ala	Gly	Glu	Gly	Ser	Ala	Thr	
		630			635					640				645		
gcg	atg	ctg	ttc	tgg	tgg	cct	caa	ctt	cta	ggg	gtg	ggc	acc	gat	gaa	2083
Ala	Met	Leu	Phe	Trp	Trp	Pro	Gln	Leu	Leu	Gly	Val	Gly	Thr	Asp	Glu	
				650					655					660		
aac	cca	gat	caa	gtc	aac	gat	gtg	gat	cag	gct	gct	cgt	gat	ctc	aac	2131
Asn	Pro	Asp	Val	Val	Asn	Asp	Val	Asp	Gln	Ala	Ala	Arg	Asp	Leu	Asn	
			665				670						675			
gtc	ggc	tac	ttc	atg	atc	agt	ccg	tgg	acg	ttc	tgg	gat	ttc	cag	atc	2179
Val	Gly	Tyr	Phe	Met	Ile	Ser	Pro	Trp	Thr	Phe	Trp	Asp	Phe	Gln	Ile	
		680					685					690				
ccc	aac	ttc	cgc	cag	atc	gat	ctg	ctg	tgg	caa	acc	cca	ggc	gtg	aca	2227
Pro	Asn	Phe	Arg	Gln	Ile	Asp	Leu	Leu	Trp	Gln	Thr	Pro	Gly	Val	Thr	
		695				700					705					
cgg	gtg	tgc	aag	aag	ggc	gac	tgc	gtg	atc	ttc	gca	gtc	aac	gat	atg	2275
Pro	Val	Cys	Lys	Lys	Gly	Asp	Ser	Val	Ile	Phe	Ala	Val	Asn	Asp	Met	
		710			715					720				725		
ttc	act	gac	gcc	gaa	ctg	gat	cag	atg	cgt	gca	cct	ggg	aat	tct	cca	2323
Phe	Thr	Asp	Ala	Glu	Leu	Asp	Gln	Met	Arg	Ala	Pro	Gly	Asn	Ser	Pro	
			730					735						740		
gaa	cca	ctg	cca	gag	ctt	cct	acc	ttg	ggc	gag	ctt	ggg	ttg	gct	gaa	2371
Glu	Pro	Leu	Pro	Glu	Leu	Pro	Thr	Leu	Gly	Glu	Leu	Gly	Leu	Ala	Glu	
			745					750					755			
act	gaa	gac	gag	gta	gat	cag	act	tat	tac	cat	cgt	cca	acg	gtt	cct	2419
Thr	Glu	Asp	Glu	Val	Asp	Gln	Thr	Tyr	Tyr	His	Arg	Pro	Thr	Val	Pro	

760										765										770										
gct	ggt	gtg	aac	tca	gag	atg	cct	tca	gcc	gaa	act	ctg	tat	gca	ccg	2467														
Ala	Gly	Val	Asn	Ser	Glu	Met	Pro	Ser	Ala	Glu	Thr	Leu	Tyr	Ala	Pro															
775					780					785																				
gat cca acg aag ccg cat acg gtc cct aac taatcacaaa gagtattcag																2517														
Asp	Pro	Thr	Lys	Pro	His	Thr	Val	Pro	Asn																					
790					795																									
taa																2520														

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<211> 799

<212> PRT

<213> Corynebacterium glutamicum

<400> 586

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Leu	Val	Val	Ser	Trp	Val	Ser	Gly	Leu	Lys	Val	Pro	Trp	Ala	Ile	Ala
			20					25					30		

Ala	Ser	Ile	Pro	Ala	Thr	Phe	Gly	Ile	Tyr	Gly	Leu	Ser	Ala	Trp	Leu
		35					40					45			

Leu	Gly	Leu	Trp	Glu	Met	Arg	Phe	Asp	Leu	His	Ser	Val	Val	Ile	Ser
	50					55					60				

Thr	Leu	Val	Phe	Ala	Ala	Val	Ala	Leu	Val	Trp	Arg	Leu	Phe	Phe	Val
	65				70					75					80

Gly	Gly	Trp	Leu	Val	Arg	Arg	Arg	Lys	Ala	Arg	Ile	Arg	Arg	Gln	Thr
			85						90					95	

Leu	Ala	Asp	Glu	Glu	Arg	Ala	Glu	Asn	Ala	Glu	Val	Ser	Ala	Gly	Glu
		100					105						110		

Pro	Ala	Glu	Ser	Ser	Thr	Asn	Glu	Ala	Ala	Glu	Ser	Glu	Ser	Glu	Thr
		115				120						125			

Ser	Glu	Arg	Arg	Gly	Ile	Trp	Arg	Val	Ile	Phe	Asp	Tyr	Met	Arg	Asp
	130				135						140				

Gly	Gly	Ile	Leu	Asp	His	Arg	Trp	Leu	Leu	Pro	Ala	Ala	Gly	Ala	Ile
	145				150					155				160	

Thr	Gly	Ala	Trp	Leu	Ile	Ile	Asp	Arg	Ala	Val	Asp	Leu	Leu	Leu	Ser
			165					170						175	

Thr	Glu	His	Gly	Leu	Gly	Asp	Ile	Val	Gln	Gly	Trp	Asp	Val	His	Trp
		180					185						190		

His	Ala	Ser	Thr	Val	Arg	Phe	Ile	Asp	Glu	Thr	Gly	Ile	Ala	Ser	Ser
		195					200					205			

Thr	Met	Met	Gly	Gln	Leu	Arg	Asn	Ile	Glu	Thr	Gln	Gln	Asp	Leu	Phe
	210					215					220				

Tyr Pro Ser Ala Trp His Ala Gly Ala Trp Val Leu Ser Asp Val Gly
 225 230 235 240
 Asn Leu Thr Ile Val Glu Ala Thr Asn Leu Thr Gly Ile Val Leu Ser
 245 250 255
 Gly Leu Leu Leu Pro Leu Ala Val Ala Leu Ile Ala Trp Arg Met Ile
 260 265 270
 Asn Asn Arg Gly Leu Thr Ala Gln Ile Gly Ala Gly Phe Ala Gly Leu
 275 280 285
 Ile Thr Ile Ala Ser Pro Val Leu Phe Trp Val Gly Asn Tyr Val Gly
 290 295 300
 Ala Trp Pro Tyr Val Ala Ala Ile Gly Ala Ser Gly Val Val Leu Ala
 305 310 315 320
 Leu Phe Met Ser Thr Pro Ser Val Pro Val Arg Ile Phe Ala Ala Ala
 325 330 335
 Leu Ala Phe Met Gly Met Phe Gln Leu His Pro Ala Pro Ser Thr Ile
 340 345 350
 Val Ile Met Val Leu Leu Leu Trp Trp Leu Leu Lys Leu Val Val Val
 355 360 365
 Pro Ser Gln Lys Val Lys Gly Trp Lys Ala Gly Ile Gly Ile Arg Leu
 370 375 380
 Lys Asp Val Gly Ile Leu Ala Ile Thr Gly Ile Ile Gly Val Leu Phe
 385 390 395 400
 Met Leu Pro Gln Val Ile Ser Gly Ser Glu Gln Thr Glu Asp Val Leu
 405 410 415
 Ser Tyr Ser Ala Glu Glu Gln Val Thr Arg Ser Glu Ser Trp Leu Val
 420 425 430
 Ser Ile Phe Met Glu Thr Arg His Val Asp Phe Phe Gly Asn Ile Asp
 435 440 445
 Ile Val Pro Val Leu Val Phe Ala Ala Ile Gly Gly Val Val Ala Leu
 450 455 460
 Val Trp Arg Gly Asn Leu Trp Ala Pro Val Phe Tyr Phe Ala Ser Val
 465 470 475 480
 Ala Leu Thr Ala Asn Ser Leu Lys Pro Phe Glu Glu Pro Trp Gly Asp
 485 490 495
 Trp Leu Asn Ile Val Gly Gly Leu His Tyr Ser Thr Gly His Arg Leu
 500 505 510
 Ile Met Pro Val Ala Met Phe Thr Phe Ala Ala Ala Gly Ile Gly Ala
 515 520 525
 Ala Ala Val Ile Arg Leu Ile Cys Leu Gly Pro Ile Lys Lys Phe Thr
 530 535 540
 Thr Val Ser Gly Val Val Ser Val Val Met Ala Leu Val Val Ala Val

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545                550                555                560
Pro Leu Gln Thr Trp Ala Lys Asp Phe Val Glu Gly Ser Glu Thr
      565                570                575

Thr Ile Leu Ala Pro His Asn Asp Glu Arg Met Val Ser Asn Asn Asp
      580                585                590

Leu Ala Ala Trp Asp Trp Leu Ile Gln Gln Pro Gly Gly Ala Asp Met
      595                600                605

Asn Ile Met Gly Asp Pro Ala Asp Gly Asn Gly Trp Met Tyr Ala Tyr
      610                615                620

Asn Gly Leu His Ser Val Ala Arg His Tyr Ala Trp Pro Ala Ala Gly
      625                630                635                640

Glu Gly Ser Ala Thr Ala Met Leu Phe Trp Trp Pro Gln Leu Leu Gly
      645                650                655

Val Gly Thr Asp Glu Asn Pro Asp Gln Val Asn Asp Val Asp Gln Ala
      660                665                670

Ala Arg Asp Leu Asn Val Gly Tyr Phe Met Ile Ser Pro Trp Thr Phe
      675                680                685

Trp Asp Phe Gln Ile Pro Asn Phe Arg Gln Ile Asp Leu Leu Trp Gln
      690                695                700

Thr Pro Gly Val Thr Pro Val Cys Lys Lys Gly Asp Ser Val Ile Phe
      705                710                715                720

Ala Val Asn Asp Met Phe Thr Asp Ala Glu Leu Asp Gln Met Arg Ala
      725                730                735

Pro Gly Asn Ser Pro Glu Pro Leu Pro Glu Leu Pro Thr Leu Gly Glu
      740                745                750

Leu Gly Leu Ala Glu Thr Glu Asp Glu Val Asp Gln Thr Tyr Tyr His
      755                760                765

Arg Pro Thr Val Pro Ala Gly Val Asn Ser Glu Met Pro Ser Ala Glu
      770                775                780

Thr Leu Tyr Ala Pro Asp Pro Thr Lys Pro His Thr Val Pro Asn
      785                790                795

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<210> 587

<211> 638

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (40)..(615)

<223> FRXA01331

<400> 587

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Met Asn Ile Met Gly Asp

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 Pro Ala Asp Gly Asn Gly Trp Met Tyr Ala Tyr Asn Gly Leu His Ser
 10 15 20
 gtg gcc cgc cac tat gca tgg cca gca gca ggc gaa ggc tct gcc acc 153
 Val Ala Arg His Tyr Ala Trp Pro Ala Ala Gly Glu Gly Ser Ala Thr
 25 30 35
 gcg atg ctg ttc tgg tgg cct caa ctt cta ggt gtg ggc acc gat gaa 201
 Ala Met Leu Phe Trp Trp Pro Gln Leu Leu Gly Val Gly Thr Asp Glu
 40 45 50
 aac cca gat caa gtc aac gat gtg gat cag gct gct cgt gat ctc aac 249
 Asn Pro Asp Gln Val Asn Asp Val Asp Gln Ala Ala Arg Asp Leu Asn
 55 60 65 70
 gtc ggc tac ttc atg atc agt ccg tgg acg ttc tgg gat ttc cag atc 297
 Val Gly Tyr Phe Met Ile Ser Pro Trp Thr Phe Trp Asp Phe Gln Ile
 75 80 85
 ccc aac ttc cgc cag atc gat ctg ctg tgg caa acc cca ggc gtg aca 345
 Pro Asn Phe Arg Gln Ile Asp Leu Leu Trp Gln Thr Pro Gly Val Thr
 90 95 100
 ccg gtg tgc aag aag ggc gac tgg gtg atc ttc gca gtc aac gat atg 393
 Pro Val Cys Lys Lys Gly Asp Ser Val Ile Phe Ala Val Asn Asp Met
 105 110 115
 ttc act gac gcc gaa ctg gat cag atg cgt gca cct ggt aat tct cca 441
 Phe Thr Asp Ala Glu Leu Asp Gln Met Arg Ala Pro Gly Asn Ser Pro
 120 125 130
 gaa cca ctg cca gag ctt cct acc ttg ggc gag ctt ggg ttg gct gaa 489
 Glu Pro Leu Pro Glu Leu Pro Thr Leu Gly Glu Leu Gly Leu Ala Glu
 135 140 145 150
 act gaa gac gag gta gat cag act tat tac cat cgt cca acg gtt cct 537
 Thr Glu Asp Glu Val Asp Gln Thr Tyr Tyr His Val Pro Thr Val Pro
 155 160 165
 gct ggt gtg aac tca gag atg cct tca gcc gaa act ctg tat gca ccg 585
 Ala Gly Val Asn Ser Glu Met Pro Ser Ala Glu Thr Leu Tyr Ala Pro
 170 175 180
 gat cca acg aag ccg cat acg gtc cct aac taatcacaaa gattattcag 635
 Asp Pro Thr Lys Pro His Thr Val Pro Asn
 185 190
 taa 638

<210> 588

<211> 192

<212> PRT

<213> Corynebacterium glutamicum

<400> 588

 Met Asn Ile Met Gly Asp Pro Ala Asp Gly Asn Gly Trp Met Tyr Ala
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Tyr Asn Gly Leu His Ser Val Ala Arg His Tyr Ala Trp Pro Ala Ala
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Gly Glu Gly Ser Ala Thr Ala Met Leu Phe Trp Trp Pro Gln Leu Leu
    35                      40                      45

Gly Val Gly Thr Asp Glu Asn Pro Asp Gln Val Asn Asp Val Asp Gln
    50                      55                      60

Ala Ala Arg Asp Leu Asn Val Gly Tyr Phe Met Ile Ser Pro Trp Thr
    65                      70                      75                      80

Phe Trp Asp Phe Gln Ile Pro Asn Phe Arg Gln Ile Asp Leu Leu Tyr
    85                      90                      95

Gln Thr Pro Gly Val Thr Pro Val Cys Lys Lys Gly Asp Ser Val Ile
    100                     105                     110

Phe Ala Val Asn Asp Met Phe Thr Asp Ala Glu Leu Asp Gln Met Arg
    115                     120                     125

Ala Pro Gly Asn Ser Pro Glu Pro Leu Pro Glu Leu Pro Thr Leu Gly
    130                     135                     140

Glu Leu Gly Leu Ala Glu Thr Glu Asp Glu Val Asp Gln Thr Tyr Tyr
    145                     150                     155                     160

His Arg Pro Thr Val Pro Ala Gly Val Asn Ser Glu Met Pro Ser Ala
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Glu Thr Leu Tyr Ala Pro Asp Pro Thr Lys Pro His Thr Val Pro Asn
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<210> 589

<211> 892

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(892)

<223> FRXA00668

<400> 589

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                                     Met Leu Thr Thr Leu
                                     1                      5

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tgg att gcg gtg ttg gta ttt acc gtt cca gga ttg gtc gtc tcg tgg 163
Trp Ile Ala Val Leu Val Phe Thr Val Pro Gly Leu Val Val Ser Trp
    10                      15                      20

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gtt tct ggc ctt aaa gtg ccc tgg gct atc gca gcc tcc atc cca gcc 211
Val Ser Gly Leu Lys Val Pro Trp Ala Ile Ala Ala Ser Ile Pro Ala

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	Thr Phe Gly Ile Tyr Gly Leu Ser Ala Trp Leu Leu Gly Leu Trp Glu			
	40	45	50	
	atg cgt ttt gat ctc cat tct gta gtt att tcc aca ttg gtt ttc gct			307
	Met Arg Phe Asp Leu His Ser Val Val Ile Ser Thr Leu Val Phe Ala			
	55	60	65	
	gcg gtt gct ttg gta tgg cgc ttg ttt ttt gtc ggt ggt tgg ctt gta			355
	Ala Val Ala Leu Val Trp Arg Leu Phe Phe Val Gly Gly Trp Leu Val			
	70	75	80	85
	cgt cgg cgt aaa gca cgt atc cgc agg cag acg ctc gcg gat gaa gag			403
	Arg Arg Arg Lys Ala Arg Ile Arg Arg Gln Thr Leu Ala Asp Glu Glu			
	90	95	100	
	cgg gca gaa aat gct gag gta tct gca ggg gag cct gcc gaa tcg agc			451
	Arg Ala Glu Asn Ala Glu Val Ser Ala Gly Glu Pro Ala Glu Ser Ser			
	105	110	115	
	aca aac gaa gca gcc gaa tct gaa tct gaa acc tcg gag cgt cgc gga			499
	Thr Asn Glu Ala Ala Glu Ser Glu Ser Glu Thr Ser Glu Arg Arg Gly			
	120	125	130	
	atc tgg cgc gtg atc ttt gat tac atg cgc gac ggt ggc atc ttg gat			547
	Ile Trp Arg Val Ile Phe Asp Tyr Met Arg Asp Gly Gly Ile Leu Asp			
	135	140	145	
	cac cgt tgg ctg ctg cct gcc gca ggt gct atc act ggt gcg tgg ctg			595
	His Arg Trp Leu Leu Pro Ala Ala Gly Ala Ile Thr Gly Ala Trp Leu			
	150	155	160	165
	atc att gat cgt gcc gtt gat ctg ctc ttg agc acc gag cat ggt ttg			643
	Ile Ile Asp Arg Ala Val Asp Leu Leu Leu Ser Thr Glu His Gly Leu			
	170	175	180	
	ggc gat atc gtc caa ggc tgg gat gtc cat tgg cat gct tcg act gtc			691
	Gly Asp Ile Val Gln Gly Trp Asp Val His Trp His Ala Ser Thr Val			
	185	190	195	
	cgt ttt ata gat gag acc gcc att gcg tca tcc acg atg atg ggg cag			739
	Arg Phe Ile Asp Glu Thr Gly Ile Ala Ser Ser Thr Met Met Gly Gln			
	200	205	210	
	ctg cgc aat att gaa acg cag caa gat ctg ttc tac cca agc gca tgg			787
	Leu Arg Asn Ile Glu Thr Gln Gln Asp Leu Phe Tyr Pro Ser Ala Trp			
	215	220	225	
	cat gct ggt gca tgg gtg ctg tcg gat gtc gga aat ctg acg att gtt			835
	His Ala Gly Ala Trp Val Leu Ser Asp Val Gly Asn Leu Thr Ile Val			
	230	235	240	245
	gaa gcc acc aac ctc act gcc att gtg ctg tcc gga ttg ttg ctg ccg			883
	Glu Ala Thr Asn Leu Thr Gly Ile Val Leu Ser Gly Leu Leu Leu Pro			
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	tta gct gtt			892
	Leu Ala Val			

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<212> PRT

<213> Corynebacterium glutamicum

<400> 590

Met Leu Thr Thr Leu Trp Ile Ala Val Leu Val Phe Thr Val Pro Gly

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Leu Val Val Ser Trp Val Ser Gly Leu Lys Val Pro Trp Ala Ile Ala

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25

30

Ala Ser Ile Pro Ala Thr Phe Gly Ile Tyr Gly Leu Ser Ala Trp Leu

35

40

45

Leu Gly Leu Trp Glu Met Arg Phe Asp Leu His Ser Val Val Ile Ser

50

55

60

Thr Leu Val Phe Ala Ala Val Ala Leu Val Trp Arg Leu Phe Phe Val

65

70

75

80

Gly Gly Trp Leu Val Arg Arg Arg Lys Ala Arg Ile Arg Arg Gln Thr

85

90

95

Leu Ala Asp Glu Glu Arg Ala Glu Asn Ala Glu Val Ser Ala Gly Glu

100

105

110

Pro Ala Glu Ser Ser Thr Asn Glu Ala Ala Glu Ser Glu Ser Glu Thr

115

120

125

Ser Glu Arg Arg Gly Ile Trp Arg Val Ile Phe Asp Tyr Met Arg Asp

130

135

140

Gly Gly Ile Leu Asp His Arg Trp Leu Leu Pro Ala Ala Gly Ala Ile

145

150

155

160

Thr Gly Ala Trp Leu Ile Ile Asp Arg Ala Val Asp Leu Leu Leu Ser

165

170

175

Thr Glu His Gly Leu Gly Asp Ile Val Gln Gly Trp Asp Val His Trp

180

185

190

His Ala Ser Thr Val Arg Phe Ile Asp Glu Thr Gly Ile Ala Ser Ser

195

200

205

Thr Met Met Gly Gln Leu Arg Asn Ile Glu Thr Gln Gln Asp Leu Phe

210

215

220

Tyr Pro Ser Ala Trp His Ala Gly Ala Trp Val Leu Ser Asp Val Gly

225

230

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Asn Leu Thr Ile Val Glu Ala Thr Asn Leu Thr Gly Ile Val Leu Ser

245

250

255

Gly Leu Leu Leu Pro Leu Ala Val

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 <222> (1)..(750)
 <223> FRXA00674

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gcc cca tcc acc atc gtg atc atg gtg ttg ctg ctg tgg tgg ctg ctc 96
Ala Pro Ser Thr Ile Val Ile Met Val Leu Leu Leu Trp Trp Leu Leu
20 25 30

aaa ctc gtg gtg gtt cca agc cag aaa gtg aag ggc tgg aag gcg ggc 144
Lys Leu Val Val Val Pro Ser Gln Lys Val Lys Gly Trp Lys Ala Gly
35 40 45

atc ggt atc cgt ttg aag gat gtc gcc atc ctg gcc atc acg gcc atc 192
Ile Gly Ile Arg Leu Lys Asp Val Gly Ile Leu Ala Ile Thr Gly Ile
50 55 60

atc ggt gtg ctc ttc atg ctg cct cag gtg att tca ggt tcc gaa caa 240
Ile Gly Val Leu Phe Met Leu Pro Gln Val Ile Ser Gly Ser Glu Gln
65 70 75 80

acc gaa gat gtg ctg tca tat tct gct gag gaa caa gtc acc cgc agc 288
Thr Glu Asp Val Leu Ser Tyr Ser Ala Glu Gln Val Thr Arg Ser
85 90 95

gag tcc tgg ttg gtg tct att ttc atg gag acc cgc cat gtt gat ttc 336
Glu Ser Trp Leu Val Ser Ile Phe Met Glu Thr Arg His Val Asp Phe
100 105 110

ttc gga aat att gac atc gtc cca gtg ctg gta ttc gca gca atc ggt 384
Phe Gly Asn Ile Asp Ile Val Pro Val Leu Val Phe Ala Ala Ile Gly
115 120 125

ggc gtg gtt gct ttg gtg tgg cgc gga aac ttg tgg gcg ccg gtg ttt 432
Gly Val Val Ala Leu Val Trp Arg Gly Asn Leu Leu Ala Pro Val Phe
130 135 140

tac ttc gcc agc gtt gcg ttg acc gct aac tcg ctg aag cct ttt gaa 480
Tyr Phe Ala Ser Val Ala Leu Thr Ala Asn Ser Leu Lys Pro Phe Glu
145 150 155 160

gag ccg tgg ggt gat tgg ctc aac atc gtg gcc ggt ctg cat tac tcc 528
Glu Pro Trp Gly Asp Trp Leu Asn Ile Val Gly Gly Leu His Tyr Ser
165 170 175

aca gga cac cgt ttg atc atg cct gtc gcc atg ttc act ttt gct gcc 576
Thr Gly His Arg Leu Ile Met Pro Val Ala Met Phe Thr Phe Ala Ala
180 185 190

gca ggt atc gcc gct gcc gca gtg atc cgt ttg atc tgc ttg gga cca 624
Ala Gly Ile Gly Ala Ala Val Ile Arg Leu Ile Cys Leu Gly Pro
195 200 205

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 Ile Lys Lys Phe Thr Thr Val Ser Gly Val Val Ser Val Val Met Ala
 210 215 220
 ctt gtt gtg gct gtg cca ttg cag act tgg gcg aag gat ttt gta gag 720
 Leu Val Val Ala Val Pro Leu Gln Thr Trp Ala Lys Asp Phe Val Glu
 225 230 235 240
 gaa gga tcc gaa acc aca atc ctt gcg cca 750
 Glu Gly Ser Glu Thr Thr Ile Leu Ala Pro
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<400> 592
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 Ala Pro Ser Thr Ile Val Ile Met Val Leu Leu Leu Trp Trp Leu Leu
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 Lys Leu Val Val Val Pro Ser Gln Lys Val Lys Gly Trp Lys Ala Gly
 35 40 45
 Ile Gly Ile Arg Leu Lys Asp Val Gly Ile Leu Ala Ile Thr Gly Ile
 50 55 60
 Ile Gly Val Leu Phe Met Leu Pro Gln Val Ile Ser Gly Ser Glu Gln
 65 70 75 80
 Thr Glu Asp Val Leu Ser Tyr Ser Ala Glu Glu Gln Val Thr Arg Ser
 85 90 95
 Glu Ser Trp Leu Val Ser Ile Phe Met Glu Thr Arg His Val Asp Phe
 100 105 110
 Phe Gly Asn Ile Asp Ile Val Pro Val Leu Val Phe Ala Ala Ile Gly
 115 120 125
 Gly Val Val Ala Leu Val Trp Arg Gly Asn Leu Trp Ala Pro Val Phe
 130 135 140
 Tyr Phe Ala Ser Val Ala Leu Thr Ala Asn Ser Leu Lys Pro Phe Glu
 145 150 155 160
 Glu Pro Trp Gly Asp Trp Leu Asn Ile Val Gly Gly Leu His Tyr Ser
 165 170 175
 Thr Gly His Arg Leu Ile Met Pro Val Ala Met Phe Thr Phe Ala Ala
 180 185 190
 Ala Gly Ile Gly Ala Ala Ala Val Ile Arg Leu Ile Cys Leu Gly Pro
 195 200 205
 Ile Lys Lys Phe Thr Thr Val Ser Gly Val Val Ser Val Val Met Ala
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Leu Val Val Ala Val Pro Leu Gln Thr Trp Ala Lys Asp Phe Val Glu
 225 230 235 240

Glu Gly Ser Glu Thr Thr Ile Leu Ala Pro
 245 250

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 <222> (101)..(1513)
 <223> RXN01337

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 Val Thr Phe Arg Gly
 1 5
 gga aac act ggc gca aag cac gcg gtc gtt gtt ggt tct ggc ccc aat 163
 Gly Asn Thr Gly Ala Lys His Ala Val Val Val Gly Ser Gly Pro Asn
 10 15 20
 ggg ttg acc acg gcg gcg gtg ctg gcc aaa gca ggt tgg caa gta gat 211
 Gly Leu Thr Thr Ala Ala Val Leu Ala Lys Ala Gly Trp Gln Val Asp
 25 30 35
 gtg tat gag gcg gcg cca acc cct gga ggg gcg gcg cgc tca gaa agc 259
 Val Tyr Glu Ala Ala Pro Thr Pro Gly Gly Ala Ala Arg Ser Glu Ser
 40 45 50
 gtt ctg ggg gag ggg act atc agc gat ttg ggt gcc gca ggg cat cct 307
 Val Leu Gly Glu Gly Thr Ile Ser Asp Leu Gly Ala Ala Gly His Pro
 55 60 65
 ttc ggg gtg gca agc cca gct ttt cac tat ttg ggt ctg gaa gat cac 355
 Phe Gly Val Ala Ser Pro Ala Phe His Tyr Leu Gly Leu Glu Asp His
 70 75 80 85
 ggc ctg gaa tgg gcg tat tct ccc ttt gcg atg gcc cac ccg tta gat 403
 Gly Leu Glu Trp Ala Tyr Ser Pro Phe Ala Met Ala His Pro Leu Asp
 90 95 100
 tat ggc agg gcc gga ctg ctg gaa acg tca ctc cca gag acc gcc aaa 451
 Tyr Gly Arg Ala Gly Leu Leu Glu Thr Ser Leu Pro Glu Thr Ala Lys
 105 110 115
 aag ctt gga cct gat gca cgt cgt tgg aag aat ttg cac cag ggc tta 499
 Lys Leu Gly Pro Asp Ala Arg Trp Lys Asn Leu His Gln Gly Leu
 120 125 130
 acc aaa aac att gat aaa cac ttg gcc aat cta tta ggg ccg gtg ctg 547
 Thr Lys Asn Ile Asp Lys His Leu Ala Asn Leu Leu Gly Pro Val Leu
 135 140 145

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Lys Trp Pro Ala His Pro Ile Arg Met Ala Lys Phe Gly Pro Phe Ala	
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ttg ctg ccc gcg aaa cgt cta gcc agt gcc gct ttt gaa aca gaa gaa	643
Leu Leu Pro Ala Lys Arg Leu Ala Ser Ala Ala Phe Glu Thr Glu Glu	
170 175 180	
gcc cga tcc ctg ttt atc ggt tgg gcg atg cac tgg gtg act cca cca	691
Ala Arg Ser Leu Phe Ile Gly Ser Ala Met His Ser Val Thr Pro Pro	
185 190 195	
cac aag ccg atg acc gca tca ctt gga ttg ctt ttt ggc gct ctg ggg	739
His Lys Pro Met Thr Ala Ser Leu Gly Leu Leu Phe Gly Ala Leu Gly	
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Met Ser Arg Gly Trp Pro Val Ala Val Gly Gly Ser Gly Arg Ile Val	
215 220 225	
gat gct ctg gtc aat gtc ata aac cat cac ggt ggc acc att cac tgc	835
Asp Ala Leu Val Asn Val Ile Asn His His Gly Gly Thr Ile His Cys	
230 235 240 245	
gat tca cag att gat tcc ctc tca caa ttc cgc gac acc gat gcc att	883
Asp Ser Gln Ile Asp Ser Leu Ser Gln Phe Arg Asp Thr Asp Ala Ile	
250 255 260	
att ctg aac caa acc ccc tca cag gtg ctg aaa ctc aaa gga act gac	931
Ile Leu Asn Gln Thr Pro Ser Gln Val Leu Lys Leu Lys Gly Thr Asp	
265 270 275	
ctt aat gca ggg ctt ccg caa cgc atg agc acc tgg aaa cac gga cca	979
Leu Asn Ala Gly Leu Pro Gln Arg Met Ser Thr Trp Lys His Gly Pro	
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Ser Ser Tyr Lys Val Asp Tyr Leu Leu Asp Glu Pro Ile Pro Trp Ser	
295 300 305	
aat ccc cag gta ggc cag gcc aca acc gtc cat gtg ggc gga agc tct	1075
Asn Pro Gln Val Gly Gln Ala Thr Thr Val His Val Gly Gly Ser Ser	
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Glu Glu Ile Ala Phe Ala Glu Ala Glu Val Ala Ala Gly Arg Met Pro	
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gaa cgc ccg ttt atc att ttg tgc caa caa caa gtg gcg gat cct tca	1171
Glu Arg Pro Phe Ile Ile Leu Cys Gln Gln Gln Val Ala Asp Pro Ser	
345 350 355	
cgc gcc ccg gag ggg cgc cac gtc gtg tgg gcc tac gcg cat gtg ccg	1219
Arg Ala Arg Glu Gly Arg His Val Val Trp Ala Tyr Ala His Val Pro	
360 365 370	
cgg ggt ttc gtc gat aag cga gct gct tta tta atc act gcg cag att	1267
Arg Gly Phe Val Asp Lys Arg Ala Leu Leu Ile Thr Ala Gln Ile	
375 380 385	
gaa cgc ttc gcc ccc ggt ttc cgt gat cgc atc gtg cat tca gtg gat	1315

Glu Arg Phe Ala Pro Gly Phe Arg Asp Arg Ile Val His Ser Val Asp
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 acc aac gcg gag gat tta gag gcg tgg aac ccc aat ctt gtt ggc gga 1363
 Thr Asn Ala Glu Asp Leu Glu Ala Trp Asn Pro Asn Leu Val Gly Gly
 410 415 420
 gac atc acc gca ggg tcc gcg ctg ctt cgg cga atg cgg acc aaa atc 1411
 Asp Ile Thr Ala Gly Ser Ala Leu Leu Arg Arg Met Pro Thr Lys Ile
 425 430 435
 ggc gag aaa acg tac atg gca tcc gcc tcc aac gcg cgg ggc ggg gga 1459
 Gly Glu Lys Thr Tyr Met Ala Ser Ala Ser Asn Ala Pro Gly Gly Gly
 440 445 450
 gtc cac gga atg ccc ggc tgg tgg gca gcg caa gcc gtt tta gca gat 1507
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 cac agg tagaattgcg acatggagcc cac 1536
 His Arg
 470
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 <400> 594
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 35 40 45
 Ala Arg Ser Glu Ser Val Leu Gly Glu Gly Thr Ile Ser Asp Leu Gly
 50 55 60
 Ala Ala Gly His Pro Phe Gly Val Ala Ser Pro Ala Phe His Tyr Leu
 65 70 75 80
 Gly Leu Glu Asp His Gly Leu Glu Trp Ala Tyr Ser Pro Phe Ala Met
 85 90 95
 Ala His Pro Leu Asp Tyr Gly Arg Ala Gly Leu Leu Glu Thr Ser Leu
 100 105 110
 Pro Glu Thr Ala Lys Lys Leu Gly Pro Asp Ala Arg Arg Trp Lys Asn
 115 120 125
 Leu His Gln Gly Leu Thr Lys Asn Ile Asp Lys His Leu Ala Asn Leu
 130 135 140
 Leu Gly Pro Val Leu Lys Trp Pro Ala His Pro Ile Arg Met Ala Lys
 145 150 155 160
 Phe Gly Pro Phe Ala Leu Leu Pro Ala Lys Arg Leu Ala Ser Ala Ala

165										170					175				
Phe	Glu	Thr		Glu	Glu	Ala	Arg	Ser	Leu	Phe	Ile	Gly	Ser	Ala	Met	His			
			180									185				190			
Ser	Val	Thr	Pro	Pro	His	Lys		Pro	Met	Thr	Ala	Ser	Leu	Gly	Leu	Leu			
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Phe	Gly	Ala	Leu	Gly	Met	Ser	Arg	Gly	Trp	Pro	Val	Ala	Val	Gly	Gly				
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Ser	Gly	Arg	Ile	Val	Asp	Ala	Leu	Val	Asn	Val	Ile	Asn	His	His	Gly				
	225				230						235					240			
Gly	Thr	Ile	His	Cys	Asp	Ser	Gln	Ile	Asp	Ser	Leu	Ser	Gln	Phe	Arg				
				245					250					255					
Asp	Thr	Asp	Ala	Ile	Ile	Leu	Asn	Gln	Thr	Pro	Ser	Gln	Val	Leu	Lys				
		260						265					270						
Leu	Lys	Gly	Thr	Asp	Leu	Asn	Ala	Gly	Leu	Pro	Gln	Arg	Met	Ser	Thr				
		275					280					285							
Trp	Lys	His	Gly	Pro	Ser	Ser	Tyr	Lys	Val	Asp	Tyr	Leu	Leu	Asp	Glu				
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Pro	Ile	Pro	Trp	Ser	Asn	Pro	Gln	Val	Gly	Gln	Ala	Thr	Thr	Val	His				
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Val	Gly	Gly	Ser	Ser	Glu	Glu	Ile	Ala	Phe	Ala	Glu	Ala	Glu	Val	Ala				
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Ala	Gly	Arg	Met	Pro	Glu	Arg	Pro	Phe	Ile	Ile	Leu	Cys	Gln	Gln	Gln				
			340					345					350						
Val	Ala	Asp	Pro	Ser	Arg	Ala	Arg	Glu	Gly	Arg	His	Val	Val	Trp	Ala				
		355					360				365								
Tyr	Ala	His	Val	Pro	Arg	Gly	Phe	Val	Asp	Lys	Arg	Ala	Ala	Leu	Leu				
	370					375					380								
Ile	Thr	Ala	Gln	Ile	Glu	Arg	Phe	Ala	Pro	Gly	Phe	Arg	Asp	Arg	Ile				
	385				390						395				400				
Val	His	Ser	Val	Asp	Thr	Asn	Ala	Glu	Asp	Leu	Glu	Ala	Trp	Asn	Pro				
			405						410					415					
Asn	Leu	Val	Gly	Gly	Asp	Ile	Thr	Ala	Gly	Ser	Ala	Leu	Leu	Arg	Arg				
			420					425					430						
Met	Pro	Thr	Lys	Ile	Gly	Glu	Lys	Thr	Tyr	Met	Ala	Ser	Ala	Ser	Asn				
		435						440				445							
Ala	Pro	Gly	Gly	Gly	Val	His	Gly	Met	Pro	Gly	Trp	Trp	Ala	Ala	Gln				
	450					455					460								
Ala	Val	Leu	Ala	Asp	His	Arg													
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1513)
 <223> FRXA01337

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 Val Thr Phe Arg Gly
 1 5
 gga aac act ggc gca aag cac gcg gtc gtt gtt ggt tot ggc ccc aat 163
 Gly Asn Thr Gly Ala Lys His Ala Val Val Val Gly Ser Gly Pro Asn
 10 15 20
 ggg ttg acc acg gcg gcg gtg ctg gcc aaa gca ggt tgg caa gta gat 211
 Gly Leu Thr Thr Ala Ala Val Leu Ala Lys Ala Gly Trp Gln Val Asp
 25 30 35
 gtg tat gag gcg gcg cca acc cct gga ggg gcg gcg cgc tca gaa agc 259
 Val Tyr Glu Ala Ala Pro Thr Pro Gly Gly Ala Ala Arg Ser Glu Ser
 40 45 50
 gtt ctg ggg gag ggg act atc agc gat ttg ggt gcc gca ggg cat cct 307
 Val Leu Gly Glu Gly Thr Ile Ser Asp Leu Gly Ala Ala Gly His Pro
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 Phe Gly Val Ala Ser Pro Ala Phe His Tyr Leu Gly Leu Glu Asp His
 70 75 80 85
 ggc ctg gaa tgg gcg tat tct ccc ttt gcg atg gcc cac ccg tta gat 403
 Gly Leu Glu Trp Ala Tyr Ser Pro Phe Ala Met Ala His Pro Leu Asp
 90 95 100
 tat ggc agg gcc gga ctg ctg gaa acg tca ctc cca gag acc gcc aaa 451
 Tyr Gly Arg Ala Gly Leu Leu Glu Thr Ser Leu Pro Glu Thr Ala Lys
 105 110 115
 aag ctt gga cct gat gca cgt cgt tgg aag aat ttg cac cag ggc tta 499
 Lys Leu Gly Pro Asp Ala Arg Arg Trp Lys Asn Leu His Gln Gly Leu
 120 125 130
 acc aaa aac att gat aaa cac ttg gcc aat cta tta ggg ccg gtg ctg 547
 Thr Lys Asn Ile Asp Lys His Leu Ala Asn Leu Leu Gly Pro Val Leu
 135 140 145
 aaa tgg cca gca cat ccg att ccg atg gca aag ttt ggc cca ttt gcg 595
 Lys Trp Pro Ala His Pro Ile Arg Met Ala Lys Phe Gly Pro Phe Ala
 150 155 160 165
 ttg ctg ccc gcg aaa cgt cta gcc agt gcc gct ttt gaa aca gaa gaa 643
 Leu Leu Pro Ala Lys Arg Leu Ala Ser Ala Ala Phe Glu Thr Glu Glu
 170 175 180
 gcc cga tcc ctg ttt atc ggt tcg gcg atg cac tcg gtg act cca cca 691

Ala Arg Ser Leu Phe Ile Gly Ser Ala Met His Ser Val Thr Pro Pro	
185 190 195	
cac aag ccg atg acc gca tca ctt gga ttg ctt ttt ggc gct ctg ggg	739
His Lys Pro Met Thr Ala Ser Leu Gly Leu Leu Phe Gly Ala Leu Gly	
200 205 210	
atg tcg cga gga tgg ccg gtt gca gtt ggg gga agc gga cgg atc gtc	787
Met Ser Arg Gly Trp Pro Val Ala Val Gly Gly Ser Gly Arg Ile Val	
215 220 225	
gat gct ctg gtc aat gtc ata aac cat cac ggt ggc acc att cac tgc	835
Asp Ala Leu Val Asn Val Ile Asn His His Gly Gly Thr Ile His Cys	
230 235 240 245	
gat tca cag att gat tcc ctc tca caa ttc cgc gac acc gat gcc att	883
Asp Ser Gln Ile Asp Ser Leu Ser Gln Phe Arg Asp Thr Asp Ala Ile	
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att ctg aac caa acc ccc tca cag gtg ctg aaa ctc aaa gga act gac	931
Ile Leu Asn Gln Thr Pro Ser Gln Val Leu Lys Leu Lys Gly Thr Asp	
265 270 275	
ctt aat gca ggg ctt ccg caa cgc atg agc acc tgg aaa cac gga cca	979
Leu Asn Ala Gly Leu Pro Gln Arg Met Ser Thr Trp Lys His Gly Pro	
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Ser Ser Tyr Lys Val Asp Tyr Leu Leu Asp Glu Pro Ile Pro Trp Ser	
295 300 305	
aat ccc cag gta ggc cag gcc aca acc gtc cat gtg ggc gga agc tct	1075
Asn Pro Gln Val Gly Gln Ala Thr Thr Val His Val Gly Gly Ser Ser	
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Glu Arg Pro Phe Ile Ile Leu Cys Gln Gln Val Ala Asp Pro Ser	
345 350 355	
cgc gcc ccg gag ggg cgc cac gtc gtg tgg gcc tac gcg cat gtg ccg	1219
Arg Ala Arg Glu Gly Arg His Val Val Trp Ala Tyr Ala His Val Pro	
360 365 370	
cgg ggt ttc gtc gat aag cga gct gct tta tta atc act gcg cag att	1267
Arg Gly Phe Val Asp Lys Arg Ala Ala Leu Leu Ile Thr Ala Gln Ile	
375 380 385	
gaa cgc ttc gcc ccc ggt ttc cgt gat cgc atc gtg cat tca gtg gat	1315
Glu Arg Phe Ala Pro Gly Phe Arg Asp Arg Ile Val His Ser Val Asp	
390 395 400 405	
acc aac gcg gag gat tta gag gcg tgg aac ccc aat ctt gtt ggc gga	1363
Thr Asn Ala Glu Asp Leu Glu Ala Trp Asn Pro Asn Leu Val Gly Gly	
410 415 420	
gac atc acc gca ggg tcc gcg ctg ctt cgg cga atg ccg acc aaa atc	1411
Asp Ile Thr Ala Gly Ser Ala Leu Leu Arg Arg Met Pro Thr Lys Ile	

425

430

435

ggc gag aaa acg tac atg gca tcc gcc tcc aac gcg ccg ggc ggg gga 1459
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 440 445 450

gtc cac gga atg ccc ggc tgg tgg gca gcg caa gcc gtt tta gca gat 1507
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cac agg tagaattgagc acatggagcc cac 1536
 His Arg
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<210> 596

<211> 471

<212> PRT

<213> Corynebacterium glutamicum

<400> 596

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Gly Trp Gln Val Asp Val Tyr Glu Ala Ala Pro Thr Pro Gly Gly Ala
 35 40 45

Ala Arg Ser Glu Ser Val Leu Gly Glu Gly Thr Ile Ser Asp Leu Gly
 50 55 60

Ala Ala Gly His Pro Phe Gly Val Ala Ser Pro Ala Phe His Tyr Leu
 65 70 75 80

Gly Leu Glu Asp His Gly Leu Glu Trp Ala Tyr Ser Pro Phe Ala Met
 85 90 95

Ala His Pro Leu Asp Tyr Gly Arg Ala Gly Leu Leu Glu Thr Ser Leu
 100 105 110

Pro Glu Thr Ala Lys Lys Leu Gly Pro Asp Ala Arg Arg Trp Lys Asn
 115 120 125

Leu His Gln Gly Leu Thr Lys Asn Ile Asp Lys His Leu Ala Asn Leu
 130 135 140

Leu Gly Pro Val Leu Lys Trp Pro Ala His Pro Ile Arg Met Ala Lys
 145 150 155 160

Phe Gly Pro Phe Ala Leu Leu Pro Ala Lys Arg Leu Ala Ser Ala Ala
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Phe Glu Thr Glu Glu Ala Arg Ser Leu Phe Ile Gly Ser Ala Met His
 180 185 190

Ser Val Thr Pro Pro His Lys Pro Met Thr Ala Ser Leu Gly Leu Leu
 195 200 205

Phe Gly Ala Leu Gly Met Ser Arg Gly Trp Pro Val Ala Val Gly Gly

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Ser Gly Arg Ile Val 225	Asp Ala Leu Val 230	Asn Val Ile Asn His His Gly 235 240
Gly Thr Ile His Cys 245	Asp Ser Gln Ile 250	Asp Ser Leu Ser Gln Phe Arg 255
Asp Thr Asp Ala Ile 260	Ile Leu Asn Gln Thr 265	Pro Ser Gln Val Leu Lys 270
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Trp Lys His Gly Pro 290	Ser Ser Tyr Lys 295	Val Asp Tyr Leu Leu Asp Glu 300
Pro Ile Pro Trp Ser 305	Asn Pro Gln Val 310	Gly Gln Ala Thr Thr Val His 315 320
Val Gly Gly Ser Ser 325	Glu Glu Ile Ala 330	Phe Ala Glu Ala Glu Val Ala 335
Ala Gly Arg Met Pro 340	Glu Arg Pro Phe 345	Ile Ile Leu Cys Gln Gln Gln 350
Val Ala Asp Pro Ser 355	Arg Ala Arg Glu 360	Gly Arg His Val Val Trp Ala 365
Tyr Ala His Val Pro 370	Arg Gly Phe Val 375	Asp Lys Arg Ala Ala Leu Leu 380
Ile Thr Ala Gln Ile 385	Glu Arg Phe Ala 390	Pro Gly Phe Arg Asp Arg Ile 395 400
Val His Ser Val Asp 405	Thr Asn Ala Glu 410	Asp Leu Glu Ala Trp Asn Pro 415
Asn Leu Val Gly Gly 420	Asp Ile Thr Ala 425	Gly Ser Ala Leu Leu Arg Arg 430
Met Pro Thr Lys Ile 435	Gly Glu Lys Thr 440	Tyr Met Ala Ser Ala Ser Asn 445
Ala Pro Gly Gly Gly 450	Val His Gly Met 455	Pro Gly Trp Trp Ala Ala Gln 460
Ala Val Leu Ala Asp 465	His Arg 470	

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Thr Leu Ala Lys Thr Ala Val Asp Arg Gly Ile Asp Leu Val Tyr Gly
 35 40 45

Gly Gly Lys Val Gly Leu Met Gly Ile Val Ala Asp Ala Phe Leu Glu
 50 55 60

Ser Gly Gly Glu Ala Phe Gly Val Ile Thr Glu Ser Leu Met Lys Gly
 65 70 75 80

Glu Leu Gly His Glu Lys Leu Thr Glu Leu Glu Ile Val Pro Asp Met
 85 90 95

His Ile Arg Lys Arg Arg Met Ala Glu Leu Gly Asp Gly Phe Ile Ala
 100 105 110

Met Pro Gly Gly Ala Gly Thr Leu Glu Glu Leu Phe Glu Val Trp Thr
 115 120 125

Trp Gln Gln Leu Gly Ile His Gln Lys Pro Val Ala Leu Tyr Asp Val
 130 135 140

Asp Gly Phe Trp Gln Pro Leu Leu Glu Met Leu Glu Gln Met Thr Gln
 145 150 155 160

Arg Gly Phe Ile Lys Arg Asp Phe Phe Glu Cys Leu Ile Val Glu Ser
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Asp Pro His Ala Leu Leu Lys Ala Met Gln Thr Trp Thr Pro Pro Ala
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Pro Lys Trp
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acc cag cat gct cgc acg gcc acc cac ctt tat gat tcc ctg cag ctg 96
 Thr Gln His Ala Arg Thr Gly Thr His Leu Tyr Asp Ser Leu Gln Leu
 20 25 30

ctg ttc act ctg gtg gat aaa ggc cac cac cca aca gat gct aag gct 144
 Leu Phe Thr Leu Val Asp Lys Gly His His Pro Thr Asp Ala Lys Ala
 35 40 45

gta gct ttt gat gcc gag gct gga gaa gaa ggc ctg cac ttc cgc aac 192
 Val Ala Phe Asp Ala Glu Ala Gly Glu Glu Gly Leu His Phe Arg Asn
 50 55 60

ctt tca gcg gat ctc ttc ctc cct gca gcc aca gaa ctt att gat cga 240
 Leu Ser Ala Asp Leu Phe Leu Pro Ala Ala Thr Glu Leu Ile Asp Arg
 65 70 75 80

gtt ggt ctt tcc aat gaa gcc cta aac aag gtc ttg gaa aac ctc ctg 288
 Val Gly Leu Ser Asn Glu Ala Leu Asn Lys Val Leu Glu Asn Leu Leu
 85 90 95

ctc tcc cgg gtg caa tcc ggt aaa gac cgc ggc ttt atc tcc tat gcc 336
 Leu Ser Arg Val Gln Ser Gly Lys Asp Arg Gly Phe Ile Ser Tyr Ala
 100 105 110

acc ttg ggt gtt acc gag ctt ggc caa gtt tat gag ggt ctg atg tcc 384
 Thr Leu Gly Val Thr Glu Leu Gly Gln Val Tyr Glu Gly Leu Met Ser
 115 120 125

tat acc ggc ttt atc gcc cag gaa gat ctt ttt gag gtt gca cca cat 432
 Tyr Thr Gly Phe Ile Ala Gln Glu Asp Leu Phe Glu Val Ala Pro His
 130 135 140

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 Gly Lys Ala Asp Lys Gly Ser Trp Met Leu Pro Val Ser Lys Ala Asp
 145 150 155 160

gaa gtc cct gcc gat agc ttt atc gaa gtt gat caa gaa gcc cct ggt 528
 Glu Val Pro Ala Asp Ser Phe Ile Glu Val Asp Gln Glu Ala Pro Gly
 165 170 175

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 Gly Gly Val Ile Lys Val Arg Lys Arg His Pro Arg Gly Ser Phe Val
 180 185 190

ttc cgt cag tcc tct cgt gac cgc gaa cgc tca gcg tcc ttc tac acc 624
 Phe Arg Gln Ser Ser Arg Asp Arg Glu Arg Ser Ala Ser Phe Tyr Thr
 195 200 205

cca caa gta ctc acc agc ttt act gtc acc cag gct att gaa gaa ctc 672
 Pro Gln Val Leu Thr Ser Phe Thr Val Thr Gln Ala Ile Glu Glu Leu
 210 215 220

cag gca tca aag cgc atc acc aca gcc aat gat gtt ctc agc ctc acc 720
 Gln Ala Ser Lys Arg Ile Thr Thr Ala Asn Asp Val Leu Ser Leu Thr
 225 230 235 240

atc tgt gaa cct gcc atg ggt tcc ggc gcc ttc gct gtg gaa gca gta 768
 Ile Cys Glu Pro Ala Met Gly Ser Gly Ala Phe Ala Val Glu Ala Val
 245 250 255

cgc caa tta gca gag ctt tat ttg gaa ttg cgc caa gaa gaa cta gag 816
 Arg Gln Leu Ala Glu Leu Tyr Leu Glu Leu Arg Gln Glu Glu Leu Glu
 260 265 270

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Gln Gln Ile Pro Ala Glu Asp Arg Ala Lys Glu Leu Gln Lys Val Lys	
275 280 285	
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Ala His Ile Ala Leu His Gln Val Tyr Gly Val Asp Leu Asn Ser Thr	
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gct gtg gag ttg gcg gaa atc tcg ctg tgg cta gac acc atg aat gca	960
Ala Val Glu Leu Ala Glu Ile Ser Leu Trp Leu Asp Thr Met Asn Ala	
305 310 315 320	
gaa atg gac gca cct tgg tat ggc ctg cac ctg cgt aat ggt aac tcc	1008
Glu Met Asp Ala Pro Trp Tyr Gly Leu His Leu Arg Asn Gly Asn Ser	
325 330 335	
ctc gtt ggt gcc acc cgt tcg ctg tat gca cct agt ctg ctt aat aaa	1056
Leu Val Gly Ala Thr Arg Ser Leu Tyr Ala Pro Ser Leu Leu Asn Lys	
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aaa gcc tgg tta act gct act cca acc cgc tat cgg ctt gat gat atc	1104
Lys Ala Trp Leu Thr Ala Thr Pro Thr Arg Tyr Arg Leu Asp Asp Ile	
355 360 365	
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Ala Gln Ala Ile Asp Glu Asn Lys Ala Glu Pro Leu Phe Asn His Gly	
370 375 380	
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Ile His His Phe Leu Leu Pro Ser Thr Gly Trp Gly Ala Thr Ala Asp	
385 390 395 400	
gcc aaa gat ctt aaa gat ctt atg gct act gaa atc aag gag ctt aaa	1248
Ala Lys Asp Leu Lys Asp Leu Met Ala Thr Glu Ile Lys Glu Leu Lys	
405 410 415	
tct tgg cgt act tcc atc cgt gcg tct ttg agt aaa act cag att aag	1296
Ser Trp Arg Thr Ser Ile Arg Ala Ser Leu Ser Lys Thr Gln Ile Lys	
420 425 430	
cag ctc aat aac ctt gcc cta cgc gtg gaa aca cta tgg cga ttt gtg	1344
Gln Leu Asn Asn Leu Ala Leu Arg Val Glu Thr Leu Trp Arg Phe Val	
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Leu Met Arg Ile Arg Ile Ala Glu Ser Gln Ile Ser Arg Ser Thr Thr	
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Leu Trp Gly Gln Glu Pro Ala Glu Val Ser Glu Val Val Thr Arg Glu	
465 470 475 480	
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Gln Ile Glu Gln Asp Leu Phe Gly Asn Ile Asp Gly Ala Tyr Asn Arg	
485 490 495	
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Leu Arg Leu Val Met Asp Ala Trp Cys Ala Leu Trp Phe Trp Pro Leu	
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Leu	Asp	Glu	Trp	Leu	Ala	Thr	Leu	Thr	Glu	Ile	Leu	Gly	Ile	Asp	Leu	
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cct	ctg	aag	tcc	aaa	aac	gaa	aat	cag	att	gtc	tta	ggg	cca	gat	acc	1680
Pro	Leu	Lys	Ser	Lys	Asn	Glu	Asn	Gln	Ile	Val	Leu	Gly	Pro	Asp	Thr	
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Asn	Trp	Leu	Ala	Ile	Asn	Asp	Ala	Glu	Ala	Thr	Asp	Leu	Gly	Phe	Ser	
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Gly	Ala	Leu	Ser	Phe	Glu	Arg	Val	Ser	Ala	Asn	His	Pro	Trp	Ile	Asn	
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gtt	gcc	cgc	caa	gtg	gct	aaa	caa	cag	agc	ttc	ttc	cac	tgg	gat	cta	1824
Val	Ala	Arg	Gln	Val	Ala	Lys	Gln	Gln	Ser	Phe	Phe	His	Trp	Asp	Leu	
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gac	ttc	gcc	cac	gtt	ttt	gcc	aag	ggg	gga	ttt	gat	ctg	cag	gtt	ggg	1872
Asp	Phe	Ala	His	Val	Phe	Ala	Lys	Gly	Gly	Phe	Asp	Leu	Gln	Val	Gly	
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Asn	Pro	Pro	Trp	Val	Arg	Pro	Asp	Val	Asn	Phe	Glu	Asp	Leu	Leu	Ala	
	625					630				635				640		
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Glu	His	Asp	Pro	Trp	Trp	Ala	Val	Met	Ser	Lys	Pro	Thr	Gln	Ala	Ser	
				645					650					655		
aaa	aaa	gaa	cgc	cag	aag	aat	ttt	cac	aac	aat	cct	aag	agc	ctc	gaa	2016
Lys	Lys	Glu	Arg	Gln	Lys	Asn	Phe	His	Asn	Asn	Pro	Lys	Ser	Leu	Glu	
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cat	gtg	gtc	agt	ggg	gca	ggg	gaa	ccc	gtg	gct	act	tct	gcg	atc	ctc	2064
His	Val	Val	Ser	Gly	Ala	Gly	Glu	Pro	Val	Ala	Thr	Ser	Ala	Ile	Leu	
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Gly	Ser	Val	Thr	Leu	Tyr	Pro	His	Leu	Lys	Asp	Gln	Arg	Pro	Asp	Leu	
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tac	cgg	ggc	ttt	atg	gaa	aag	act	tgg	tct	aat	gcc	tcc	ccg	gca	ggg	2160
Tyr	Arg	Gly	Phe	Met	Glu	Lys	Thr	Trp	Ser	Asn	Ala	Ser	Pro	Ala	Gly	
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gcg	atc	tca	ctg	atc	cac	ccc	gaa	tcc	cac	ttc	act	gag	aaa	aaa	gct	2208
Ala	Ile	Ser	Leu	Ile	His	Pro	Glu	Ser	His	Phe	Thr	Glu	Lys	Lys	Ala	
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Ala	Pro	Leu	Arg	Arg	Gly	Ala	Tyr	Glu	Arg	Leu	Arg	Arg	His	Trp	Gln	
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ttc	att	aat	gag	ttg	att	ctt	ttt	gac	gtc	cac	gac	ttg	gtt	aaa	tat	2304
Phe	Ile	Asn	Glu	Leu	Ile	Leu	Phe	Asp	Val	His	Asp	Leu	Val	Lys	Tyr	

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Ala Ala Ser Leu Tyr His Pro Gln Thr Val Leu Asp Ser Phe Asp His			
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Asp Gly Ser Gly Asn Leu Pro Gly Leu Lys Asp Asp Asn Gly Asn Trp			
805	810	815	
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Asp Arg Arg Pro His Lys Asp Arg Ile Gln Leu Val Asn Ala Asp Thr			
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Leu Thr Val Trp Lys Ser Ile Leu Glu Asp Glu Gln Thr Pro Tyr Leu			
835	840	845	
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Asp Thr Arg Met Val Tyr Thr Val Asn Thr Glu Ala Ala Ala Leu			
850	855	860	
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Glu Lys Leu Ala Ser Ala Pro Arg Ile Lys Glu Leu Gly Leu Gln Phe			
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885	890	895	
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Val Gly Trp Gly Tyr Pro Ala Ser Trp Ser Asp Ala Ile Leu Gln Gly			
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Pro His Leu Gly Val Ala Thr Pro Met Ile Lys Gln Pro Asn Pro Thr			
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Met Lys His Asn Gln Asp Trp Ser Glu Ile Asp Phe Glu Ala Ile Pro			
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Ala Asn Phe Ile Pro Ala Thr Ala Tyr Gln Pro Asp Arg Gln Thr Lys			
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Pro Thr Tyr Asp Ala Asp Tyr Gly Thr Trp Thr Phe Gly Asp Lys Gln			
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Val Pro Val Ala Asp Thr Phe Arg Ile Ala Trp Arg Glu Met Ala Ala			
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Thr Thr Gly Phe Arg Thr Val Tyr Pro Ser Val Ile Pro Pro Gly Ala			
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 Tyr Leu Arg Leu Asn Cys Leu Thr Ser Ala Tyr Ala Pro Leu Trp Glu
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 Glu Ile Thr Gly Glu Pro Trp Asp Val Gln Val Pro Leu Arg Asn Ala
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 Phe Pro Val Met Arg Arg Tyr Asp Gln Glu Asp His Phe Asp Ala Asn
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 1185 1190 1195 1200
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 Glu Pro

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<211> 1218

<212> PRT

<213> Corynebacterium glutamicum

<400> 600

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 Leu Phe Thr Leu Val Asp Lys Gly His His Pro Thr Asp Ala Lys Ala
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 Val Ala Phe Asp Ala Glu Ala Gly Glu Glu Gly Leu His Phe Arg Asn
 50 55 60
 Leu Ser Ala Asp Leu Phe Leu Pro Ala Ala Thr Glu Leu Ile Asp Arg
 65 70 75 80
 Val Gly Leu Ser Asn Glu Ala Leu Asn Lys Val Leu Glu Asn Leu Leu
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 Leu Ser Arg Val Gln Ser Gly Lys Asp Arg Gly Phe Ile Ser Tyr Ala
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 Thr Leu Gly Val Thr Glu Leu Gly Gln Val Tyr Glu Gly Leu Met Ser
 115 120 125
 Tyr Thr Gly Phe Ile Ala Gln Glu Asp Leu Phe Glu Val Ala Pro His
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 Gly Lys Ala Asp Lys Gly Ser Trp Met Leu Pro Val Ser Lys Ala Asp
 145 150 155 160
 Glu Val Pro Ala Asp Ser Phe Ile Glu Val Asp Gln Glu Ala Pro Gly
 165 170 175
 Gly Gly Val Ile Lys Val Arg Lys Arg His Pro Arg Gly Ser Phe Val
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 Phe Arg Gln Ser Ser Arg Asp Arg Glu Arg Ser Ala Ser Phe Tyr Thr
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 Pro Gln Val Leu Thr Ser Phe Thr Val Thr Gln Ala Ile Glu Glu Leu
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 Gln Ala Ser Lys Arg Ile Thr Thr Ala Asn Asp Val Leu Ser Leu Thr
 225 230 235 240
 Ile Cys Glu Pro Ala Met Gly Ser Gly Ala Phe Ala Val Glu Ala Val
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 Arg Gln Leu Ala Glu Leu Tyr Leu Glu Leu Arg Gln Glu Glu Leu Glu
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 Gln Gln Ile Pro Ala Glu Asp Arg Ala Lys Glu Leu Gln Lys Val Lys
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 Ala His Ile Ala Leu His Gln Val Tyr Gly Val Asp Leu Asn Ser Thr
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 Ala Val Glu Leu Ala Glu Ile Ser Leu Trp Leu Asp Thr Met Asn Ala

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Glu Met Asp Ala Pro	Trp Tyr Gly Leu His	Leu Arg Asn Gly Asn Ser				
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Leu Val Gly Ala Thr	Arg Ser Leu Tyr Ala Pro	Ser Leu Leu Asn Lys				
	340		345			350
Lys Ala Trp Leu Thr	Ala Thr Pro Tar Arg Tyr	Arg Leu Asp Asp Ile				
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Ala Gln Ala Ile Asp	Glu Asn Lys Ala Glu Pro	Leu Phe Asn His Gly				
	370		375			380
Ile His His Phe Leu	Leu Pro Ser Tar Gly Trp	Gly Ala Thr Ala Asp				
	385		390			400
Ala Lys Asp Leu Lys	Asp Leu Met Ala Thr Glu Ile	Lys Glu Leu Lys				
	405		410			415
Ser Trp Arg Thr Ser	Ile Arg Ala Ser Leu Ser	Lys Thr Gln Ile Lys				
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Gln Leu Asn Asn Leu	Ala Leu Arg Val Glu Thr	Leu Trp Arg Phe Val				
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Leu Arg Leu Val Met	Asp Ala Trp Cys Ala Leu Trp	Phe Trp Pro Leu				
	500		505			510
Asp Ala Val Ala Thr	Ala Glu His Pro Glu Arg	Pro Ala Leu Pro Asp				
	515		520			525
Leu Asp Glu Trp Leu	Ala Thr Leu Thr Glu Ile	Leu Gly Ile Asp Leu				
	530		535			540
Pro Leu Lys Ser Lys	Asn Glu Asn Gln Ile Val	Leu Gly Pro Asp Thr				
	545		550			555
Asn Trp Leu Ala Ile	Asn Asp Ala Glu Ala Thr	Asp Leu Gly Phe Ser				
	565		570			575
Gly Ala Leu Ser Phe	Glu Arg Val Ser Ala Asn His	Pro Trp Ile Asn				
	580		585			590
Val Ala Arg Gln Val	Ala Lys Gln Gln Ser Phe Phe	His Trp Asp Leu				
	595		600			605
Asp Phe Ala His Val	Phe Ala Lys Gly Gly Phe	Asp Leu Gln Val Gly				
	610		615			620
Asn Pro Pro Trp Val	Arg Pro Asp Val Asn Phe	Glu Asp Leu Leu Ala				
	625		630			635
						640

Glu His Asp Pro Trp Trp Ala Val Met Ser Lys Pro Thr Gln Ala Ser
 645 650 655
 Lys Lys Glu Arg Gln Lys Asn Phe His Asn Asn Pro Lys Ser Leu Glu
 660 665 670
 His Val Val Ser Gly Ala Gly Glu Pro Val Ala Thr Ser Ala Ile Leu
 675 680 685
 Gly Ser Val Thr Leu Tyr Pro His Leu Lys Asp Gln Arg Pro Asp Leu
 690 695 700
 Tyr Arg Gly Phe Met Glu Lys Thr Trp Ser Asn Ala Ser Pro Ala Gly
 705 710 715 720
 Ala Ile Ser Leu Ile His Pro Glu Ser His Phe Thr Glu Lys Lys Ala
 725 730 735
 Ala Pro Leu Arg Arg Gly Ala Tyr Glu Arg Leu Arg Arg His Trp Gln
 740 745 750
 Phe Ile Asn Glu Leu Ile Leu Phe Asp Val His Asp Leu Val Lys Tyr
 755 760 765
 Gly Val His Val Tyr Gly Ala Pro Gln Glu Ser Ile Asn Phe Leu Ser
 770 775 780
 Ala Ala Ser Leu Tyr His Pro Gln Thr Val Leu Asp Ser Phe Asp His
 785 790 795 800
 Asp Gly Ser Gly Asn Leu Pro Gly Leu Lys Asp Asp Asn Gly Asn Trp
 805 810 815
 Asp Arg Arg Pro His Lys Asp Arg Ile Gln Leu Val Asn Ala Asp Thr
 820 825 830
 Leu Thr Val Trp Lys Ser Ile Leu Glu Asp Glu Gln Thr Pro Tyr Leu
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 Asp Thr Arg Met Val Tyr Thr Val Asn Thr Glu Ala Ala Ala Leu
 850 855 860
 Glu Lys Leu Ala Ser Ala Pro Arg Ile Lys Glu Leu Gly Leu Gln Phe
 865 870 875 880
 Ser Ser Gly Trp Asn Glu Thr Thr Asp Lys Lys Lys Gly Tyr Phe Asp
 885 890 895
 Val Gly Trp Gly Tyr Pro Ala Ser Trp Ser Asp Ala Ile Leu Gln Gly
 900 905 910
 Pro His Leu Gly Val Ala Thr Pro Met Ile Lys Gln Pro Asn Pro Thr
 915 920 925
 Met Lys His Asn Gln Asp Trp Ser Glu Ile Asp Phe Glu Ala Ile Pro
 930 935 940
 Ala Asn Phe Ile Pro Ala Thr Ala Tyr Gln Pro Asp Arg Gln Thr Lys
 945 950 955 960

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Pro Thr Tyr Asp Ala Asp Tyr Gly Thr Trp Thr Phe Gly Asp Lys Gln
      965                      970                      975

Val Pro Val Ala Asp Thr Phe Arg Ile Ala Trp Arg Glu Met Ala Ala
      980                      985                      990

Thr Thr Gly Phe Arg Thr Val Tyr Pro Ser Val Ile Pro Pro Gly Ala
      995                      1000                      1005

Asn His Val His Thr Val Asn Ser Ala Ala Ser Arg Ser Asn Leu Lys
      1010                      1015                      1020

Thr Ile Leu Val Gly Ala Gln Leu Gly Ala Ile Leu Ser Asp Tyr Phe
      1025                      1030                      1035                      1040

Ala Arg Ser Ser Gly Ser Ser His Ile Phe Asn Asp Ile Val Arg Lys
      1045                      1050                      1055

Ile Pro Leu Pro Asn Phe Thr Ser Leu Glu Lys Gln Phe Ala Arg Thr
      1060                      1065                      1070

Tyr Leu Arg Leu Asn Cys Leu Thr Ser Ala Tyr Ala Pro Leu Trp Glu
      1075                      1080                      1085

Glu Ile Thr Gly Glu Pro Trp Asp Val Gln Val Pro Leu Arg Asn Ala
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Glu Gln Arg Arg Ala Ala Gln Asn Asp Ile Asp Ala Met Val Ala Leu
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Ser Leu Gly Ile Ser Ala Asp Glu Leu Cys Met Ile Tyr Arg Thr Gln
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Phe Pro Val Met Arg Arg Tyr Asp Gln Glu Asp His Phe Asp Ala Asn
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Gly Arg Lys Val Pro Lys Glu Ile Ile Lys Leu Gln Gln Lys Leu Lys
      1155                      1160                      1165

Asp Gly Gln Glu Leu Ser Val Glu Lys Arg Thr Trp Val His Pro Gln
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Ser Glu Val Ser Tyr Thr Phe Glu Tyr Pro Phe Arg Val Leu Asp Arg
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Glu Pro

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<223> FRXA01362

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 gta cat gtc tat ggc gct ccg cag gaa tct att aac ttt tta agt gct 96
 Val His Val Tyr Gly Ala Pro Gln Glu Ser Ile Asn Phe Leu Ser Ala 30
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 gcg tgc ctt tat cac cca caa aca gtg ctt gat tca ttt gat cat gac 144
 Ala Ser Leu Tyr His Pro Gln Thr Val Leu Asp Ser Phe Asp His Asp 35 40 45
 ggt tca ggt aat ctc cct ggt ctt aaa gac gac aat ggc aac tgg gac 192
 Gly Ser Gly Asn Leu Pro Gly Leu Lys Asp Asp Asn Gly Asn Trp Asp 50 55 60
 cgt cgc cca cac aag gac cgt atc caa ctg gtc aat gcc gat act ttg 240
 Arg Arg Pro His Lys Asp Arg Ile Gln Leu Val Asn Ala Asp Thr Leu 65 70 75 80
 acg gtg tgg aag tcc atc ctg gag gat gaa caa acg cca tac ttg gat 288
 Thr Val Trp Lys Ser Ile Leu Glu Asp Glu Gln Thr Pro Tyr Leu Asp 85 90 95
 acc cgc atg gtt tat acc gtc aac acg gaa gca gca gca ggc ttg gaa 336
 Thr Arg Met Val Tyr Thr Val Asn Thr Glu Ala Ala Ala Leu Glu 100 105 110
 aag ttg gct tct gca cct cgt atc aaa gaa ctg ggg ctg cag ttc tcc 384
 Lys Leu Ala Ser Ala Pro Arg Ile Lys Glu Leu Gly Leu Gln Phe Ser 115 120 125
 agt ggc tgg aat gaa acc acc gat aag aaa aag gga tac ttt gac gtt 432
 Ser Gly Trp Asn Glu Thr Thr Asp Lys Lys Lys Gly Tyr Phe Asp Val 130 135 140
 ggt tgg ggc tac cca gct tcc tgg tct gat gcc att ttg cag ggg ccg 480
 Gly Trp Gly Tyr Pro Ala Ser Trp Ser Asp Ala Ile Leu Gln Gly Pro 145 150 155 160
 cac ctg ggt gtt gct aca cca atg atc aag cag ccc aat ccg aca atg 528
 His Leu Gly Val Ala Thr Pro Met Ile Lys Gln Pro Asn Pro Thr Met 165 170 175
 aag cat aat caa gat tgg tct gaa att gat ttc gag gcc att cct gca 576
 Lys His Asn Gln Asp Trp Ser Glu Ile Asp Phe Glu Ala Ile Pro Ala 180 185 190
 aac ttc ata cct gca acg gcg tac cag ccc gat cgc caa aca aag ccc 624
 Asn Phe Ile Pro Ala Thr Ala Tyr Gln Pro Asp Arg Gln Thr Lys Pro 195 200 205
 act tat gat gct gac tac ggc acc tgg act ttc ggg gac aag cag gta 672
 Thr Tyr Asp Ala Asp Tyr Gly Thr Trp Thr Phe Gly Asp Lys Gln Val 210 215 220
 cca gtt gca gac act ttc cga att gca tgg agg gag atg gct gcc acc 720
 Pro Val Ala Asp Thr Phe Arg Ile Ala Trp Arg Glu Met Ala Ala Thr 225 230 235 240

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 Gly Ser Gly Asn Leu Pro Gly Leu Lys Asp Asp Asn Gly Asn Trp Asp
 50 55 60
 Arg Arg Pro His Lys Asp Arg Ile Gln Leu Val Asn Ala Asp Thr Leu
 65 70 75 80
 Thr Val Trp Lys Ser Ile Leu Glu Asp Glu Gln Thr Pro Tyr Leu Asp
 85 90 95
 Thr Arg Met Val Tyr Thr Val Asn Thr Glu Ala Ala Ala Leu Glu
 100 105 110
 Lys Leu Ala Ser Ala Pro Arg Ile Lys Glu Leu Gly Leu Gln Phe Ser
 115 120 125
 Ser Gly Trp Asn Glu Thr Thr Asp Lys Lys Lys Gly Tyr Phe Asp Val
 130 135 140
 Gly Trp Gly Tyr Pro Ala Ser Trp Ser Asp Ala Ile Leu Gln Gly Pro
 145 150 155 160
 His Leu Gly Val Ala Thr Pro Met Ile Lys Gln Pro Asn Pro Thr Met
 165 170 175
 Lys His Asn Gln Asp Trp Ser Glu Ile Asp Phe Glu Ala Ile Pro Ala
 180 185 190
 Asn Phe Ile Pro Ala Thr Ala Tyr Gln Pro Asp Arg Gln Thr Lys Pro
 195 200 205
 Thr Tyr Asp Ala Asp Tyr Gly Thr Trp Thr Phe Gly Asp Lys Gln Val
 210 215 220
 Pro Val Ala Asp Thr Phe Arg Ile Ala Trp Arg Glu Met Ala Ala Thr
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 Thr Gly Phe Arg Thr Val Tyr Pro Ser Val Ile Pro Pro Gly Ala Asn
 245 250 255
 His Val His Thr Val Asn Ser Ala Ala Ser Arg Ser Asn Leu Lys Thr
 260 265 270
 Ile Leu Val Gly Ala Gln Leu Gly Ala Ile Leu Ser Asp Tyr Phe Ala
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Arg Ser Ser Gly Ser Ser His Ile Phe Asn Asp Ile Val Arg Lys Ile
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Pro Leu Pro Asn Phe Thr Ser Leu Glu Lys Gln Phe Ala Arg Thr Tyr
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Gln Arg Arg Ala Ala Gln Asn Asp Ile Asp Ala Met Val Ala Leu Ser
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Leu Gly Ile Ser Ala Asp Glu Leu Cys Met Ile Tyr Arg Thr Gln Phe
370                375                380

Pro Val Met Arg Arg Tyr Asp Gln Glu Asp His Phe Asp Ala Asn Gly
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Gly Gln Glu Leu Ser Val Glu Lys Arg Thr Trp Val His Pro Gln Ser
420                425                430

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Asp Lys Gly His His Pro Thr Asp Ala Lys Ala Val Ala Phe Asp Ala
20 25 30

gag gct gga gaa gaa ggc ctg cac ttc cgc aac ctt tca gcg gat ctc 144
Glu Ala Gly Glu Glu Gly Leu His Phe Arg Asn Leu Ser Ala Asp Leu
35 40 45

ttc ctc cct gca gcc aca gaa ctt att gat cga gtt ggt ctt tcc aat 192

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Glu	Ala	Leu	Asn	Lys	Val	Leu	Glu	Asn	Leu	Leu	Leu	Ser	Arg	Val	Gln	
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Ser	Gly	Lys	Asp	Arg	Gly	Phe	Ile	Ser	Tyr	Ala	Thr	Leu	Gly	Val	Thr	
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Glu	Leu	Gly	Gln	Val	Tyr	Glu	Gly	Leu	Met	Ser	Tyr	Thr	Gly	Phe	Ile	
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gcc	cag	gaa	gat	ctt	ttt	gag	gtt	gca	cca	cat	ggc	aaa	gcc	gat	aaa	384
Ala	Gln	Glu	Asp	Leu	Phe	Glu	Val	Ala	Pro	His	Gly	Lys	Ala	Asp	Lys	
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Gly	Ser	Trp	Met	Leu	Pro	Val	Ser	Lys	Ala	Asp	Glu	Val	Pro	Ala	Asp	
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Ser	Phe	Ile	Glu	Val	Asp	Gln	Glu	Ala	Pro	Gly	Gly	Gly	Val	Ile	Lys	
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Val	Arg	Lys	Arg	His	Pro	Arg	Gly	Ser	Phe	Val	Phe	Arg	Gln	Ser	Ser	
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Arg	Asp	Arg	Glu	Arg	Ser	Ala	Ser	Phe	Tyr	Thr	Pro	Gln	Val	Leu	Thr	
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Ser	Phe	Thr	Val	Thr	Gln	Ala	Ile	Glu	Glu	Leu	Gln	Ala	Ser	Lys	Arg	
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Ile	Thr	Thr	Ala	Asn	Asp	Val	Leu	Ser	Leu	Thr	Ile	Cys	Glu	Pro	Ala	
210																
atg	ggt	tcc	ggc	gcc	ttc	gct	gtg	gaa	gca	gta	cgc	caa	tta	gca	gag	720
Met	Gly	Ser	Gly	Ala	Phe	Ala	Val	Ala	Ala	Val	Arg	Gln	Leu	Ala	Glu	
225																
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Leu	Tyr	Leu	Glu	Leu	Arg	Gln	Glu	Glu	Leu	Glu	Gln	Gln	Ile	Pro	Ala	
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Glu	Asp	Arg	Ala	Lys	Glu	Leu	Gln	Lys	Val	Lys	Ala	His	Ile	Ala	Leu	
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cac	cag	gtt	tat	ggt	gtg	gac	ctt	aac	Ser	act	gct	gtg	gag	ttg	gcg	864
His	Gln	Val	Tyr	Gly	Val	Asp	Leu	Asn	Ser	Thr	Ala	Val	Glu	Leu	Ala	
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gat ctt atg gct act Asp Leu Met Ala Thr 385	gaa atc aag gag ctt aaa Glu Ile Lys Glu Leu Lys 390	tct tgg cgt act tcc Ser Trp Arg Thr Ser 395	1200
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aac gaa aat cag att Asn Glu Asn Gln Ile 530	gtc tta ggt cca gat Val Leu Gly Pro Asp 535	acc aat tgg cta gcc att Thr Asn Trp Leu Ala Ile 540	1632

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Ser Gly Lys Asp Arg Gly Phe Ile Ser Tyr Ala Thr Leu Gly Val Thr
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Glu Leu Gly Gln Val Tyr Glu Gly Leu Met Ser Tyr Thr Gly Phe Ile
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Gly Ser Trp Met Leu Pro Val Ser Lys Ala Asp Glu Val Pro Ala Asp
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Ser Phe Ile Glu Val Asp Gln Glu Ala Pro Gly Gly Gly Val Ile Lys
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Val Arg Lys Arg His Pro Arg Gly Ser Phe Val Phe Arg Gln Ser Ser
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 Ser Phe Thr Val Thr Gln Ala Ile Glu Glu Leu Gln Ala Ser Lys Arg
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 Ile Thr Thr Ala Asn Asp Val Leu Ser Leu Thr Ile Cys Glu Pro Ala
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 Met Gly Ser Gly Ala Phe Ala Val Glu Ala Val Arg Gln Leu Ala Glu
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 Leu Tyr Leu Glu Leu Arg Gln Glu Glu Leu Glu Gln Gln Ile Pro Ala
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 Glu Asp Arg Ala Lys Glu Leu Gln Lys Val Lys Ala His Ile Ala Leu
 260 265 270
 His Gln Val Tyr Gly Val Asp Leu Asn Ser Thr Ala Val Glu Leu Ala
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 Trp Tyr Gly Leu His Leu Arg Asn Gly Asn Ser Leu Val Gly Ala Thr
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 385 390 395 400
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 Leu Phe Gly Asn Ile Asp Gly Ala Tyr Asn Arg Leu Arg Leu Val Met
 465 470 475 480
 Asp Ala Trp Cys Ala Leu Trp Phe Trp Pro Leu Asp Ala Val Ala Thr
 485 490 495
 Ala Glu His Pro Glu Arg Pro Ala Leu Pro Asp Leu Asp Glu Trp Leu

500					505					510				
Ala Thr	Leu Thr	Glu Ile	Leu Gly	Ile Asp	Leu Pro	Leu Lys	Ser Lys							
	515		520			525								
Asn Glu	Asn Gln	Ile Val	Leu Gly	Pro Asp	Thr Asn	Trp Leu	Ala Ile							
	530		535			540								
Asn Asp	Ala Glu	Ala Thr	Asp Leu	Gly Phe	Ser Gly	Ala Leu	Ser Phe							
	545		550		555		560							
Glu Arg	Val Ser	Ala Asn	His Pro	Trp Ile	Asn Val	Ala Arg	Gln Val							
		565		570			575							
Ala Lys	Gln Gln	Ser Phe	Phe His	Trp Asp	Leu Asp	Phe Ala	His Val							
		580		585			590							
Phe Ala	Lys Gly	Gly Phe	Asp Leu	Gln Val	Gly Asn	Pro Pro	Trp Val							
		595		600			605							
Arg Pro	Asp Val	Asn Phe	Glu Asp	Leu Leu	Ala Glu	His Asp								
			615				620							

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<210> 605
<211> 1042
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> {101}..(1042)
<223> RXN01379
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<400> 605															
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cttcgcgcgc cgcgaacttt gaacaccgag gtttaacaca															
Met agt gca ttt gat															115
1 Ser Ala Phe Asp															5
tcg atc cta aat gtt gaa gag tgg atc agt gac cac tac ctc acc aat															163
Ser Ile Leu Asn Val Glu Glu Trp Ile Ser Asp His Tyr Leu Thr Asn															20
10 15 20															
gac gat gcc aaa ggt gcc tca ttt tcc aag cgg gtg cgc gag cgc att															211
Asp Asp Ala Lys Lys Gly Ala Ser Phe Ser Lys Arg Val Arg Glu Arg Ile															35
25 30 35															
aaa gaa tgg aaa acc acc gag gac gca acc cag cag agt ggc cct tta															259
Lys Glu Trp Lys Thr Thr Glu Asp Ala Thr Gln Gln Ser Gly Pro Leu															40 45 50
40 45 50															
act cgt ttt tcc agc aac cgc ctg cag ttg cag cat gct ctt tct gag															307
Thr Arg Phe Ser Ser Asn Arg Leu Gln Leu Gln His Ala Leu Ser Glu															55 60 65
55 60 65															
ctt gac gac gcc acc acc gcc gcc agt tta gtg gcc tct gca ctg ggg															355
Leu Asp Asp Ala Thr Thr Ala Ala Ser Leu Val Ala Ser Ala Leu Gly															70 75 80 85
70 75 80 85															

tat ggt gtc ccc agc gcg cgc cac gcg cag cgc ggc tcc gac aca ata	403
Tyr Gly Val Pro Ser Ala Arg His Ala Gln Arg Gly Ser Asp Thr Ile	
90 95 100	
tcc tat tcc tct tgg gtg gga aat gcc ggc agt gtg gaa ttt ctt gca	451
Ser Tyr Ser Ser Trp Val Gly Asn Ala Gly Ser Val Glu Phe Leu Ala	
105 110 115	
gcg act ccc gct gaa agc ttt gaa gag aac ttc cga tcc ctt ccc ctt	499
Ala Thr Pro Ala Glu Ser Phe Glu Glu Asn Phe Arg Ser Leu Pro Leu	
120 125 130	
gag cca gta gcg gtc aat gac aag ccc cag gat atc acc gca gcc aaa	547
Glu Pro Val Ala Val Asn Asp Lys Pro Gln Asp Ile Thr Ala Ala Lys	
135 140 145	
ttg gtg ggc cag att ttc ctt agt gat act ccc cct gct ttt gtt gtt	595
Leu Val Gly Gln Ile Phe Leu Ser Asp Thr Pro Pro Ala Phe Val Val	
150 155 160 165	
atc acc gct ggt aaa tgg gtg gtt tta gcc gag cgt gaa acc tgg cct	643
Ile Thr Ala Gly Lys Trp Val Val Leu Ala Glu Arg Glu Thr Trp Pro	
170 175 180	
cta ggc cgc cac cta gct att gat att tcc ctg gtg gtg gaa cgt aat	691
Leu Gly Arg His Leu Ala Ile Asp Ile Ser Leu Val Val Glu Arg Asn	
185 190 195	
gac acc aaa gcc cag ggt gag atg cag cag acg gtc gta gca cta gcc	739
Asp Thr Lys Ala Gln Gly Glu Met Gln Gln Thr Val Val Ala Leu Ala	
200 205 210	
cgc gaa aat acc gag cgt gcc gcc gat gcc acc acc tgg tgg gaa gaa	787
Arg Glu Asn Thr Glu Arg Ala Ala Asp Gly Thr Thr Trp Trp Glu Glu	
215 220 225	
acc att gag caa tcc cgc gaa cat gct gtc aag gtt tct gcc gag cta	835
Thr Ile Glu Gln Ser Arg Glu His Ala Val Lys Val Ser Gly Glu Leu	
230 235 240 245	
cgc agt gcg gtg cgt gaa tcc att gaa atc ctg ggc aat gac gtg ctc	883
Arg Ser Ala Val Arg Glu Ser Ile Glu Ile Leu Gly Asn Asp Val Leu	
250 255 260	
aca cgc tat gaa gct aaa gag ctc tcc acc gct gag atc gac ggt ggc	931
Thr Arg Tyr Glu Ala Lys Glu Leu Ser Thr Ala Glu Ile Asp Gly Gly	
265 270 275	
gag cta gct aag caa tct ttg cgc tat ctc tac cgc att ttg ttc ctg	979
Glu Leu Ala Lys Gln Ser Leu Arg Tyr Leu Tyr Arg Ile Leu Phe Leu	
280 285 290	
ctt ttt gcc gag gct tca cca gag ott gaa atc ctg cca acc gcc acc	1027
Leu Phe Ala Glu Ala Ser Pro Glu Leu Glu Ile Leu Pro Thr Gly Thr	
295 300 305	
ccg gaa tat gac gag	1042
Pro Glu Tyr Asp Glu	
310	

<210> 606

<211> 314

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 606

Met Ser Ala Phe Asp Ser Ile Leu Asn Val Glu Glu Trp Ile Ser Asp
 1 5 10 15

His Tyr Leu Thr Asn Asp Asp Ala Lys Gly Ala Ser Phe Ser Lys Arg
 20 25 30

Val Arg Glu Arg Ile Lys Glu Trp Lys Thr Thr Glu Asp Ala Thr Gln
 35 40 45

Gln Ser Gly Pro Leu Thr Arg Phe Ser Ser Asn Arg Leu Gln Leu Gln
 50 55 60

His Ala Leu Ser Glu Leu Asp Asp Ala Thr Thr Ala Ala Ser Leu Val
 65 70 75 80

Ala Ser Ala Leu Gly Tyr Gly Val Pro Ser Ala Arg His Ala Gln Arg
 85 90 95

Gly Ser Asp Thr Ile Ser Tyr Ser Ser Trp Val Gly Asn Ala Gly Ser
 100 105 110

Val Glu Phe Leu Ala Ala Thr Pro Ala Glu Ser Phe Glu Glu Asn Phe
 115 120 125

Arg Ser Leu Pro Leu Glu Pro Val Ala Val Asn Asp Lys Pro Gln Asp
 130 135 140

Ile Thr Ala Ala Lys Leu Val Gly Gln Ile Phe Leu Ser Asp Thr Pro
 145 150 155 160

Pro Ala Phe Val Val Ile Thr Ala Gly Lys Trp Val Val Leu Ala Glu
 165 170 175

Arg Glu Thr Trp Pro Leu Gly Arg His Leu Ala Ile Asp Ile Ser Leu
 180 185 190

Val Val Glu Arg Asn Asp Thr Lys Ala Gln Gly Glu Met Gln Gln Thr
 195 200 205

Val Val Ala Leu Ala Arg Glu Asn Thr Glu Arg Ala Ala Asp Gly Thr
 210 215 220

Thr Trp Trp Glu Glu Thr Ile Glu Gln Ser Arg Glu His Ala Val Lys
 225 230 235 240

Val Ser Gly Glu Leu Arg Ser Ala Val Arg Glu Ser Ile Glu Ile Leu
 245 250 255

Gly Asn Asp Val Leu Thr Arg Tyr Glu Ala Lys Glu Leu Ser Thr Ala
 260 265 270

Glu Ile Asp Gly Gly Glu Leu Ala Lys Gln Ser Leu Arg Tyr Leu Tyr
 275 280 285

Arg Ile Leu Phe Leu Leu Phe Ala Glu Ala Ser Pro Glu Leu Glu Ile

290

295

300

Leu Pro Thr Gly Thr Pro Glu Tyr Asp Glu
305 310

<210> 607

<211> 921

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(921)

<223> FRXA01379

<400> 607

cta aat gtt gaa gag tgg atc agt gac cac tac ctc acc aat gac gat 48
Leu Asn Val Glu Glu Trp Ile Ser Asp His Tyr Leu Thr Asn Asp Asp
1 5 10 15

gcc aaa ggt gcc tca ttt tcc aag cgg gtg cgc gag cgc att aaa gaa 96
Ala Lys Gly Ala Ser Phe Ser Lys Arg Val Arg Glu Arg Ile Lys Glu
20 25 30

tgg aaa acc acc gag gac gca acc cag cag agt ggc cct tta act cgt 144
Trp Lys Thr Thr Glu Asp Ala Thr Gln Gln Ser Gly Pro Leu Thr Arg
35 40 45

ttt tcc agc aac cgc ctg cag ttg cag cat gct ctt tct gag ctt gac 192
Phe Ser Ser Asn Arg Leu Gln Leu Gln His Ala Ser Glu Leu Asp
50 55 60

gac gcc acc acc gcc gcc agt tta gtg gcc tct gca ctg ggg tat ggt 240
Asp Ala Thr Thr Ala Ala Ser Leu Val Ala Ser Ala Leu Gly Tyr Gly
65 70 75 80

gtc ccc agc gcg cgc cac gcg cag cgc ggc tcc gac aca ata tcc tat 288
Val Pro Ser Ala Arg His Ala Gln Arg Gly Ser Asp Thr Ile Ser Tyr
85 90 95

tcc tct tgg gtg gga aat gcc ggc agt gtg gaa ttt ctt gca gcg act 336
Ser Ser Trp Val Gly Asn Ala Gly Ser Val Glu Phe Leu Ala Ala Thr
100 105 110

ccc gct gaa agc ttt gaa gag aac ttc cga tcc ctt ccc ctt gag cca 384
Pro Ala Glu Ser Phe Glu Glu Asn Phe Arg Ser Leu Pro Leu Glu Pro
115 120 125

gta gcg gtc aat gac aag ccc cag gat atc acc gca gcc aaa ttg gtg 432
Val Ala Val Asn Asp Lys Pro Gln Asp Ile Thr Ala Ala Lys Leu Val
130 135 140

ggc cag att ttc ctt agt gat act ccc cct gct ttt gtt gtt atc acc 480
Gly Gln Ile Phe Leu Ser Asp Thr Pro Pro Ala Phe Val Val Ile Thr
145 150 155 160

gct ggt aaa tgg gtg gtt tta gcc gag cgt gaa acc tgg cct cta gcc 528
Ala Gly Lys Trp Val Val Leu Ala Glu Arg Glu Thr Trp Pro Leu Gly
165 170 175

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cgc cac cta gct att gat att tcc ctg gtg gtg gaa cgt aat gac acc 576
Arg His Leu Ala Ile Asp Ile Ser Leu Val Val Glu Arg Asn Asp Thr
      180                      185                      190

aaa gcc cag ggt gag atg cag cag acg gtc gta gca cta gcc cgc gaa 624
Lys Ala Gln Gly Glu Met Gln Gln Thr Val Val Ala Leu Ala Arg Glu
      195                      200                      205

aat acc gag cgt gcc gcc gat ggc acc acc tgg tgg gaa gaa acc att 672
Asn Thr Glu Arg Ala Ala Asp Gly Thr Thr Trp Trp Glu Glu Thr Ile
      210                      215                      220

gag caa tcc cgc gaa cat gct gtc aag gtt tct ggc gag cta cgc agt 720
Glu Gln Ser Arg Glu His Ala Val Lys Val Ser Gly Glu Leu Arg Ser
      225                      230                      235

gcg gtg cgt gaa tcc att gaa atc ctg gcc aat gac gtg ctc aca cgc 768
Ala Val Arg Glu Ser Ile Glu Ile Leu Gly Asn Asp Val Leu Thr Arg
      245                      250                      255

tat gaa gct aaa gag ctc tcc acc gct gag atc gac ggt gcc gag cta 816
Tyr Glu Ala Lys Glu Leu Ser Thr Ala Glu Ile Asp Gly Gly Glu Leu
      260                      265                      270

gct aag caa tct ttg cgc tat ctc tac cgc att ttg ttc ctg ctt ttt 864
Ala Lys Gln Ser Leu Arg Tyr Leu Tyr Arg Ile Leu Phe Leu Leu Phe
      275                      280                      285

gcc gag gct tca cca gag ctt gaa atc ctg cca acc gcc acc ccg gaa 912
Ala Glu Ala Ser Pro Glu Leu Glu Ile Leu Pro Thr Gly Thr Pro Glu
      290                      295                      300

tat gac gag 921
Tyr Asp Glu
305

<210> 608
<211> 307
<212> PRT
<213> Corynebacterium glutamicum

<400> 608
Leu Asn Val Glu Glu Trp Ile Ser Asp His Tyr Leu Thr Asn Asp Asp
  1                      5                      10                      15

Ala Lys Gly Ala Ser Phe Ser Lys Arg Val Arg Glu Arg Ile Lys Glu
  20                      25                      30

Trp Lys Thr Thr Glu Asp Ala Thr Gln Gln Ser Gly Pro Leu Thr Arg
  35                      40                      45

Phe Ser Ser Asn Arg Leu Gln Leu Gln His Ala Leu Ser Glu Leu Asp
  50                      55                      60

Asp Ala Thr Thr Ala Ala Ser Leu Val Ala Ser Ala Leu Gly Tyr Gly
  65                      70                      75                      80

Val Pro Ser Ala Arg His Ala Gln Arg Gly Ser Asp Thr Ile Ser Tyr
      85                      90                      95

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Ser Ser Trp Val Gly Asn Ala Gly Ser Val Glu Phe Leu Ala Ala Thr
 100 105 110
 Pro Ala Glu Ser Phe Glu Glu Asn Phe Arg Ser Leu Pro Leu Glu Pro
 115 120 125
 Val Ala Val Asn Asp Lys Pro Gln Asp Ile Thr Ala Ala Lys Leu Val
 130 135 140
 Gly Gln Ile Phe Leu Ser Asp Thr Pro Pro Ala Phe Val Val Ile Thr
 145 150 155 160
 Ala Gly Lys Trp Val Val Leu Ala Glu Arg Glu Thr Trp Pro Leu Gly
 165 170 175
 Arg His Leu Ala Ile Asp Ile Ser Leu Val Val Glu Arg Asn Asp Thr
 180 185 190
 Lys Ala Gln Gly Glu Met Gln Gln Thr Val Val Ala Leu Ala Arg Glu
 195 200 205
 Asn Thr Glu Arg Ala Ala Asp Gly Thr Thr Trp Trp Glu Glu Thr Ile
 210 215 220
 Glu Gln Ser Arg Glu His Ala Val Lys Val Ser Gly Glu Leu Arg Ser
 225 230 235 240
 Ala Val Arg Glu Ser Ile Glu Ile Leu Gly Asn Asp Val Leu Thr Arg
 245 250 255
 Tyr Glu Ala Lys Glu Leu Ser Thr Ala Glu Ile Asp Gly Gly Glu Leu
 260 265 270
 Ala Lys Gln Ser Leu Arg Tyr Leu Tyr Arg Ile Leu Phe Leu Leu Phe
 275 280 285
 Ala Glu Ala Ser Pro Glu Leu Glu Ile Leu Pro Thr Gly Thr Pro Glu
 290 295 300
 Tyr Asp Glu
 305

<210> 609

<211> 780

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(757)

<223> RXN01390

<400> 609

cggtccagata atcaatctgc gaagccagtg gcttccgaag ctccaacaac tattacgccg 60

gcaagctctg gtgcattagc atccgatgct ccgacgtctt atg ttc agg cgc agc 115
 Met Phe Arg Arg Ser
 1 5

ctt ccc agc aac aag aca tcc tca gca agt tcc gcc agc tcc gcc gac 163

Leu Pro Ser Asn Lys Thr Ser Ser Ala Ser Ser Ala Ser Ser Ala Asp
 10 15 20
 aca agt tac tca gtc aga tta ggc cgt cct gaa gag cct ggt tac cag 211
 Thr Ser Tyr Ser Val Arg Leu Gly Arg Pro Glu Glu Pro Gly Tyr Gln
 25 30
 cca gaa cag tct tat tgc gag cct tac act gac tct gat ttc ggc cca 259
 Pro Glu Pro Ser Tyr Ser Glu Pro Tyr Thr Asp Ser Asp Phe Ala Pro
 40 45 50
 gca ggt gcg gcc gct gcg gca gct gca gta gct cca cca atg att gcg 307
 Ala Gly Ala Ala Ala Ala Ala Ala Val Ala Pro Met Ile Ala
 55 60 65
 gaa cag cca caa att gtt gaa gat gcc cgc cga ggt acc ctc gat ttc 355
 Glu Gln Pro Gln Ile Val Glu Asp Ala Arg Gly Thr Leu Asp Phe
 70 75 80 85
 ggc ctg ttg att atc cgc gca gtc att ggt gtc tat ttg atc gtc cgt 403
 Gly Leu Leu Ile Ile Arg Ala Val Ile Gly Val Tyr Leu Ile Val Arg
 90 95 100
 gga gtc ttt aca ttc ttc acc ctt gga gga tct gcc ggt ctt gct ggc 451
 Gly Val Phe Thr Phe Phe Thr Leu Gly Gly Ser Ala Gly Leu Ala Gly
 105 110 115
 ctc gag gca gag ttc gct ggt tac cag tgg cct gaa atc ctc gcg atc 499
 Leu Glu Ala Glu Phe Ala Gly Tyr Gln Trp Pro Glu Ile Leu Ala Ile
 120 125 130
 ctg ctt cca tct att gaa ctt gcg gct ggt gtc ttc ctg ctc ctt ggt 547
 Leu Leu Pro Ser Ile Glu Leu Ala Ala Gly Val Phe Leu Leu Leu Gly
 135 140 145
 ctg atg acc cca gtg gca gca gcg gta gcc acg gtg gcg aca tcc ttt 595
 Leu Met Thr Pro Val Ala Ala Ala Val Ala Thr Val Ala Thr Ser Phe
 150 155 160 165
 acc acc ctt cac caa gtc aac act cat gaa ggt ggt tgg ggt gaa ctt 643
 Thr Thr Leu His Gln Val Asn Thr His Glu Gly Gly Trp Gly Glu Leu
 170 175 180
 agt gag cca ttg atg ctg gca ctg atc ctc act atc gtg gtt gtc gga 691
 Ser Glu Pro Leu Met Leu Ala Leu Ile Leu Thr Ile Val Val Val Gly
 185 190 195
 ctt cag ttc acc ggc ccc ggc aag att tcc ctt gac tct ggc cga ggt 739
 Leu Gln Phe Thr Gly Pro Gly Lys Ile Ser Leu Asp Ser Gly Arg Gly
 200 205 210
 tgg caa agc gtc cac tgg tgagctcgtg gatcttcgtg gtc 780
 Trp Gln Ser Val His Trp
 215

<210> 610

<211> 219

<212> FRT

<213> Corynebacterium glutamicum

<400> 610

Met Phe Arg Arg Ser Leu Pro Ser Asn Lys Thr Ser Ser Ala Ser Ser
 1 5 10 15

Ala Ser Ser Ala Asp Thr Ser Tyr Ser Val Arg Leu Gly Arg Pro Glu
 20 25 30

Glu Pro Gly Tyr Gln Pro Glu Pro Ser Tyr Ser Glu Pro Tyr Thr Asp
 35 40 45

Ser Asp Phe Ala Pro Ala Gly Ala Ala Ala Ala Ala Ala Val Ala
 50 55 60

Pro Pro Met Ile Ala Glu Gln Pro Gln Ile Val Glu Asp Ala Arg Arg
 65 70 75 80

Gly Thr Leu Asp Phe Gly Leu Leu Ile Ile Arg Ala Val Ile Gly Val
 85 90 95

Tyr Leu Ile Val Arg Gly Val Phe Thr Phe Phe Thr Leu Gly Gly Ser
 100 105 110

Ala Gly Leu Ala Gly Leu Glu Ala Glu Phe Ala Gly Tyr Gln Trp Pro
 115 120 125

Glu Ile Leu Ala Ile Leu Leu Pro Ser Ile Glu Leu Ala Ala Gly Val
 130 135 140

Phe Leu Leu Leu Gly Leu Met Thr Pro Val Ala Ala Ala Val Ala Thr
 145 150 155 160

Val Ala Thr Ser Phe Thr Thr Leu His Gln Val Asn Thr His Glu Gly
 165 170 175

Gly Trp Gly Glu Leu Ser Glu Pro Leu Met Leu Ala Leu Ile Leu Thr
 180 185 190

Ile Val Val Val Gly Leu Gln Phe Thr Gly Pro Gly Lys Ile Ser Leu
 195 200 205

Asp Ser Gly Arg Gly Trp Gln Ser Val His Trp
 210 215

<210> 611

<211> 780

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(757)

<223> FRXA01390

<400> 611

cgtccagata atcaatctgc gaagccagtg gcttccgaag ctccaacaac tattacgccg 60

gcaagctctg gtgcattagc atccgatgct ccgacgtctt atg ttc agg cgc agc 115
 Met Phe Arg Arg Ser
 1 5

ctt ccc agc aac aag aca tcc tca gca agt tcc gcc agc tcc gcc gac 163
 Leu Pro Ser Asn Lys Thr Ser Ser Ala Ser Ser Ala Ser Ser Ala Asp
 10 15 20

aca agt tac tca gtc aga tta ggc cgt cct gaa gag cct ggt tac cag 211
 Thr Ser Tyr Ser Val Arg Leu Gly Arg Pro Glu Glu Pro Gly Tyr Gln
 25 30 35

cca gaa ccg tct tat tgc gag cct tac act gac tct gat ttc gcg cca 259
 Pro Glu Pro Ser Tyr Ser Glu Pro Tyr Thr Asp Ser Asp Phe Ala Pro
 40 45 50

gca ggt gcg gcc gct gcg gca gct gca gta gct cca cca atg att gcg 307
 Ala Gly Ala Ala Ala Ala Ala Ala Val Ala Pro Pro Met Ile Ala
 55 60 65

gaa cag cca caa att gtt gaa gat gcc cgc cga ggt acc ctc gat ttc 355
 Glu Gln Pro Gln Ile Val Glu Asp Ala Arg Arg Gly Thr Leu Asp Phe
 70 75 80 85

ggc ctg ttg att atc cgc gca gtc att ggt gtc tat ttg atc gtc cgt 403
 Gly Leu Leu Ile Ile Arg Ala Val Ile Gly Val Tyr Leu Ile Val Arg
 90 95 100

gga gtc ttt aca ttc ttc acc ctt gga gga tct gcc ggt ctt gct ggc 451
 Gly Val Phe Thr Phe Phe Thr Leu Gly Gly Ser Ala Gly Leu Ala Gly
 105 110 115

ctc gag gca gag ttc gct ggt tac cag tgg cct gaa atc ctc gcg atc 499
 Leu Glu Ala Glu Phe Ala Gly Tyr Gln Trp Pro Glu Ile Leu Ala Ile
 120 125 130

ctg ctt cca tct att gaa ctt gcg gct ggt gtc ttc ctg ctc ctt ggt 547
 Leu Leu Pro Ser Ile Glu Leu Ala Ala Gly Val Phe Leu Leu Leu Gly
 135 140 145

ctg atg acc cca gtg gca gca gcg gta gcc acg gtg gcg aca tcc ttt 595
 Leu Met Thr Pro Val Ala Ala Ala Val Ala Thr Val Ala Thr Ser Phe
 150 155 160 165

acc acc ctt cac caa gtc aac act cat gaa ggt ggt tgg ggt gaa ctt 643
 Thr Thr Leu His Gln Val Asn Thr His Glu Gly Gly Trp Gly Glu Leu
 170 175 180

agt gag cca ttg atg ctg gca ctg atc ctc act atc gtg gtt gtc gga 691
 Ser Glu Pro Leu Met Leu Ala Leu Ile Leu Thr Ile Val Val Val Gly
 185 190 195

ctt cag ttc acc gcg ccc gcg aag att tcc ctt gac tct ggc cga ggt 739
 Leu Gln Phe Thr Gly Pro Gly Lys Ile Ser Leu Asp Ser Gly Arg Gly
 200 205 210

tgg caa agc gtc cac tgg tgagctcgtg gatcttcgtg gtc 780
 Trp Gln Ser Val His Trp
 215

<210> 612

<211> 219

<212> PRT

<213> Corynebacterium glutamicum

<400> 612

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Met Phe Arg Arg Ser Leu Pro Ser Asn Lys Thr Ser Ser Ala Ser Ser
 1          5          10          15

Ala Ser Ser Ala Asp Thr Ser Tyr Ser Val Arg Leu Gly Arg Pro Glu
          20          25          30

Glu Pro Gly Tyr Gln Pro Glu Pro Ser Tyr Ser Glu Pro Tyr Thr Asp
          35          40          45

Ser Asp Phe Ala Pro Ala Gly Ala Ala Ala Ala Ala Val Ala
 50          55          60

Pro Pro Met Ile Ala Glu Gln Pro Gln Ile Val Glu Asp Ala Arg Arg
 65          70          75          80

Gly Thr Leu Asp Phe Gly Leu Leu Ile Ile Arg Ala Val Ile Gly Val
          85          90          95

Tyr Leu Ile Val Arg Gly Val Phe Thr Phe Phe Thr Leu Gly Gly Ser
          100          105          110

Ala Gly Leu Ala Gly Leu Glu Ala Glu Phe Ala Gly Tyr Gln Trp Pro
          115          120          125

Glu Ile Leu Ala Ile Leu Leu Pro Ser Ile Glu Leu Ala Ala Gly Val
          130          135          140

Phe Leu Leu Leu Gly Leu Met Thr Pro Val Ala Ala Val Ala Thr
          145          150          155          160

Val Ala Thr Ser Phe Thr Thr Leu His Gln Val Asn Thr His Glu Gly
          165          170          175

Gly Trp Gly Glu Leu Ser Glu Pro Leu Met Leu Ala Leu Ile Leu Thr
          180          185          190

Ile Val Val Val Gly Leu Gln Phe Thr Gly Pro Gly Lys Ile Ser Leu
          195          200          205

Asp Ser Gly Arg Gly Trp Gln Ser Val His Trp
          210          215

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<210> 613

<211> 813

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(790)

<223> RXN01391

<400> 613

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aaagtgtaaa agtgtaatat ccagcatcat cagcattgcc  gtg gct gca gtc gct 115
                                     Val Ala Ala Val Ala
                                     1          5

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ttt gca gct tac gtt ata gat ggt ggg gta gaa gag gcg tct gga aca 163
 Phe Ala Ala Tyr Val Ile Asp Gly Gly Val Glu Glu Ala Ser Gly Thr
 10 15 20

ccg acg tct tcg gaa agc tcg gta gcg gca act gct cca gcg gca tct 211
 Pro Thr Ser Ser Glu Ser Ser Val Ala Ala Thr Ala Pro Ala Ala Ser
 25 30 35

agc gag act gcg gct gaa tac cgt gcg atg ctc gct tcc ctt gac gtt 259
 Ser Glu Thr Ala Ala Glu Tyr Arg Ala Met Leu Ala Ser Leu Asp Val
 40 45 50

aaa ggt cgt gcg cca gga aca gga tat gac gcg gaa tta ttc gga cca 307
 Lys Gly Arg Ala Pro Gly Thr Gly Tyr Asp Arg Glu Leu Phe Gly Pro
 55 60 65

gca tgg acc gac act gtt tcc gtg gaa tat gga cac aat gcc tgc gat 355
 Ala Trp Thr Asp Thr Val Ser Val Glu Tyr Gly His Asn Gly Cys Asp
 70 75 80 85

acc gcg aac gac atc ctg caa gcg gac ctg gat gac atc caa ctt gcg 403
 Thr Arg Asn Asp Ile Leu Gln Arg Asp Leu Asp Asp Ile Gln Leu Arg
 90 95 100

gaa ggc acc aag gat tgt atc gtc acg agc ggc ctg ctc agc gat cca 451
 Glu Gly Thr Lys Asp Cys Ile Val Thr Ser Gly Leu Leu Ser Asp Pro
 105 110 115

ttt tct ggc gaa ctt att gat ttc gtt gcg ggt gaa cgt tcc gcc gac 499
 Phe Ser Gly Glu Leu Ile Asp Phe Val Arg Gly Glu Arg Ser Gly Asp
 120 125 130

gtg cag atc gat cac ctg gtc cca tta cat gac gca tgg gtc aag gga 547
 Val Gln Ile Asp His Leu Val Pro Leu His Asp Ala Trp Val Lys Gly
 135 140 145

gca cag cag tgg gat gag caa act cga aag aac ttt gcc aac gat ccc 595
 Ala Gln Gln Trp Asp Glu Gln Thr Arg Lys Asn Phe Ala Asn Asp Pro
 150 155 160 165

gac aac ctt ctc gcc gtt aaa ggt acg ctt aac cag caa aaa ggt gca 643
 Asp Asn Leu Leu Ala Val Lys Gly Thr Leu Asn Gln Gln Lys Gly Ala
 170 175 180

gcc gat gca gca acc tgg ctt cca cca aac aca gct ttt agg tgc gat 691
 Gly Asp Ala Ala Thr Trp Leu Pro Pro Asn Thr Ala Phe Arg Cys Asp
 185 190 195

tac gca aag aaa atc atc acc gtt aaa gat gcg tac aac gtg tgg gtg 739
 Tyr Ala Lys Lys Ile Ile Thr Val Lys Asp Arg Tyr Asn Val Trp Val
 200 205 210

act gag gct gaa gca agc gcc ctg gaa gcg caa tta gat acg tgt gct 787
 Thr Glu Ala Glu Ala Ser Ala Leu Glu Arg Gln Leu Asp Thr Cys Ala
 215 220 225

gca taacagtcac ataagcattt ggg 813
 Ala
 230

<210> 614
 <211> 230
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 614
 Val Ala Ala Val Ala Phe Ala Ala Tyr Val Ile Asp Gly Gly Val Glu
 1 5 10 15
 Glu Ala Ser Gly Thr Pro Thr Ser Ser Glu Ser Ser Val Ala Ala Thr
 20 25 30
 Ala Pro Ala Ala Ser Ser Glu Thr Ala Ala Glu Tyr Arg Ala Met Leu
 35 40 45
 Ala Ser Leu Asp Val Lys Gly Arg Ala Pro Gly Thr Gly Tyr Asp Arg
 50 55 60
 Glu Leu Phe Gly Pro Ala Trp Thr Asp Thr Val Ser Val Glu Tyr Gly
 65 70 75 80
 His Asn Gly Cys Asp Thr Arg Asn Asp Ile Leu Gln Arg Asp Leu Asp
 85 90
 Asp Ile Gln Leu Arg Glu Gly Thr Lys Asp Cys Ile Val Thr Ser Gly
 100 105 110
 Leu Leu Ser Asp Pro Phe Ser Gly Glu Leu Ile Asp Phe Val Arg Gly
 115 120 125
 Glu Arg Ser Gly Asp Val Gln Ile Asp His Leu Val Pro Leu His Asp
 130 135 140
 Ala Trp Val Lys Gly Ala Gln Gln Trp Asp Glu Gln Thr Arg Lys Asn
 145 150 155 160
 Phe Ala Asn Asp Pro Asp Asn Leu Leu Ala Val Lys Gly Thr Leu Asn
 165 170 175
 Gln Gln Lys Gly Ala Gly Asp Ala Ala Thr Trp Leu Pro Pro Asn Thr
 180 185 190
 Ala Phe Arg Cys Asp Tyr Ala Lys Lys Ile Ile Thr Val Lys Asp Arg
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 Tyr Asn Val Trp Val Thr Glu Ala Glu Ala Ser Ala Leu Glu Arg Gln
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 <222> (101)..(790)

<223> FRXA01391

<400> 615

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 Val Ala Ala Val Ala
 1 5

ttt gca gct tac gtt ata gat ggt ggg gta gaa gag gcg tct gga aca 163
 Phe Ala Ala Tyr Val Ile Asp Gly Gly Val Glu Glu Ala Ser Gly Thr
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ccg acg tct tcg gaa agc tcg gta gcg gca act gct cca gcg gca tot 211
 Pro Thr Ser Ser Glu Ser Ser Val Ala Ala Thr Ala Pro Ala Ala Ser
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agc gag act gcg gct gaa tac cgt gcg atg ctc gct tcc ctt gac gtt 259
 Ser Glu Thr Ala Ala Glu Tyr Arg Ala Met Leu Ala Ser Leu Asp Val
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aaa ggt cgt gcg cca gga aca gga tat gac cgc gaa tta ttc gga cca 307
 Lys Gly Arg Ala Pro Gly Thr Gly Tyr Asp Arg Glu Leu Phe Gly Pro
 55 60 65

gca tgg acc gac act gtt tcc gtg gaa tat gga cac aat ggc tgc gat 355
 Ala Trp Thr Asp Thr Val Ser Val Glu Tyr Gly His Asn Gly Cys Asp
 70 75 80 85

acc cgc aac gac atc ctg caa cgc gac ctg gat gac atc caa ctt cgc 403
 Thr Arg Asn Asp Ile Leu Gln Arg Asp Leu Asp Asp Ile Gln Leu Arg
 90 95 100

gaa ggc acc aag gat tgt atc gtc acg agc ggc ctg ctc agc gat cca 451
 Glu Gly Thr Lys Asp Cys Ile Val Thr Ser Gly Leu Leu Ser Asp Pro
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 Phe Ser Gly Glu Leu Ile Asp Phe Val Arg Gly Glu Arg Ser Gly Asp
 120 125 130

gtg cag atc gat cac ctg gtc cca tta cat gac gca tgg gtc aag gga 547
 Val Gln Ile Asp His Leu Val Pro Leu His Asp Ala Trp Val Lys Gly
 135 140 145

gca cag cag tgg gat gag caa act cga aag aac ttt gcc aac gat ccc 595
 Ala Gln Gln Trp Asp Glu Gln Thr Arg Lys Asn Phe Ala Asn Asp Pro
 150 155 160 165

gac aac ctt ctc gcc gtt aaa ggt acg ctt aac cag caa aaa ggt gca 643
 Asp Asn Leu Leu Ala Val Lys Gly Thr Leu Asn Gln Gln Lys Gly Ala
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ggc gat gca gca acc tgg ctt cca cca aac aca gct ttt agg tgc gat 691
 Gly Asp Ala Ala Thr Trp Leu Pro Pro Asn Thr Ala Phe Arg Cys Asp
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tac gca aag aaa atc atc acc gtt aaa gat cgc tac aac gtg tgg gtg 739
 Tyr Ala Lys Lys Ile Ile Thr Val Lys Asp Arg Tyr Asn Val Trp Val
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act gag gct gaa gca agc gcc ctg gaa cgc caa tta gat acg tgt gct 787
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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 616

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Ala Ser Leu Asp Val Lys Gly Arg Ala Pro Gly Thr Gly Tyr Asp Arg
 50 55 60

Glu Leu Phe Gly Pro Ala Trp Thr Asp Thr Val Ser Val Glu Tyr Gly
 65 70 75 80

His Asn Gly Cys Asp Thr Arg Asn Asp Ile Leu Gln Arg Asp Leu Asp
 85 90 95

Asp Ile Gln Leu Arg Glu Gly Thr Lys Asp Cys Ile Val Thr Ser Gly
 100 105 110

Leu Leu Ser Asp Pro Phe Ser Gly Glu Leu Ile Asp Phe Val Arg Gly
 115 120 125

Glu Arg Ser Gly Asp Val Gln Ile Asp His Leu Val Pro Leu His Asp
 130 135 140

Ala Trp Val Lys Gly Ala Gln Gln Trp Asp Glu Gln Thr Arg Lys Asn
 145 150 155 160

Phe Ala Asn Asp Pro Asp Asn Leu Leu Ala Val Lys Gly Thr Leu Asn
 165 170 175

Gln Gln Lys Gly Ala Gly Asp Ala Ala Thr Trp Leu Pro Pro Asn Thr
 180 185 190

Ala Phe Arg Cys Asp Tyr Ala Lys Lys Ile Ile Thr Val Lys Asp Arg
 195 200 205

Tyr Asn Val Trp Val Thr Glu Ala Glu Ala Ser Ala Leu Glu Arg Gln
 210 215 220

Leu Asp Thr Cys Ala Ala
 225 230

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				Met	Ala	Ile	Ser	Val									211		
				1				5									259		
tct	atg	cct	aag	gcg	atc	agc	cgt	gag	gaa	ttg	gag	cgc	gcg	tgg	ctt			307	
Ser	Met	Pro	Lys	Ala	Ile	Ser	Arg	Glu	Glu	Leu	Glu	Arg	Ala	Trp	Leu			355	
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gaa	gtg	att	gaa	cg	cac	ggc	acc	ttg	cg	aca	gta	ttt	agc	acg	gga			451	
Glu	Val	Ile	Glu	Arg	His	Gly	Thr	Leu	Arg	Thr	Val	Phe		Ser	Thr	Gly			499
				25				30					35					547	
atg	ggt	ggg	gaa	gtg	cag	caa	cac	cg	att	gat	gtg	ggc	ccg	gga	aaa			595	
Met	Gly	Gly	Glu	Val	Gln	Gln	His	Arg	Ile	Asp	Val	Gly	Pro	Gly	Lys			643	
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Trp	Ile	Asp	His	Ala	Val	Ala	Pro	Gly	Glu	Ser	Ile	Asn	Glu	Ala	Leu				
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cgg	gcg	gtg	ttg	aat	cgg	cag	tgt	tcg	ccg	tac	tcg	agg	cca	tcg	cat				
Arg	Ala	Val	Leu	Asn	Arg	Gln	Cys	Ser	Pro	Tyr	Ser	Arg	Pro	Ser	His				
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agt	ttg	tgc	att	att	gat	gcg	cat	ccg	cgt	ccc	acg	gtg	att	att	ggt				
Ser	Leu	Cys	Ile	Ile	Asp	Ala	His	Pro	Arg	Pro	Thr	Val	Ile	Ile	Gly				
				90					95					100					
agt	gat	cat	tcg	cat	gtg	gat	atg	tgg	tcc	atg	ctg	gtg	att	gtg	cg				
Ser	Asp	His	Ser	His	Val	Asp	Met	Trp	Ser	Met	Leu	Val	Ile	Val	Arg				
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gat	ttg	ttg	gct	gcg	ctc	gat	atg	gaa	ctt	ccc	gtt	gag	ccg	ccg	ttg				
Asp	Leu	Leu	Ala	Ala	Leu	Asp	Met	Glu	Leu	Pro	Val	Glu	Pro	Pro	Leu				
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gcg	ttt	gaa	tcg	cac	acc	gcg	gaa	ctc	ctc	gcg	gct	cca	cct	gca	ccg				
Ala	Phe	Glu	Ser	His	Thr	Ala	Glu	Leu	Leu	Ala	Ala	Pro	Arg	Ala	Pro				
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gaa cgc gtt gaa gtc cgc gac att ttc ggg gtc aat ggc ttg gcg att 691
 Glu Arg Val Glu Val Arg Asp Ile Phe Gly Val Asn Gly Leu Ala Ile
 185 190 195

tac tcg gca cgc gcc cgc gca caa cag gta agc tcc ctg gcc ttg act 739
 Tyr Ser Ala Arg Ala Arg Ala Gln Gln Val Ser Ser Leu Ala Leu Thr
 200 205 210

att tca gtg atg gct gat gtt acg gcg gcg ctg gcg gac ctt ccg ttg 787
 Ile Ser Val Met Ala Asp Val Thr Ala Ala Leu Ala Asp Leu Pro Leu
 215 220 225

cgt gct gta ttc cca gtc cat agc cgt ttc gat cag cgc tgg cac gat 835
 Arg Ala Val Phe Pro Val His Ser Arg Phe Asp Gln Arg Trp His Asp
 230 235 240 245

agt gtc ggg tgg ttt atc tcc aat tcg gtc att gag gtg cca gat tcc 883
 Ser Val Gly Trp Phe Ile Ser Asn Ser Val Ile Glu Val Pro Asp Ser
 250 255 260

gat cct cac act gca gcc caa gct gtt cgc gag gct gtt tct ttg gga 931
 Asp Pro His Thr Ala Ala Gln Ala Val Arg Glu Ala Val Ser Leu Gly
 265 270 275

agc tac ccg ctg gct gag ctg ctt gaa ccg tgg ggt ggc atg ccg gaa 979
 Ser Tyr Pro Leu Ala Glu Leu Glu Pro Trp Gly Gly Met Pro Glu
 280 285 290

acg cca gga atg ttt gct att tct tgg ctt gac ctg cgc cga ctc cca 1027
 Thr Pro Gly Met Phe Ala Ile Ser Trp Leu Asp Leu Arg Arg Leu Pro
 295 300 305

gtg agc att gac gat att ggc ctc caa gcc cag tat gtc agc gct tca 1075
 Val Ser Ile Asp Asp Ile Gly Leu Gln Ala Gln Tyr Val Ser Ala Ser
 310 315 320 325

ctg cgc acc gat ggt gtg atg ctg tgg ttt att ttg gat cgc tcc ggc 1123
 Leu Arg Thr Asp Gly Val Met Leu Trp Phe Ile Leu Asp Arg Ser Gly
 330 335 340

gcg cac ctt cgc tgt cgt tat cct gac tct ttg gtg gcg cgg gaa aat 1171
 Ala His Leu Arg Cys Arg Tyr Pro Asp Ser Leu Val Ala Arg Glu Asn
 345 350 355

gta ggc cgc tgg att gat gcg att gtt gct cag atg cgc gcc gaa gct 1219
 Val Gly Arg Trp Ile Asp Ala Ile Val Ala Gln Met Arg Ala Glu Ala
 360 365 370

ggg acg gtg aat ctg cag gcc gcc ggg gaa cag ctg aca ctt cgg cat 1267
 Gly Thr Val Asn Leu Gln Ala Gly Gly Glu Gln Leu Thr Leu Arg His
 375 380 385

gga act cgc gcc gat att tcc gag atc gcc ccg cta ctt gcc cga aac 1315
 Gly Thr Arg Ala Asp Ile Ser Glu Ile Ala Pro Leu Leu Ala Arg Asn
 390 395 400 405

gca gct gac cct tgt gag ctg gtg gat ctt gaa cat gcc ctt gac ctg 1363
 Ala Ala Asp Pro Cys Glu Leu Val Asp Leu Glu His Ala Leu Asp Leu
 410 415 420

ctg aca cac gag tct tcg cat ttc ctg gcg gtg gtt cga aac gct cgt 1411

Leu Thr His Glu Ser Ser His Phe Leu Ala Val Val Arg Asn Ala Arg
 425 430 435
 ggc aag ata atc gca gcg atg cag ttg act att gtt ccg gag ttt tcc 1459
 Gly Lys Ile Ile Ala Ala Met Gln Leu Thr Ile Val Pro Glu Phe Ser
 440 445 450
 cgc ggt ggt gcg ctt cat ctt cac atc gag ggg ccg ttc att att ccg 1507
 Arg Gly Gly Ala Leu His Leu His Ile Glu Gly Pro Phe Ile Ile Pro
 455 460 465
 gaa tat cgc acc acc gat ttg gat aaa aag ctg cgc gcc tgg gct gtg 1555
 Glu Tyr Arg Thr Thr Asp Leu Asp Lys Lys Leu Arg Ala Trp Ala Val
 470 475 480 485
 gag cat ggg cgt gcg cga ggg gtg aag gtt gag gag gtg gtg gga 1600
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<211> 500

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 618

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Val Phe Ser Thr Gly Met Gly Gly Glu Val Gln Gln His Arg Ile Asp
 35 40 45

Val Gly Pro Gly Lys Trp Ile Asp His Ala Val Ala Pro Gly Glu Ser
 50 55 60

Ile Asn Glu Ala Leu Arg Ala Val Leu Asn Arg Gln Cys Ser Pro Tyr
 65 70 75 80

Ser Arg Pro Ser His Ser Leu Cys Ile Ile Asp Ala His Pro Arg Pro
 85 90 95

Thr Val Ile Ile Gly Ser Asp His Ser His Val Asp Met Trp Ser Met
 100 105 110

Leu Val Ile Val Arg Asp Leu Leu Ala Ala Leu Asp Met Glu Leu Pro
 115 120 125

Val Glu Pro Pro Leu Ala Phe Glu Ser His Thr Ala Glu Leu Leu Ala
 130 135 140

Ala Pro Pro Ala Pro Glu Arg Ile His Gln Arg Trp Arg Glu Ile Leu
 145 150 155 160

Glu Ala Gly Gly Gly Lys Met Pro Gln Phe Pro Leu Pro Leu Gly Asp
 165 170 175

Ala Ile Ser Met Pro Glu Arg Val Glu Val Arg Asp Ile Phe Gly Val
 180 185 190
 Asn Gly Leu Ala Ile Tyr Ser Ala Arg Ala Arg Ala Gln Gln Val Ser
 195 200 205
 Ser Leu Ala Leu Thr Ile Ser Val Met Ala Asp Val Thr Ala Ala Leu
 210 215 220
 Ala Asp Leu Pro Leu Arg Ala Val Phe Pro Val His Ser Arg Phe Asp
 225 230 235 240
 Gln Arg Trp His Asp Ser Val Gly Trp Phe Ile Ser Asn Ser Val Ile
 245 250 255
 Glu Val Pro Asp Ser Asp Pro His Thr Ala Ala Gln Ala Val Arg Glu
 260 265 270
 Ala Val Ser Leu Gly Ser Tyr Pro Leu Ala Glu Leu Leu Glu Pro Trp
 275 280 285
 Gly Gly Met Pro Glu Thr Pro Gly Met Phe Ala Ile Ser Trp Leu Asp
 290 295 300
 Leu Arg Arg Leu Pro Val Ser Ile Asp Asp Ile Gly Leu Gln Ala Gln
 305 310 315 320
 Tyr Val Ser Ala Ser Leu Arg Thr Asp Gly Val Met Leu Trp Phe Ile
 325 330 335
 Leu Asp Arg Ser Gly Ala His Leu Arg Cys Arg Tyr Pro Asp Ser Leu
 340 345 350
 Val Ala Arg Glu Asn Val Gly Arg Trp Ile Asp Ala Ile Val Ala Gln
 355 360 365
 Met Arg Ala Glu Ala Gly Thr Val Asn Leu Gln Ala Gly Gly Glu Gln
 370 375 380
 Leu Thr Leu Arg His Gly Thr Arg Ala Asp Ile Ser Glu Ile Ala Pro
 385 390 395 400
 Leu Leu Ala Arg Asn Ala Ala Asp Pro Cys Glu Leu Val Asp Leu Glu
 405 410 415
 His Ala Leu Asp Leu Leu Thr His Glu Ser Ser His Phe Leu Ala Val
 420 425 430
 Val Arg Asn Ala Arg Gly Lys Ile Ile Ala Ala Met Gln Leu Thr Ile
 435 440 445
 Val Pro Glu Phe Ser Arg Gly Gly Ala Leu His Leu His Ile Glu Gly
 450 455 460
 Pro Phe Ile Ile Pro Glu Tyr Arg Thr Thr Asp Leu Asp Lys Lys Leu
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<211> 1623

<212> DNA

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<222> (101)..(1600)

<223> FRXA01400

<400> 619

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                                         Met Ala Ile Ser Val
                                         1 5

tct atg cct aag gcg atc agc cgt gag gaa ttg gag cgc gcg tgg ctt 163
Ser Met Pro Lys Ala Ile Ser Arg Glu Glu Leu Glu Arg Ala Trp Leu
                        10 15 20

gaa gtg att gaa cgg cac gcc acc ttg cgc aca gta ttt agc acg gga 211
Glu Val Ile Glu Arg His Gly Thr Leu Arg Thr Val Phe Ser Thr Gly
                        25 30 35

atg ggt ggg gaa gtg cag caa cac cgc att gat gtg gcc ccg gga aaa 259
Met Gly Gly Glu Val Gln Gln His Arg Ile Asp Val Gly Pro Gly Lys
                        40 45 50

tgg att gac cac gcc gtt gcg cct ggt gag agc att aat gag gcg ttg 307
Trp Ile Asp His Ala Val Ala Pro Gly Glu Ser Ile Asn Glu Ala Leu
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cgg gcg gtg ttg aat cgg cag tgt tgc ccg tac tgc agg cca tgc cat 355
Arg Ala Val Leu Asn Arg Gln Cys Ser Pro Tyr Ser Arg Pro Ser His
                        70 75 80 85

agt ttg tgc att att gat gcg cat ccg cgt ccc acg gtg att att ggt 403
Ser Leu Cys Ile Ile Asp Ala His Pro Arg Pro Thr Val Ile Ile Gly
                        90 95 100

agt gat cat tgc cat gtg gat atg tgg tcc atg ctg gtg att gtg cgc 451
Ser Asp His Ser His Val Asp Met Trp Ser Met Leu Val Ile Val Arg
                        105 110 115

gat ttg ttg gct gcg ctc gat atg gaa ctt ccc gtt gag ccg ccg ttg 499
Asp Leu Leu Ala Ala Leu Asp Met Glu Leu Pro Val Glu Pro Pro Leu
                        120 125 130

gcg ttt gaa tgc cac acc gcg gaa ctc ctc gcg gct cca cct gca ccg 547
Ala Phe Glu Ser His Thr Ala Glu Leu Leu Ala Ala Pro Pro Ala Pro
                        135 140 145

gag cgg att cac cag cgg tgg cgt gaa att ttg gaa gct ggt ggt gga 595
Glu Arg Ile His Gln Arg Trp Arg Glu Ile Leu Glu Ala Gly Gly Gly
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aaa atg cct cag ttc ccg ctt ccg ctt gcc gat gcc atc tcc atg cct 643

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Glu	Arg	Val	Glu	Val	Arg	Asp	Ile	Phe	Gly	Val	Asn	Gly	Leu	Ala	Ile	
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tac	tcg	gca	cgc	gcc	cgc	gca	caa	cag	gta	agc	tcc	ctg	gcc	ttg	act	739
Tyr	Ser	Ala	Arg	Ala	Arg	Ala	Gln	Gln	Val	Ser	Ser	Leu	Ala	Leu	Thr	
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Ile	Ser	Val	Met	Ala	Asp	Val	Thr	Ala	Ala	Leu	Ala	Asp	Leu	Pro	Leu	
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cgt	gct	gta	ttc	cca	gtc	cat	agc	cgt	ttc	gat	cag	cgc	tgg	cac	gat	835
Arg	Ala	Val	Phe	Pro	Val	His	Ser	Arg	Phe	Asp	Gln	Arg	Trp	His	Asp	
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agt	gtc	ggg	tgg	ttt	atc	tcc	aat	tcg	gtc	att	gag	gtg	cca	gat	tcc	883
Ser	Val	Gly	Trp	Phe	Ile	Ser	Asn	Ser	Val	Ile	Glu	Val	Pro	Asp	Ser	
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gat	cct	cac	act	gca	gcc	caa	gct	gtt	cgc	gag	gct	gtt	tct	ttg	gga	931
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Ser	Tyr	Pro	Leu	Ala	Glu	Leu	Leu	Glu	Pro	Trp	Gly	Gly	Met	Pro	Glu	
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acg	cca	gga	atg	ttt	gct	att	tct	tgg	ctt	gac	ctg	cgc	cga	ctc	cca	1027
Thr	Pro	Gly	Met	Phe	Ala	Ile	Ser	Trp	Leu	Asp	Leu	Arg	Arg	Leu	Pro	
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Val	Ser	Ile	Asp	Asp	Ile	Gly	Leu	Gln	Ala	Gln	Tyr	Val	Ser	Ala	Ser	
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ctg	cgc	acc	gat	ggt	gtg	atg	ctg	tgg	ttt	att	ttg	gat	cgc	tcc	ggc	1123
Leu	Arg	Thr	Asp	Gly	Val	Met	Leu	Trp	Phe	Ile	Leu	Asp	Arg	Ser	Gly	
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gcg	cac	ctt	cgc	tgt	cgt	tat	cct	gac	tct	ttg	gtg	gcg	cgg	gaa	aat	1171
Ala	His	Leu	Arg	Cys	Arg	Tyr	Pro	Asp	Ser	Leu	Val	Ala	Arg	Glu	Asn	
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Val	Gly	Arg	Trp	Ile	Asp	Ala	Ile	Val	Ala	Gln	Met	Arg	Ala	Glu	Ala	
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ggg	acg	gtg	aat	ctg	cag	gcc	ggc	ggg	gaa	cag	ctg	aca	ctt	cgg	cat	1267
Gly	Thr	Val	Asn	Leu	Gln	Ala	Gly	Gly	Glu	Gln	Leu	Thr	Leu	Arg	His	
			375			380					385					
gga	act	cgc	gcc	gat	att	tcc	gag	atc	gcc	ccg	cta	ctt	gcc	cga	aac	1315
Gly	Thr	Arg	Ala	Asp	Ile	Ser	Glu	Ile	Ala	Pro	Leu	Leu	Ala	Arg	Asn	
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gca	gct	gac	cct	tgt	gag	ctg	gtg	gat	ctt	gaa	cat	gcc	ctt	gac	ctg	1363
Ala	Ala	Asp	Pro	Cys	Glu	Leu	Val	Asp	Leu	Glu	His	Ala	Leu	Asp	Leu	

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Leu Thr His Glu Ser Ser His Phe Leu Ala Val Val Arg Asn Ala Arg				
	425	430	435	
ggc aag ata atc gca gcg atg cag ttg act att gtt ccg gag ttt tcc				1459
Gly Lys Ile Ile Ala Ala Met Gln Leu Thr Ile Val Pro Glu Phe Ser				
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cgc ggt ggt gcg ctt cat ctt cac atc gag ggg ccg ttc att att ccg				1507
Arg Gly Glu Ala Leu His Leu His Ile Glu Gly Pro Phe Ile Ile Pro				
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gaa tat cgc acc acc gat ttg gat aaa aag ctg cgc gcc tgg gct gtg				1555
Glu Tyr Arg Thr Thr Asp Leu Asp Lys Lys Leu Arg Ala Trp Ala Val				
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Val Gly Pro Gly Lys Trp Ile Asp His Ala Val Ala Pro Gly Glu Ser				
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65 70 75 80				
Ser Arg Pro Ser His Ser Leu Cys Ile Ile Asp Ala His Pro Arg Pro				
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Thr Val Ile Ile Gly Ser Asp His Ser His Val Asp Met Trp Ser Met				
100 105 110				
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115 120 125				
Val Glu Pro Pro Leu Ala Phe Glu Ser His Thr Ala Glu Leu Leu Ala				
130 135 140				
Ala Pro Pro Ala Pro Glu Arg Ile His Gln Arg Trp Arg Glu Ile Leu				
145 150 155 160				

Glu Ala Gly Gly Lys Met Pro Gln Phe Pro Leu Pro Leu Gly Asp
 165 170 175
 Ala Ile Ser Met Pro Glu Arg Val Glu Val Arg Asp Ile Phe Gly Val
 180 185 190
 Asn Gly Leu Ala Ile Tyr Ser Ala Arg Ala Arg Ala Gln Gln Val Ser
 195 200 205
 Ser Leu Ala Leu Thr Ile Ser Val Met Ala Asp Val Thr Ala Ala Leu
 210 215 220
 Ala Asp Leu Pro Leu Arg Ala Val Phe Pro Val His Ser Arg Phe Asp
 225 230 235 240
 Gln Arg Trp His Asp Ser Val Gly Trp Phe Ile Ser Asn Ser Val Ile
 245 250 255
 Glu Val Pro Asp Ser Asp Pro His Thr Ala Ala Gln Ala Val Arg Glu
 260 265 270
 Ala Val Ser Leu Gly Ser Tyr Pro Leu Ala Glu Leu Leu Glu Pro Trp
 275 280 285
 Gly Gly Met Pro Glu Thr Pro Gly Met Phe Ala Ile Ser Trp Leu Asp
 290 295 300
 Leu Arg Arg Leu Pro Val Ser Ile Asp Asp Ile Gly Leu Gln Ala Gln
 305 310 315 320
 Tyr Val Ser Ala Ser Leu Arg Thr Asp Gly Val Met Leu Trp Phe Ile
 325 330 335
 Leu Asp Arg Ser Gly Ala His Leu Arg Cys Arg Tyr Pro Asp Ser Leu
 340 345 350
 Val Ala Arg Glu Asn Val Gly Arg Trp Ile Asp Ala Ile Val Ala Gln
 355 360 365
 Met Arg Ala Glu Ala Gly Thr Val Asn Leu Gln Ala Gly Gly Glu Gln
 370 375 380
 Leu Thr Leu Arg His Gly Thr Arg Ala Asp Ile Ser Glu Ile Ala Pro
 385 390 395 400
 Leu Leu Ala Arg Asn Ala Ala Asp Pro Cys Glu Leu Val Asp Leu Glu
 405 410 415
 His Ala Leu Asp Leu Leu Thr His Glu Ser Ser His Phe Leu Ala Val
 420 425 430
 Val Arg Asn Ala Arg Gly Lys Ile Ile Ala Ala Met Gln Leu Thr Ile
 435 440 445
 Val Pro Glu Phe Ser Arg Gly Gly Ala Leu His Leu His Ile Glu Gly
 450 455 460
 Pro Phe Ile Ile Pro Glu Tyr Arg Thr Thr Asp Leu Asp Lys Lys Leu
 465 470 475 480
 Arg Ala Trp Ala Val Glu His Gly Arg Ala Arg Gly Val Lys Val Glu

485

490

495

Glu Val Val Gly
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<210> 621

<211> 845

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

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<223> RXN01409

<400> 621

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cag ctg acc cct cat gta gat ttc ggt cct ttc ttc cgc cac ccc aag 96
Gln Leu Thr Pro His Val Asp Phe Gly Pro Phe Phe Arg His Pro Lys
20 25 30

gca gac gat gat ctc gtg gca gcc ctg aaa aag cgt gcc aag gat gcc 144
Ala Asp Asp Asp Leu Val Ala Ala Leu Lys Lys Arg Ala Lys Asp Ala
35 40 45

gga gtc acc att cct gca ctg ttg cca gtg cag cgt att tcc tgg ccg 192
Gly Val Thr Ile Pro Ala Leu Leu Pro Val Gln Arg Ile Ser Trp Pro
50 55 60

gag gaa acc cag cgt gtt gca gca gta cgc aac atc aag cgc atc atc 240
Glu Glu Thr Gln Arg Val Ala Ala Val Arg Asn Ile Lys Arg Ile Ile
65 70 75 80

cag ttg gcc gtt gat ctg gaa gta gac acc ctc aac acg gag ttt tct 289
Gln Leu Ala Val Asp Leu Glu Val Asp Thr Leu Asn Thr Glu Phe Ser
85 90 95

gga cgc cca gaa cgc tcc gag gat tcc gaa gat gcc ttc tac cgc tcc 336
Gly Arg Pro Glu Arg Ser Glu Asp Ser Glu Asp Ala Phe Tyr Arg Ser
100 105 110

atg gaa gaa ctc ctg cca atc ctg gaa aaa gag ggc atc aag ttc aac 384
Met Glu Glu Leu Leu Pro Ile Leu Glu Lys Glu Gly Ile Lys Phe Asn
115 120 125

atc gac cca cac cct gat gat ttc gtg gaa aac ggt att gaa gca tgg 432
Ile Asp Pro His Pro Asp Asp Phe Val Glu Asn Gly Ile Glu Ala Trp
130 135 140

cga gtc atc cgc ggt ctg aac tcc aag cag gtg ggc ttt gtt tac gtg 480
Arg Val Ile Arg Gly Leu Asn Ser Lys Gln Val Gly Phe Val Tyr Val
145 150 155 160

gca cct cac tca ttc cac atg ggt gat cag gct gag gca atc ctg cca 528
Ala Pro His Ser Phe His Met Gly Asp Gln Ala Glu Ala Ile Leu Pro
165 170 175

gca gta ggc gat cgc ctt ggg gct gtg tac ctg tca gat acc ttc gac 576
 Ala Val Gly Asp Arg Leu Gly Ala Val Tyr Leu Ser Asp Thr Phe Asp
 180 185 190

cac cac aaa tcc cac ggc ctg cgc tac atc act aac cct cca ggc aac 624
 His His Lys Ser His Gly Leu Arg Tyr Ile Thr Asn Pro Pro Gly Asn
 195 200 205

gca gtg cgc gtg cac cag cac cta aaa atc ggt gat ggc gat gtg aac 672
 Ala Val Arg Val His Gln His Leu Lys Ile Gly Asp Gly Asp Val Asn
 210 215 220

ttt gaa gag atc ttc tca ctg ctg cgc tct acc ggt tac ctt gac cgt 720
 Phe Glu Glu Ile Phe Ser Leu Leu Arg Ser Thr Gly Tyr Leu Asp Arg
 225 230 235 240

gaa gat gca ctg ttg gtc tcc aac gtg ttt gca gaa gat gaa gca gca 768
 Glu Asp Ala Leu Leu Val Ser Asn Val Phe Ala Glu Asp Glu Ala Ala
 245 250 255

gat gaa gta tcc cgc tac cag ctg gag aaa atc cgc tca ctc atc gaa 816
 Asp Glu Val Ser Arg Tyr Gln Leu Glu Lys Ile Arg Ser Leu Ile Glu
 260 265 270

aac gca tagagttatc tcgaaactac caa 845
 Asn Ala

<210> 622
 <211> 274
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 622
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 35 40 45
 Gly Val Thr Ile Pro Ala Leu Leu Pro Val Gln Arg Ile Ser Trp Pro
 50 55 60
 Glu Glu Thr Gln Arg Val Ala Ala Val Arg Asn Ile Lys Arg Ile Ile
 65 70 75 80
 Gln Leu Ala Val Asp Leu Glu Val Asp Thr Leu Asn Thr Glu Phe Ser
 85 90 95
 Gly Arg Pro Glu Arg Ser Glu Asp Ser Glu Asp Ala Phe Tyr Arg Ser
 100 105 110
 Met Glu Glu Leu Leu Pro Ile Leu Glu Lys Glu Gly Ile Lys Phe Asn
 115 120 125
 Ile Asp Pro His Pro Asp Asp Phe Val Glu Asn Gly Ile Glu Ala Trp
 130 135 140

Arg Val Ile Arg Gly Leu Asn Ser Lys Gln Val Gly Phe Val Tyr Val
145 150 155 160

Ala Pro His Ser Phe His Met Gly Asp Gln Ala Glu Ala Ile Leu Pro
165 170 175

Ala Val Gly Asp Arg Leu Gly Ala Val Tyr Leu Ser Asp Thr Phe Asp
180 185 190

His His Lys Ser His Gly Leu Arg Tyr Ile Thr Asn Pro Pro Gly Asn
195 200 205

Ala Val Arg Val His Gln His Leu Lys Ile Gly Asp Gly Asp Val Asn
210 215 220

Phe Glu Glu Ile Phe Ser Leu Leu Arg Ser Thr Gly Tyr Leu Asp Arg
225 230 235 240

Glu Asp Ala Leu Leu Val Ser Asn Val Phe Ala Glu Asp Glu Ala Ala
245 250 255

Asp Glu Val Ser Arg Tyr Gln Leu Glu Lys Ile Arg Ser Leu Ile Glu
260 265 270

Asn Ala

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<211> 839

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(816)

<223> FRXA01409

<400> 623

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acc cct cat gta gat ttc ggt cct ttc ttc cgc cac ccc aag gca gac 96
Thr Pro His Val Asp Phe Gly Pro Phe Phe Arg His Pro Lys Ala Asp
20 25 30

gat gat ctc gtg gca gcc ctg aaa aag cgt gcc aag gat gcc gga gtc 144
Asp Asp Leu Val Ala Ala Leu Lys Lys Arg Ala Lys Asp Ala Gly Val
35 40 45

acc att cct gca ctg ttg cca gtg cag cgt att tcc tgg ccg gag gaa 192
Thr Ile Pro Ala Leu Leu Pro Val Gln Arg Ile Ser Trp Pro Glu Glu
50 55 60

acc cag cgt gtt gca gca gta cgc aac atc aag cgc atc atc cag ttg 240
Thr Gln Arg Val Ala Ala Val Arg Asn Ile Lys Arg Ile Ile Gln Leu
65 70 75 80

gcc gtt gat ctg gaa gta gac acc ctc aac acg gag ttt tct gga cgc 288

Ala Val Asp Leu Glu Val Asp Thr Leu Asn Thr Glu Phe Ser Gly Arg
85 90 95

cca gaa cgc tcc gag gat tcc gaa gat gcc ttc tac cgc tcc atg gaa 336
Pro Glu Arg Ser Glu Asp Ser Glu Asp Ala Phe Tyr Arg Ser Met Glu
100 105 110

gaa ctc ctg cca atc ctg gaa aaa gag ggc atc aag ttc aac atc gac 384
Glu Leu Leu Pro Ile Leu Glu Lys Glu Gly Ile Lys Phe Asn Ile Asp
115 120 125

cca cac cct gat gat ttc gtg gaa aac ggt att gaa gca tgg cga gtc 432
Pro His Pro Asp Asp Phe Val Glu Asn Gly Ile Glu Ala Trp Arg Val
130 135 140

atc cgc ggt ctg aac tcc aag cag gtg ggc ttt gtt tac gtg gca cct 480
Ile Arg Gly Leu Asn Ser Lys Gln Val Gly Phe Val Tyr Val Ala Pro
145 150 155 160

cac tca ttc cac atg ggt gat cag gct gag gca atc ctg cca gca gta 528
His Ser Phe His Met Gly Asp Gln Ala Glu Ala Ile Leu Pro Ala Val
165 170 175

ggc gat cgc ctt ggg gct gtg tac ctg tca gat acc ttc gac cac cac 576
Gly Asp Arg Leu Gly Ala Val Tyr Leu Ser Asp Thr Phe Asp His His
180 185 190

aaa tcc cac ggc ctg cgc tac atc act aac cct cca ggc aac gca gtg 624
Lys Ser His Gly Leu Arg Tyr Ile Thr Asn Pro Pro Gly Asn Ala Val
195 200 205

cgc gtg cac cag cac cta aaa atc ggt gat ggc gat gtg aac ttt gaa 672
Arg Val His Gln His Leu Lys Ile Gly Asp Gly Asp Val Asn Phe Glu
210 215 220

gag atc ttc tca ctg ctg cgc tct acc ggt tac ctt gac cgt gaa gat 720
Glu Ile Phe Ser Leu Leu Arg Ser Thr Gly Tyr Leu Asp Arg Glu Asp
225 230 235 240

gca ctg ttg gtc tcc aac gtg ttt gca gaa gat gaa gca gca gat gaa 768
Ala Leu Leu Val Ser Asn Val Phe Ala Glu Asp Glu Ala Ala Asp Glu
245 250 255

gta tcc cgc tac cag ctg gag aaa atc cgc tca ctc atc gaa aac gca 816
Val Ser Arg Tyr Gln Leu Glu Lys Ile Arg Ser Leu Ile Glu Asn Ala
260 265 270

tagagttatc tcgaaactac caa 839

<210> 624
<211> 272
<212> PRT
<213> Corynebacterium glutamicum

<400> 624
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Thr Pro His Val Asp Phe Gly Pro Phe Phe Arg His Pro Lys Ala Asp
20 25 30

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Thr Ile Pro Ala Leu Leu Pro Val Gln Arg Ile Ser Trp Pro Glu Glu
    50                                55                                60

Thr Gln Arg Val Ala Ala Val Arg Asn Ile Lys Arg Ile Ile Gln Leu
    65                                70                                75                                80

Ala Val Asp Leu Glu Val Asp Thr Leu Asn Thr Glu Phe Ser Gly Arg
    85                                90                                95

Pro Glu Arg Ser Glu Asp Ser Glu Asp Ala Phe Tyr Arg Ser Met Glu
   100                                105                                110

Glu Leu Leu Pro Ile Leu Glu Lys Glu Gly Ile Lys Phe Asn Ile Asp
   115                                120                                125

Pro His Pro Asp Asp Phe Val Glu Asn Gly Ile Glu Ala Trp Arg Val
   130                                135                                140

Ile Arg Gly Leu Asn Ser Lys Gln Val Gly Phe Val Tyr Val Ala Pro
   145                                150                                155                                160

His Ser Phe His Met Gly Asp Gln Ala Glu Ala Ile Leu Pro Ala Val
   165                                170                                175

Gly Asp Arg Leu Gly Ala Val Tyr Leu Ser Asp Thr Phe Asp His His
   180                                185                                190

Lys Ser His Gly Leu Arg Tyr Ile Thr Asn Pro Pro Gly Asn Ala Val
   195                                200                                205

Arg Val His Gln His Leu Lys Ile Gly Asp Gly Asp Val Asn Phe Glu
   210                                215                                220

Glu Ile Phe Ser Leu Leu Arg Ser Thr Gly Tyr Leu Asp Arg Glu Asp
   225                                230                                235                                240

Ala Leu Leu Val Ser Asn Val Phe Ala Glu Asp Glu Ala Ala Asp Glu
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Val Ser Arg Tyr Gln Leu Glu Lys Ile Arg Ser Leu Ile Glu Asn Ala
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<211> 3075

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(3052)

<223> RXN01434

<400> 625

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 aacactgccacacacgtgcc caacctgatc actggaaatc gtg ttg ggt gcg gtg 115
 Val Leu Gly Ala Val
 1 5
 ctg aca tcg ctg gtt att ccg gtc ctt acc cgc gcg gaa aaa gaa gac 163
 Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg Ala Glu Lys Glu Asp
 10 15 20
 gcc gac gcc ggt tcc ggg ttc ttc agg cgg ctg ctc acc ctg tcg gtg 211
 Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu Leu Thr Leu Ser Val
 25 30 35
 acg ctg ctg ggt ggt gtc acc atc ctg tcg att atc ggc gcg ccg ctg 259
 Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile Ile Gly Ala Pro Leu
 40 45 50
 ctg aca cgg atg atg ctg tcc tct gag gga caa gtc aac gtg gtc atg 307
 Leu Thr Arg Met Met Ser Ser Glu Gly Gln Val Asn Val Val Met
 55 60 65
 tcc acg gcc ttt gcg tat tgg ctg ctg cca cag att ttc ttc tac gcc 355
 Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln Ile Phe Phe Tyr Gly
 70 75 80 85
 ctg ttt gcc ctg ttc atg gct gtg ttg aac acc cgt gaa gtg ttc aaa 403
 Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr Arg Glu Val Phe Lys
 90 95 100
 ccc gcc gcg tgg gca cct gtt gtc aac aat gtg atc acc ttg acc gtg 451
 Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val Ile Thr Leu Thr Val
 105 110 115
 ctg gcc gtg tac atg gtg ctg cct gcg cgt ttg cac ccg cat gag cag 499
 Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu His Pro His Glu Gln
 120 125 130
 gtg gcc att ttt gat ccg cag atc att ttc ctc ggc gtg gcc acc acc 547
 Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu Gly Val Gly Thr Thr
 135 140 145
 ctt ggt gtg gtt gca cag tgt cta atc atg att ccg tac ctg cgt cgc 595
 Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile Pro Tyr Leu Arg Arg
 150 155 160 165
 gcg gcc att gat atg cgc cct ctg tgg ggt atc gat gcg cgt ttg aag 643
 Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile Asp Ala Arg Leu Lys
 170 175 180
 caa ttc ggt gcc atg gcg atg gcg atc atc gtg tac gtg gca atc tcc 691
 Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val Tyr Val Ala Ile Ser
 185 190 195
 cag ttc ggt tac atc atc acc act cgc att gcg tcg att gca gac gat 739
 Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala Ser Ile Ala Asp Asp
 200 205 210
 got gcg ccg ttt att tat cag cag cac tgg atg ttg ctg caa gtt cct 787
 Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met Leu Leu Gln Val Pro
 215 220 225

tat ggc atc atc ggc gtc acc ttg ctc acc gcg att atg ccg cga ctg Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala Ile Met Pro Arg Leu 230 235 240 245	835
tcc cgc aac gcg gca gac ggc gat gat agg gca gta gtc tct gac ctt Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala Val Val Ser Asp Leu 250 255 260	883
cag ttg ggt tcc aag cta acc ttc atc gca ctg atc ccc atc gtg gtg Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu Ile Pro Ile Val Val 265 270 275	931
ttc ttc acc gcc ttc ggt gtc cct att gcc aat ggc ctt ttt gcc tac Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn Gly Leu Phe Ala Tyr 280 285 290	979
ggc caa ttc gat gcc aac gcc gcc aac atc ctt ggt tgg act ctg agc Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu Gly Trp Thr Leu Ser 295 300 305	1027
ttc tct gct ttc acg ctg att cct tac gct ttg gtg ctg cta cat ctg Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu Val Leu Leu His Leu 310 315 320 325	1075
cgt gtg ttt tat gcg cgt gaa gag gtc tgg acc cca acc ttc atc atc Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr Pro Thr Phe Ile Ile 330 335 340	1123
gcc ggc atc acc gcc acc aag gtc gtg ctt tcc ctg ttg gca ccg ctg Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser Leu Ala Pro Leu 345 350 355	1171
ctg tcg agc tcc ccg gag cgt gtg gtg gtg ctt ctt ggt gcg gcc aac Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu Leu Gly Ala Ala Asn 360 365 370	1219
ggt ttc agt ttc atc acc gcc gcg gtc atc gcc gcg tat ctg ttg cgc Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly Ala Tyr Leu Leu Arg 375 380 385	1267
aac aaa ctc ggc ctg ttg ggt atg cgc tct ttg gct aaa acc tcc ctg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu Ala Lys Thr Ser Leu 390 395 400 405	1315
tgg gcg ttg ggc tct gcg gcg gtt ggt gca gca gca gca tgg gcg ttg Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala Ala Ala Trp Ala Leu 410 415 420	1363
ggg tgg ctg att caa gcc gtc gtg gcc gat ttc ttg ctg gcc act cta Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe Leu Leu Gly Thr Leu 425 430 435	1411
agc tcc gta ggc tac ttg ttg aac ctg gct gtg ttg ggt gtc ttc ttc Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val Leu Gly Val Phe Phe 440 445 450	1459
atc ttc gtc acc gcc atc gtg ttg tca cgt tct ggt ttg ccg gag gtc Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser Gly Leu Pro Glu Val 455 460 465	1507

caa aac ttg ggc cag gca ctg acc cgc atc cca ggt ttg agc cgg ttt 1555
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 470 475 480 485

att cgc ccg aat acc aag atc tct ttg gat gtc ggc gaa gtc tcc gag 1603
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 490 495 500

cag gat ttc tcc acc cag ctg gtc gcg cca agc gag ttc gca gca acc 1651
 Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser Glu Phe Ala Ala Thr
 505 510 515

cct gtg cgc cca cgc atg tcc gcc ggt att gtc cgc gga cct cgc ctg 1699
 Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val Arg Gly Pro Arg Leu
 520 525 530

gtt ccc ggc gcc cca gtc gcg gac ggt cgt ttc cgt ctg ctc gcc gat 1747
 Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe Arg Leu Leu Ala Asp
 535 540 545

cac ggc ggc gtc caa ggc gcg cgt ttc tgg cag gcc cgc gag atc gcc 1795
 His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln Ala Arg Glu Ile Ala
 550 555 560 565

acc ggc aag gaa gtc gcg ctg atc ttt gtg gat act tcc gcc aac gcc 1843
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 570 575 580

cca ttt gcg cca ctg tct tcg gca gcc gca gcg gcc atc gcc tac gag 1891
 Pro Phe Ala Leu Ser Ser Ala Ala Ala Gly Ile Ala Tyr Glu
 585 590 595

gtg cag cgc cgc acc aag aag ctg gcc agc ttg gcc agc ttg gcg gta 1939
 Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu Gly Ser Leu Ala Val
 600 605 610

gcc ccc aac atc cac tcc gag gcg tac cgc aac ggt tgc ctc att gtg 1987
 Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn Gly Cys Leu Ile Val
 615 620 625

gcc gat tgg gtg cct gcc tcc agc ttg agc gcc gtc gcg gaa tcc ggt 2035
 Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala Val Ala Glu Ser Gly
 630 635 640 645

gcc gat ccc cgc gcc gcc gcg ttc gcg ctc gcg gaa cta act gaa acc 2083
 Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala Glu Leu Thr Glu Thr
 650 655 660

atc ggc gag gcc cac gag atg ggt atc cgc gcc gcc ttg gac aac aag 2131
 Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala Gly Leu Asp Asn Lys
 665 670 675

tgc cga att cgt atc aac acc gac gcc cat gcc gtc ctc gcc ttg cgc 2179
 Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro
 680 685 690

gcg att ttg ccc gat gcc tca gag ctc cgc gac gcc aag tcc ctg gcc 2227
 Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp Ala Lys Ser Leu Ala
 695 700 705

tcg gcc gcc gag atg ctt atc gac gcg acc ctc gct ccc agc gac gtc 2275

Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu Ala Pro Ser Asp Val	
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Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala Thr Glu Asp Asn Pro	
730 735 740	
gat tac gca tca ctt gcc atg gcg atg cgc acc tgc gga ctg ttc acc	2371
Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr Cys Gly Leu Phe Thr	
745 750 755	
gag gaa cca acc cac ctt gtg gtg aag aag gaa aag aca cca aag cct	2419
Glu Glu Pro Thr His Leu Val Val Lys Lys Glu Lys Thr Pro Lys Pro	
760 765 770	
gcg aca cgt gat ggt ttc ggt gcc tcc gac tac acc gtc aag ggc atg	2467
Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met	
775 780 785	
gca gcc atc gcc gct gtg gtg atc atc ttg gtt tcc ctg gtg gcc gcc	2515
Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val Ser Leu Val Ala Ala	
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Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser Ser Thr Asn Glu Gln	
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tcc ccg ttg gcc tct gtt gaa gcc acc acc tct gca aca cca gaa cct	2611
Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser Ala Thr Pro Glu Pro	
825 830 835	
gtg ggg cca ccg gtc tac ctg gat ctg gat caa gcc cgc acg tgg gat	2659
Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln Ala Arg Thr Trp Asp	
840 845 850	
gac ggt gca gga aca gat gtc acc gac gtc acc gac ggc aac acc tcc	2707
Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser	
855 860 865	
acc gca tgg acc tcc acc gcc ggc gac ggc ctc cta gtt gac ctg tcc	2755
Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu Leu Val Asp Leu Ser	
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acg cct gcc cgc ctc gac cgc gtc atc ttg acc acc ggc acc ggc tcc	2803
Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr Thr Gly Thr Gly Ser	
890 895 900	
gac agc aac gtg acc tcg acc gtg aag atc tac gca ttc aac gac gcc	2851
Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr Ala Phe Asn Asp Ala	
905 910 915	
tca cca cac tcc ctg tcg gaa ggc atc gag atc ggc acc gtg gat tat	2899
Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile Gly Thr Val Asp Tyr	
920 925 930	
tcc ggc cgc agt ctc agc cac agc atc cgc gat tcc tcc aag ctt ccg	2947
Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp Ser Ser Lys Leu Pro	
935 940 945	
ggc cag gtg gaa tcc gtg gtg att ctg gtc gat gag gtt cgt tcc tca	2995
Gly Gln Val Glu Ser Val Val Ile Leu Val Asp Glu Val Arg Ser Ser	

950 955 960 965

caa acc tca gac acc aat cca cag atg cag atc gct gaa gta caa ctt 3043
 Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile Ala Glu Val Gln Leu
 970 975 980

gtt ggt tgg taaattacgc gttgtgatt gac 3075
 Val Gly Trp

<210> 626

<211> 984

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 626

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Leu Thr Leu Ser Val Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile
 35 40 45

Ile Gly Ala Pro Leu Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln
 50 55 60

Val Asn Val Val Met Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln
 65 70 75 80

Ile Phe Phe Tyr Gly Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr
 85 90 95

Arg Glu Val Phe Lys Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val
 100 105 110

Ile Thr Leu Thr Val Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu
 115 120 125

His Pro His Glu Gln Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu
 130 135 140

Gly Val Gly Thr Thr Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile
 145 150 155 160

Pro Tyr Leu Arg Arg Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile
 165 170 175

Asp Ala Arg Leu Lys Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val
 180 185 190

Tyr Val Ala Ile Ser Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala
 195 200 205

Ser Ile Ala Asp Asp Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met
 210 215 220

Leu Leu Gln Val Pro Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala
 225 230 235 240

Ile Met Pro Arg Leu Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala
 245 250 255
 Val Val Ser Asp Leu Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu
 260 265 270
 Ile Pro Ile Val Val Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn
 275 280 285
 Gly Leu Phe Ala Tyr Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu
 290 295 300
 Gly Trp Thr Leu Ser Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu
 305 310 315 320
 Val Leu Leu His Leu Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr
 325 330 335
 Pro Thr Phe Ile Ile Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser
 340 345 350
 Leu Leu Ala Pro Leu Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu
 355 360 365
 Leu Gly Ala Ala Asn Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly
 370 375 380
 Ala Tyr Leu Leu Arg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu
 385 390 395 400
 Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala
 405 410 415
 Ala Ala Trp Ala Leu Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe
 420 425 430
 Leu Leu Gly Thr Leu Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val
 435 440 445
 Leu Gly Val Phe Phe Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser
 450 455 460
 Gly Leu Pro Glu Val Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro
 465 470 475 480
 Gly Leu Ser Arg Phe Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val
 485 490 495
 Gly Glu Val Ser Glu Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser
 500 505 510
 Glu Phe Ala Ala Thr Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val
 515 520 525
 Arg Gly Pro Arg Leu Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe
 530 535 540
 Arg Leu Leu Ala Asp His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln
 545 550 555 560

Ala Arg Glu Ile Ala Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp
 565 570 575
 Thr Ser Gly Asn Ala Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala
 580 585 590
 Gly Ile Ala Tyr Glu Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu
 595 600 605
 Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn
 610 615 620
 Gly Cys Leu Ile Val Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala
 625 630 635 640
 Val Ala Glu Ser Gly Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala
 645 650 655
 Glu Leu Thr Glu Thr Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala
 660 665 670
 Gly Leu Asp Asn Lys Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala
 675 680 685
 Val Leu Ala Leu Pro Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp
 690 695 700
 Ala Lys Ser Leu Ala Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu
 705 710 715 720
 Ala Pro Ser Asp Val Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala
 725 730 735
 Thr Glu Asp Asn Pro Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr
 740 745 750
 Cys Gly Leu Phe Thr Glu Glu Pro Thr His Leu Val Val Lys Lys Glu
 755 760 765
 Lys Thr Pro Lys Pro Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr
 770 775 780
 Thr Val Lys Gly Met Ala Ala Ile Ala Val Val Ile Ile Leu Val
 785 790 795 800
 Ser Leu Val Ala Ala Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser
 805 810 815
 Ser Thr Asn Glu Gln Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser
 820 825 830
 Ala Thr Pro Glu Pro Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln
 835 840 845
 Ala Arg Thr Trp Asp Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr
 850 855 860
 Asp Gly Asn Thr Ser Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu
 865 870 875 880
 Leu Val Asp Leu Ser Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr

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      885                      890                      895
Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr
      900                      905
Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile
      915                      920                      925
Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp
      930                      935                      940
Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu Val Asp
      945                      950                      955                      960
Glu Val Arg Ser Ser Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile
      965                      970                      975
Ala Glu Val Gln Leu Val Gly Trp
      980

<210> 627
<211> 389
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(366)
<223> FRXA01434

<400> 627
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ggc ctc cta gtt gac ctg tcc acg cct gcc cgc ctc gac cgc gtc atc 96
Gly Leu Leu Val Asp Leu Ser Thr Pro Ala Arg Leu Asp Arg Val Ile
20 25 30
ttg acc acc ggc acc ggc tcc gac agc aac gtg acc tcg acc gtg aag 144
Leu Thr Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys
35 40 45
atc tac gca ttc aac gac gcc tca cca cac tcc ctg tcg gaa ggc atc 192
Ile Tyr Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Glu Gly Ile
50 55 60
gag atc ggc acc gtg gat tat tcc ggc cgc agt ctc agc cac agc atc 240
Glu Ile Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile
65 70 75 80
cgc gat tcc tcc aag ctt ccg ggt cag gtg gaa tcc gtg gtg att ctg 288
Arg Asp Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu
85 90 95
gtc gat gag gtt cgt tcc tca caa acc tca gac acc aat cca cag atg 336
Val Asp Glu Val Arg Ser Ser Gln Thr Ser Asp Thr Asn Pro Gln Met
100 105 110
cag atc gct gaa gta caa ctt gtt ggt tgg taaattacgc gtttgtgatt 386

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Gln Ile Ala Glu Val Gln Leu Val Gly Trp
 115 120

gac

389

<210> 628

<211> 122

<212> PRT

<213> Corynebacterium glutamicum

<400> 628

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Gly Leu Leu Val Asp Leu Ser Thr Pro Ala Arg Leu Asp Arg Val Ile
 20 25 30

Leu Thr Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys
 35 40 45

Ile Tyr Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Glu Gly Ile
 50 55 60

Glu Ile Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile
 65 70 75 80

Arg Asp Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu
 85 90 95

Val Asp Glu Val Arg Ser Ser Gln Thr Ser Asp Thr Asn Pro Gln Met
 100 105 110

Gln Ile Ala Glu Val Gln Leu Val Gly Trp
 115 120

<210> 629

<211> 1290

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> {101}..(1267)

<223> RXN01448

<400> 629

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tctcatgctc ttgtgaatat gcatagctaa tcttgaggcc atg gca aag aag aaa 115
 Met Ala Lys Lys Lys
 1 5

ctg ggg act gtc gcc aga ctg tct gaa ctg gat aag tcc ctg cgc aat 163
 Leu Gly Thr Val Ala Arg Leu Ser Glu Leu Asp Lys Ser Leu Arg Asn
 10 15 20

aga ttg ctg egg gtt cgt tcc cga ctg ctg ttt att gtt cat tcc gca 211
 Arg Leu Leu Arg Val Arg Ser Arg Leu Leu Phe Ile Val His Ser Ala
 25 30 35

att ggt gcg ggt gtg gcg tat tgg atc gcc gtg gaa gtg atc aaa cac 259
 Ile Gly Ala Gly Val Ala Tyr Trp Ile Ala Val Glu Val Ile Lys His
 40 45 50

gga caa ccg ttt ttc gca ccg atg tcc gcg gtg att att ttg ggt ctc 307
 Gly Gln Pro Phe Phe Ala Pro Met Ser Ala Val Ile Ile Leu Gly Leu
 55 60 65

tcc gga gga gac cgc atc aaa aga gcc acg gaa ctc acc ctg ggc tgt 355
 Ser Gly Gly Asp Arg Ile Lys Arg Ala Thr Glu Leu Thr Leu Gly Cys
 70 75 80 85

gct tta ggc gtt ggt ttg ggt gat tta ctg atc atg caa atc ggc acg 403
 Ala Leu Gly Val Gln Leu Gly Asp Leu Ile Met Gln Ile Gly Thr
 90 95 100

ggc tat tgg cag ata ttt gtg gta gtt gga tta gcg ctg ctg gtg gcc 451
 Gly Tyr Trp Gln Ile Phe Val Val Gly Leu Ala Leu Val Ala
 105 110 115

tcg ttt gtt tca ccg gca ccg ttg gtg agt aat cag atg gcc att ggt 499
 Ser Phe Val Ser Pro Ala Pro Leu Val Ser Asn Gln Met Ala Ile Gly
 120 125 130

ggc att ttg att gcc acg atg ttc ccg cca ggt gat ggt gga agc att 547
 Gly Ile Leu Ile Ala Thr Met Phe Pro Pro Gly Asp Gly Gly Ser Ile
 135 140 145

gac cgt atg atc gac gcc ttc att ggt ggt ggc gtg gga att ttg gtc 595
 Asp Arg Met Ile Asp Ala Phe Ile Gly Gly Val Gly Ile Leu Val
 150 155 160 165

atc gca ctt ctt ccc tca tct cct ctt gac gca ggc cgg cat caa gtg 643
 Ile Ala Leu Leu Pro Ser Ser Pro Leu Asp Ala Gly Arg His Gln Val
 170 175 180

gcc aac gtt ttg ggg atc gca gct agt gtg ctg gaa gac gtg gca gct 691
 Ala Asn Val Leu Gly Ile Ala Ala Ser Val Leu Glu Asp Val Ala Ala
 185 190 195

tcc cta aaa gcc aag gat gca gcc aaa ctc aac aat gct ttg gaa gca 739
 Ser Leu Lys Ala Lys Asp Ala Ala Lys Leu Asn Asn Ala Leu Glu Ala
 200 205 210

ttg aga agg tcg cag gcg tcg gtg aac aag ctg gaa act gcg gca tct 787
 Leu Arg Arg Ser Gln Ala Ser Val Asn Lys Leu Glu Thr Ala Ala Ser
 215 220 225

tca ggc aag gaa gca acc acc gta tcg cca ttt tta tgg gga gat agg 835
 Ser Gly Lys Glu Ala Thr Thr Val Ser Pro Phe Leu Trp Gly Asp Arg
 230 235 240 245

gcc cgc gtg aga tcg ctg tat cgc att ctg gcg cca gtg gac aac gtc 883
 Ala Arg Val Arg Ser Leu Tyr Arg Ile Leu Ala Pro Val Asp Asn Val
 250 255 260

atc cga aat gct cga gtc ctt gcg cga cgg gca gtg gtg ctg acc gaa 931
 Ile Arg Asn Ala Arg Val Leu Ala Arg Ala Val Val Leu Thr Glu
 265 270 275

gac aat gac acc gtc agt gat gaa caa atc cac gtg att gag gaa atc 979
 Asp Asn Asp Thr Val Ser Asp Glu Gln Ile His Val Ile Glu Glu Ile
 280 285 290

gca gac att gca ctg cga ctg tca gac ctt tat gag cac cac aaa gaa 1027
 Ala Asp Ile Ala Leu Arg Leu Ser Asp Leu Tyr Glu His His Lys Glu
 295 300 305

atc agt gaa gca ctg gaa att cct gag ttg gtt aac cga ctg cgt caa 1075
 Ile Ser Glu Ala Leu Glu Ile Pro Glu Leu Val Asn Arg Leu Arg Gln
 310 315 320 325

ctg ggc agt gaa gtg ggc gag gac atc gcc gaa gat cga gtg cta tcc 1123
 Leu Gly Ser Glu Val Gly Glu Asp Ile Ala Glu Asp Arg Val Leu Ser
 330 335 340

gca caa gta att ttg gcg caa tcg cga tcc atc att gtg gac ctg ttg 1171
 Ala Gln Val Ile Leu Ala Gln Ser Arg Ser Ile Ile Val Asp Leu Leu
 345 350 355

cag atc tgc ggc atg tcc agg gaa tct gcg gtg gca gtg ttg gtt ccg 1219
 Gln Ile Cys Gly Met Ser Arg Glu Ser Ala Val Ala Val Leu Val Pro
 360 365 370

acc tca gag agt ccg gct tac cct ccg gag ctg tgg gat gac gaa gac 1267
 Thr Ser Glu Ser Pro Ala Tyr Pro Pro Glu Leu Trp Asp Asp Glu Asp
 375 380 385

tagcctttta tcgcggttcg gtt 1290

<210> 630
 <211> 389
 <212> FRT
 <213> *Corynebacterium glutamicum*

<400> 630
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Lys Ser Leu Arg Asn Arg Leu Leu Arg Val Arg Ser Arg Leu Leu Phe
 20 25 30

Ile Val His Ser Ala Ile Gly Ala Gly Val Ala Tyr Trp Ile Ala Val
 35 40 45

Glu Val Ile Lys His Gly Gln Pro Phe Phe Ala Pro Met Ser Ala Val
 50 55 60

Ile Ile Leu Gly Leu Ser Gly Gly Asp Arg Ile Lys Arg Ala Thr Glu
 65 70 75 80

Leu Thr Leu Gly Cys Ala Leu Gly Val Gly Leu Gly Asp Leu Leu Ile
 85 90 95

Met Gln Ile Gly Thr Gly Tyr Trp Gln Ile Phe Val Val Val Gly Leu
 100 105 110

Ala Leu Leu Val Ala Ser Phe Val Ser Pro Ala Pro Leu Val Ser Asn
 115 120 125

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Gln Met Ala Ile Gly Gly Ile Leu Ile Ala Thr Met Phe Pro Pro Gly
130                      135                      140

Asp Gly Gly Ser Ile Asp Arg Met Ile Asp Ala Phe Ile Gly Gly Gly
145                      150                      155                      160

Val Gly Ile Leu Val Ile Ala Leu Leu Pro Ser Ser Pro Leu Asp Ala
165                      170                      175

Gly Arg His Gln Val Ala Asn Val Leu Gly Ile Ala Ala Ser Val Leu
180                      185                      190

Glu Asp Val Ala Ala Ser Leu Lys Ala Lys Asp Ala Ala Lys Leu Asn
195                      200                      205

Asn Ala Leu Glu Ala Leu Arg Arg Ser Gln Ala Ser Val Asn Lys Leu
210                      215                      220

Glu Thr Ala Ala Ser Ser Gly Lys Glu Ala Thr Thr Val Ser Pro Phe
225                      230                      235                      240

Leu Trp Gly Asp Arg Ala Arg Val Arg Ser Leu Tyr Arg Ile Leu Ala
245                      250                      255

Pro Val Asp Asn Val Ile Arg Asn Ala Arg Val Leu Ala Arg Arg Ala
260                      265                      270

Val Val Leu Thr Glu Asp Asn Asp Thr Val Ser Asp Glu Gln Ile His
275                      280                      285

Val Ile Glu Glu Ile Ala Asp Ile Ala Leu Arg Leu Ser Asp Leu Tyr
290                      295                      300

Glu His His Lys Glu Ile Ser Glu Ala Leu Glu Ile Pro Glu Leu Val
305                      310                      315                      320

Asn Arg Leu Arg Gln Leu Gly Ser Glu Val Gly Glu Asp Ile Ala Glu
325                      330                      335

Asp Arg Val Leu Ser Ala Gln Val Ile Leu Ala Gln Ser Arg Ser Ile
340                      345                      350

Ile Val Asp Leu Leu Gln Ile Cys Gly Met Ser Arg Glu Ser Ala Val
355                      360                      365

Ala Val Leu Val Pro Thr Ser Glu Ser Pro Ala Tyr Pro Pro Glu Leu
370                      375                      380

Trp Asp Asp Glu Asp
385

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<210> 631
<211> 842
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (40)..(819)
<223> FRXA01448

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<400> 631

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                                     Met Ala Ile Gly Gly Ile
                                     1           5

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Leu Ile Ala Thr Met Phe Pro Pro Gly Asp Gly Gly Ser Ile Asp Arg
                10                15                20

atg atc gac gcc ttc att ggt ggt ggc gtg gga att ttg gtc atc gca 153
Met Ile Asp Ala Phe Ile Gly Gly Gly Val Gly Ile Leu Val Ile Ala
                25                30                35

ctt ctt ccc tca tct cct ctt gac gca ggc cgg cat caa gtg gcc aac 201
Leu Leu Pro Ser Ser Pro Leu Asp Ala Gly Arg His Gln Val Ala Asn
                40                45                50

gtt ttg ggg atc gca gct agt gtg ctg gaa gac gtg gca gct tcc cta 249
Val Leu Gly Ile Ala Ala Ser Val Leu Glu Asp Val Ala Ala Ser Leu
                55                60                65                70

aaa gcc aag gat gca gcc aaa ctc aac aat gct ttg gaa gca ttg aga 297
Lys Ala Lys Asp Ala Ala Lys Leu Asn Asn Ala Leu Glu Ala Leu Arg
                75                80                85

agg tcg cag gcg tcg gtg aac aag ctg gaa act gcg gca tct tca ggc 345
Arg Ser Gln Ala Ser Val Asn Lys Leu Glu Thr Ala Ala Ser Ser Gly
                90                95                100

aag gaa gca acc acc gta tcg cca ttt tta tgg gga gat agg gcc cgc 393
Lys Glu Ala Thr Thr Val Ser Pro Phe Leu Trp Gly Asp Arg Ala Arg
                105                110                115

gtg aga tcg ctg tat cgc att ctg gcg cca gtg gac aac gtc atc cga 441
Val Arg Ser Leu Tyr Arg Ile Leu Ala Pro Val Asp Asn Val Ile Arg
                120                125                130

aat gct cga gtc ctt gcg cga cgg gca gtg gtg ctg acc gaa gac aat 489
Asn Ala Arg Val Leu Ala Arg Arg Ala Val Val Leu Thr Glu Asp Asn
                135                140                145                150

gac acc gtc agt gat gaa caa atc cac gtg att gag gaa atc gca gac 537
Asp Thr Val Ser Asp Glu Gln Ile His Val Ile Glu Glu Ile Ala Asp
                155                160                165

att gca ctg cga ctg tca gac ctt tat gag cac cac aaa gaa atc agt 585
Ile Ala Leu Arg Leu Ser Asp Leu Tyr Glu His His Lys Glu Ile Ser
                170                175                180

gaa gca ctg gaa att cct gag ttg gtt aac cga ctg cgt caa ctg ggc 633
Glu Ala Leu Glu Ile Pro Glu Leu Val Asn Arg Leu Arg Gln Leu Gly
                185                190                195

agt gaa gtg ggc gag gac atc gcc gaa gat cga gtg cta tcc gca caa 681
Ser Glu Val Gly Glu Asp Ile Ala Glu Asp Arg Val Leu Ser Ala Gln
                200                205                210

gta att ttg gcg caa tcg cga tcc atc att gtg gac ctg ttg cag atc 729
Val Ile Leu Ala Gln Ser Arg Ser Ile Ile Val Asp Leu Leu Gln Ile
                215                220                225                230

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tgc ggc atg tcc agg gaa tct gcg gtg gca gtg ttg gtt ccg acc tca 777
 Cys Gly Met Ser Arg Glu Ser Ala Val Ala Val Leu Val Pro Thr Ser
 235 240 245

gag agt ccg gct tac cct ccg gag ctg tgg gat gac gaa gac 819
 Glu Ser Pro Ala Tyr Pro Pro Glu Leu Trp Asp Asp Glu Asp
 250 255 260

tagcctttta tcgcggttcg gtt 842

<210> 632

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 632

Met Ala Ile Gly Gly Ile Leu Ile Ala Thr Met Phe Pro Pro Gly Asp
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Gly Gly Ser Ile Asp Arg Met Ile Asp Ala Phe Ile Gly Gly Gly Val
 20 25 30

Gly Ile Leu Val Ile Ala Leu Leu Pro Ser Ser Pro Leu Asp Ala Gly
 35 40 45

Arg His Gln Val Ala Asn Val Leu Gly Ile Ala Ala Ser Val Leu Glu
 50 55 60

Asp Val Ala Ala Ser Leu Lys Ala Lys Asp Ala Ala Lys Leu Asn Asn
 65 70 75 80

Ala Leu Glu Ala Leu Arg Arg Ser Gln Ala Ser Val Asn Lys Leu Glu
 85 90 95

Thr Ala Ala Ser Ser Gly Lys Glu Ala Thr Thr Val Ser Pro Phe Leu
 100 105 110

Trp Gly Asp Arg Ala Arg Val Arg Ser Leu Tyr Arg Ile Leu Ala Pro
 115 120 125

Val Asp Asn Val Ile Arg Asn Ala Arg Val Leu Ala Arg Arg Ala Val
 130 135 140

Val Leu Thr Glu Asp Asn Asp Thr Val Ser Asp Glu Gln Ile His Val
 145 150 155 160

Ile Glu Glu Ile Ala Asp Ile Ala Leu Arg Leu Ser Asp Leu Tyr Glu
 165 170 175

His His Lys Glu Ile Ser Glu Ala Leu Glu Ile Pro Glu Leu Val Asn
 180 185 190

Arg Leu Arg Gln Leu Gly Ser Glu Val Gly Glu Asp Ile Ala Glu Asp
 195 200 205

Arg Val Leu Ser Ala Gln Val Ile Leu Ala Gln Ser Arg Ser Ile Ile
 210 215 220

Val Asp Leu Leu Gln Ile Cys Gly Met Ser Arg Glu Ser Ala Val Ala

Val Leu Val Pro Thr Ser Glu Ser Pro Ala Tyr Pro Pro Glu Leu Trp

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Asp Asp Glu Asp
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<210> 633

<211> 933

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

 $\langle 222 \rangle$ (101) .. (910)

<223> RXN01459

<400> 633

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togtagcaat aggaaatagt tgccttgtag attggtaaat atg aac tct aat ggc 115
Met Asn Ser Asn Gly
1 5

ttt ggt ttc tct ttt ggc aac aac gat gac gac gat gac aaa aac cgc 163
Phe Gly Phe Ser Phe Gly Asn Asn Asp Asp Asp Asp Lys Asn Arg
10 15 20

aac aac gac cca ttc ggc ctt ttc ggt ggc aac ttc gga ttc gga gga 211
Asn Asn Asp Pro Phe Gly Leu Phe Gly Gly Asn Phe Gly Phe Gly Gly
25 30 35

caa ggt ggc gct ggt ggc ccc ggc gga tta ggc gat att tta aac cag 259
Gln Gly Gly Ala Gly Gly Pro Gly Gly Leu Gly Asp Ile Leu Asn Gln
40 45 50

ttc ggc cag atg ctg tcc gga atg gga gat tgc atg aac tcc ccc gaa 307
Phe Gly Gln Met Leu Ser Gly Met Gly Asp Ser Met Asn Ser Pro Glu
55 60 65

gca gca ggc cgg gtt aat tat gat tta gca gca cgc atc gcc cgc cag 355
Ala Ala Gly Pro Val Asn Tyr Asp Leu Ala Ala Arg Ile Ala Arg Gln
70 75 80 85

cag att ggt cgc gta gcg cgg gtg aag gat tct gag aag gaa gca gtc 403
Gln Ile Gly Arg Val Ala Pro Val Lys Asp Ser Glu Lys Glu Ala Val
90 95 100

gaa gag tcc ctt cgc ctt gct gaa ctc tgg ctc gat aac gcc acc cag 451
Glu Glu Ser Leu Arg Leu Ala Glu Leu Trp Leu Asp Asn Ala Thr Gln
105 110 115

ctc ccc act tcc ggg cac cgc gtc gaa gcg tgg aat cca gaa aac tgg 499
Leu Pro Thr Ser Gly His Arg Val Glu Ala Trp Asn Pro Glu Asn Trp
120 125 130

tta gaa aac acc ctg cct gtg tgg aag cgt ctt gtc tcc cct gtt gcg 547
Leu Glu Asn Thr Leu Pro Val Trp Lys Arg Leu Val Ser Pro Val Ala
135 140 145

gag caa atg aac aaa gcc caa tta gaa aac ctc cct gaa gaa gcc cgc 595
 Glu Gln Met Asn Lys Ala Gln Leu Glu Asn Leu Pro Glu Glu Ala Arg
 150 155 160 165

gag atg atg ggc cgc atg tct tct ttg atg aac tcc atg tct tcg atg 643
 Glu Met Met Gly Pro Met Ser Ser Leu Met Asn Ser Met Ser Ser Met
 170 175 180

aac ttc gga gtt caa tta gga aat gcg ctg ggc gac ctc gca aag cag 691
 Asn Phe Gly Val Gln Leu Gly Asn Ala Leu Gly Asp Leu Ala Lys Gln
 185 190 195

acc ctc acc ggc tct gac ttc ggt ttg cct atc tcc cca gtc ggc gta 739
 Thr Leu Thr Gly Ser Asp Phe Gly Leu Pro Ile Ser Pro Val Gly Val
 200 205 210

tct gcc gtc ctg ccc ggc aac atc gcc gaa gca tcc aaa ggc ctc aac 787
 Ser Ala Val Leu Pro Gly Asn Ile Ala Glu Ala Ser Lys Gly Leu Asn
 215 220 225

gtg gca ccg caa gaa atg ctc gtt tac atc tgt gcc cgc gaa gcc gcc 835
 Val Ala Pro Gln Glu Met Leu Val Tyr Ile Cys Ala Arg Glu Ala Ala
 230 235 240 245

gcc aac gcc tct tca agc acg tgc cgt gcc ttg tcg agc gcc tcg ttt 883
 Ala Asn Ala Ser Ser Ser Thr Cys Arg Gly Leu Ser Ser Ala Ser Phe
 250 255 260

cct ccg ttg agg aat acg ccg tcg gcc tagaaatcga cacctcacac 930
 Pro Pro Leu Arg Asn Thr Pro Ser Ala
 265 270

att 933

<210> 634
 <211> 270
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 634
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 Phe Gly Phe Gly Gly Gln Gly Gly Ala Gly Gly Pro Gly Gly Leu Gly
 35 40 45
 Asp Ile Leu Asn Gln Phe Gly Gln Met Leu Ser Gly Met Gly Asp Ser
 50 55 60
 Met Asn Ser Pro Glu Ala Ala Gly Pro Val Asn Tyr Asp Leu Ala Ala
 65 70 75 80
 Arg Ile Ala Arg Gln Gln Ile Gly Arg Val Ala Pro Val Lys Asp Ser
 85 90 95
 Glu Lys Glu Ala Val Glu Glu Ser Leu Arg Leu Ala Glu Leu Trp Leu

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100              105              110
Asp Asn Ala Thr Gln Leu Pro Thr Ser Gly His Arg Val Glu Ala Trp
115              120
Asn Pro Glu Asn Trp Leu Glu Asn Thr Leu Pro Val Trp Lys Arg Leu
130              135              140
Val Ser Pro Val Ala Glu Gln Met Asn Lys Ala Gln Leu Glu Asn Leu
145              150              155
Pro Glu Glu Ala Arg Glu Met Met Gly Pro Met Ser Ser Leu Met Asn
165              170              175
Ser Met Ser Ser Met Asn Phe Gly Val Gln Leu Gly Asn Ala Leu Gly
180              185              190
Asp Leu Ala Lys Gln Thr Leu Thr Gly Ser Asp Phe Gly Leu Pro Ile
195              200              205
Ser Pro Val Gly Val Ser Ala Val Leu Pro Gly Asn Ile Ala Glu Ala
210              215              220
Ser Lys Gly Leu Asn Val Ala Pro Gln Glu Met Leu Val Tyr Ile Cys
225              230              235              240
Ala Arg Glu Ala Ala Ala Asn Ala Ser Ser Ser Thr Cys Arg Gly Leu
245              250              255
Ser Ser Ala Ser Phe Pro Pro Leu Arg Asn Thr Pro Ser Ala
260              265              270

<210> 635
<211> 933
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(910)
<223> FRXA01459

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tcgtagcaat aggaatatgt tgcctttagt attggtataat atg aac tct aat ggc 115
Met Asn Ser Asn Gly
1
ttt ggt ttc tct ttt ggc aac aac gat gac gac gat gac aaa aac cgc 163
Phe Gly Phe Ser Phe Gly Asn Asn Asp Asp Asp Asp Asp Lys Asn Arg
10              15              20
aac aac gac cca ttc ggc ctt ttc ggt ggc aac ttc gga ttc gga gga 211
Asn Asn Asp Pro Phe Gly Leu Phe Gly Gly Asn Phe Gly Phe Gly Gly
25              30              35
caa ggt ggc gct ggt ggc ccc ggc gga tta ggc gat att tta aac cag 259
Gln Gly Gly Ala Gly Gly Pro Gly Gly Leu Gly Asp Ile Leu Asn Gln
40              45              50

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ttc ggc cag atg ctg tcc gga atg gga gat tgc atg aac tcc ccc gaa 307
 Phe Gly Gln Met Leu Ser Gly Met Gly Asp Ser Met Asn Ser Pro Glu
 55 60 65

gca gca ggc ccg gtt aat tat gat tta gca gca cgc atc gcc cgc cag 355
 Ala Ala Gly Pro Val Asn Tyr Asp Leu Ala Ala Arg Ile Ala Arg Gln
 70 75 80 85

cag att ggt cgc gta gcg ccg gtg aag gat tct gag aag gaa gca gtc 403
 Gln Ile Gly Arg Val Ala Pro Val Lys Asp Ser Glu Lys Glu Ala Val
 90 95 100

gaa gag tcc ctt cgc ctt gct gaa ctc tgg ctc gat aac gcc acc cag 451
 Glu Glu Ser Leu Arg Leu Ala Glu Leu Trp Leu Asp Asn Ala Thr Gln
 105 110 115

ctc ccc act tcc ggg cac cgc gtc gaa gcg tgg aat cca gaa aac tgg 499
 Leu Pro Thr Ser Gly His Arg Val Glu Ala Trp Asn Pro Glu Asn Trp
 120 125 130

tta gaa aac acc ctg cct gtg tgg aag cgt ctt gtc tcc cct gtt gcg 547
 Leu Glu Asn Thr Leu Pro Val Trp Lys Arg Leu Val Ser Pro Val Ala
 135 140 145

gag caa atg aac aaa gcc caa tta gaa aac ctc cct gaa gaa gcc cgc 595
 Glu Gln Met Asn Lys Ala Gln Leu Glu Asn Leu Pro Glu Glu Ala Arg
 150 155 160 165

gag atg atg ggc ccg atg tct tct ttg atg aac tcc atg tct tgc atg 643
 Glu Met Met Gly Pro Met Ser Ser Leu Met Asn Ser Met Ser Ser Met
 170 175 180

aac ttc gga gtt caa tta gga aat gcg ctg gcc gac ctc gca aag cag 691
 Asn Phe Gly Val Gln Leu Gly Asn Ala Leu Gly Asp Leu Ala Lys Gln
 185 190 195

acc ctc acc gcc tct gac ttc ggt ttg cct atc tcc cca gtc gcc gta 739
 Thr Leu Thr Gly Ser Asp Phe Gly Leu Pro Ile Ser Pro Val Gly Val
 200 205 210

tct gcc gtc ctg ccc gcc aac atc gcc gaa gca tcc aaa gcc ctc aac 787
 Ser Ala Val Leu Pro Gly Asn Ile Ala Glu Ala Ser Lys Gly Leu Asn
 215 220 225

gtg gca ccg caa gaa atg ctc gtt tac atc tgt gcc cgc gaa gcc gcc 835
 Val Ala Pro Gln Glu Met Leu Val Tyr Ile Cys Ala Arg Glu Ala Ala
 230 235 240 245

gcc aac gcc tct tca agc acg tgc cgt gcc ttg tgc agc gcc tgc ttt 883
 Ala Asn Ala Ser Ser Thr Cys Arg Gly Leu Ser Ser Ala Ser Phe
 250 255 260

cct ccg ttg agg aat acg ccg tgc gcc tagaaatcga cacctcacac 930
 Pro Pro Leu Arg Asn Thr Pro Ser Ala
 265 270

att 933

<211> 270

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 636

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Phe Gly Phe Gly Gly Gln Gly Gly Ala Gly Gly Pro Gly Gly Leu Gly
 35 40 45

Asp Ile Leu Asn Gln Phe Gly Gln Met Leu Ser Gly Met Gly Asp Ser
 50 55 60

Met Asn Ser Pro Glu Ala Ala Gly Pro Val Asn Tyr Asp Leu Ala Ala
 65 70 75 80

Arg Ile Ala Arg Gln Ile Gly Arg Val Ala Pro Val Lys Asp Ser
 85 90 95

Glu Lys Glu Ala Val Glu Glu Ser Leu Arg Leu Ala Glu Leu Trp Leu
 100 105 110

Asp Asn Ala Thr Gln Leu Pro Thr Ser Gly His Arg Val Glu Ala Trp
 115 120 125

Asn Pro Glu Asn Trp Leu Glu Asn Thr Leu Pro Val Trp Lys Arg Leu
 130 135 140

Val Ser Pro Val Ala Glu Gln Met Asn Lys Ala Gln Leu Glu Asn Leu
 145 150 155 160

Pro Glu Glu Ala Arg Glu Met Met Gly Pro Met Ser Ser Leu Met Asn
 165 170 175

Ser Met Ser Ser Met Asn Phe Gly Val Gln Leu Gly Asn Ala Leu Gly
 180 185 190

Asp Leu Ala Lys Gln Thr Leu Thr Gly Ser Asp Phe Gly Leu Pro Ile
 195 200 205

Ser Pro Val Gly Val Ser Ala Val Leu Pro Gly Asn Ile Ala Glu Ala
 210 215 220

Ser Lys Gly Leu Asn Val Ala Pro Gln Glu Met Leu Val Tyr Ile Cys
 225 230 235 240

Ala Arg Glu Ala Ala Ala Asn Ala Ser Ser Ser Thr Cys Arg Gly Leu
 245 250 255

Ser Ser Ala Ser Phe Pro Pro Leu Arg Asn Thr Pro Ser Ala
 260 265 270

<210> 637

<211> 417

<212> DNA

<213> *Corynebacterium glutamicum*

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Val Gly Leu Glu Ile Asp Thr Ser His Ile Gln Glu Ala Met Gly Asn
      20              25              30
Phe Gln Met Asp Asn Pro Asp Pro Glu Arg Leu Gln Glu Met Met Asn
      35              40              45
Glu Leu Gln Gly Met Asp Leu Ser Pro Arg Ile Gly Ser Arg Asn Ala
      50              55              60
Asn Ala Val Ser Arg Leu Glu Thr Leu Leu Ala Leu Val Glu Gly Trp
  65              70              75              80

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Thr Pro

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gag cgc ctc gtt tcc tcc gtt gag gaa tac gcc gtc ggc cta gaa atc 163
Glu Arg Leu Val Ser Ser Val Glu Glu Tyr Ala Val Gly Leu Glu Ile
10 15 20

gac acc tca cac att caa gag gcc atg ggc aac ttc caa atg gac aac 211
Asp Thr Ser His Ile Gln Glu Ala Met Gly Asn Phe Gln Met Asp Asn
25 30 35

cca gat cct gaa cgc ctc cag gaa atg atg aac gaa ctc caa ggt atg 259
Pro Asp Pro Glu Arg Leu Gln Glu Met Met Asn Glu Leu Gln Gly Met
40 45 50

gac ctg tcc cca cgc atc gga tcc cgc aac gcc aac gca gta tcc cgc 307
Asp Leu Ser Pro Arg Ile Gly Ser Arg Asn Ala Asn Ala Val Ser Arg
55 60 65

ctg gaa act ctc ctc gca ctc gtc gaa ggc tgg gtc gac atc gta gtt 355
Leu Glu Thr Leu Leu Ala Leu Val Glu Gly Trp Val Asp Ile Val Val
70 75 80 85

acc caa gcc ctg agc gaa cgc att cca tca ccg acg cca tgaacgaagc 404
Thr Gln Ala Leu Ser Glu Arg Ile Pro Ser Pro Thr Pro
90 95

ctggaagcgc cgc 417

<400> 640
Val Pro Trp Leu Val Glu Arg Leu Val Ser Ser Val Glu Glu Tyr Ala
1 5 10 15

Val Gly Leu Glu Ile Asp Thr Ser His Ile Gln Glu Ala Met Gly Asn

	20		25		30										
Phe	Gln	Met	Asp	Asn	Pro	Asp	Pro	Glu	Arg	Leu	Gln	Glu	Met	Met	Asn
		35				40						45			
Glu	Leu	Gln	Gly	Met	Asp	Leu	Ser	Pro	Arg	Ile	Gly	Ser	Arg	Asn	Ala
	50					55					60				
Asn	Ala	Val	Ser	Arg	Leu	Glu	Thr	Leu	Leu	Ala	Leu	Val	Glu	Gly	Trp
	65				70					75					80
Val	Asp	Ile	Val	Val	Thr	Gln	Ala	Leu	Ser	Glu	Arg	Ile	Pro	Ser	Pro
			85						90					95	
Thr	Pro														

<210> 641

<211> 930

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(907)

<223> RXN01471

<400> 641

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                                         Met Gln Ser Phe Lys
                                         1                               5
acg ctt gaa tct tgg cct gtc gac aat gtt tgc gcc agt gtc atc tcc 163
Thr Leu Glu Ser Trp Pro Val Asp Asn Val Ser Ala Ser Val Ile Ser
                        10                        15                        20
gac ggc gcc gtg cac ttt tac ggc gac gtc gat cgt gtt ttt gaa ctc 211
Asp Gly Ala Val His Phe Tyr Gly Asp Val Asp Arg Val Phe Glu Leu
                        25                        30                        35
atg agt gtg aca aaa ctc ctg gcc acc tac ggt ttc ctt gtt gcc atc 259
Met Ser Val Thr Lys Leu Leu Ala Thr Tyr Gly Phe Leu Val Ala Ile
                        40                        45                        50
gaa gaa ggt gtt ttt gag ctc gat tca ccg atg ggt cct gaa gga tcc 307
Glu Glu Gly Val Phe Glu Leu Asp Ser Pro Met Gly Pro Glu Gly Ser
                        55                        60                        65
aca gtg agg cat ctg ctc tca cat gct tcc gcc gtg gca ttc gat aag 355
Thr Val Arg His Leu Leu Ser His Ala Ser Gly Val Ala Phe Asp Lys
                        70                        75                        80                        85
ccg gta gcg gaa aag gga gtg ggg gag cgc cgc att tac tcc tct gct 403
Pro Val Ala Glu Lys Gly Val Gly Glu Arg Arg Ile Tyr Ser Ser Ala
                        90                        95                        100
ggc atg gac atc ttg gcg gat gct gtt gcc gct gaa gct gaa atg ccg 451
Gly Met Asp Ile Leu Ala Asp Ala Val Ala Ala Glu Ala Glu Met Pro

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	105	110	115	
	ttt gca gag tat ctc cgc gag gct gtg ttc gag cct ttg gga atg gag			499
	Phe Ala Glu Tyr Leu Arg Glu Ala Val Phe Glu Pro Leu Gly Met Glu			
	120	125	130	
	aac tct gaa cta tgg ggt tct gcg ggc cac gag gcg cgc agc aca gtg			547
	Asn Ser Glu Leu Trp Gly Ser Ala Gly His Glu Ala Arg Ser Thr Val			
	135	140	145	
	gct gat ctg acc aag ttc ggc caa gag ctc acc gca cca act ctg atc			595
	Ala Asp Leu Thr Lys Phe Gly Gln Glu Leu Thr Ala Pro Thr Leu Ile			
	150	155	160	165
	tca cca gaa acc ctt gca gag gct ttc cag gtg caa ttc ccg gaa ctg			643
	Ser Pro Glu Thr Leu Ala Glu Ala Phe Gln Val Gln Phe Pro Glu Leu			
	170	175	180	
	att ggc acc gtc ccc ggt tat ggc atg cag aag ccg tgt ccg tgg gga			691
	Ile Gly Thr Val Pro Gly Tyr Gly Met Gln Lys Pro Cys Pro Trp Gly			
	185	190	195	
	ttg ggc ttt gaa att aag gga cag aag tcg ccg cac tgg aca ggt gac			739
	Leu Gly Phe Glu Ile Lys Gly Gln Lys Ser Pro His Trp Thr Gly Asp			
	200	205	210	
	ttg atg ccg gag aac act gct gga cac ttt gga cag tcg gga aca ttc			787
	Leu Met Pro Glu Asn Thr Ala Gly His Phe Gly Gln Ser Gly Thr Phe			
	215	220	225	
	ttt tgg act gtt cca ggc tca ggt caa gtc ggg gtt gtt ttg act gac			835
	Phe Trp Thr Val Pro Gly Ser Gly Gln Val Gly Val Val Leu Thr Asp			
	230	235	240	245
	cga aat ttc ggt cct tgg gct aaa ccg ttg tgg act gcc ttc aat gac			883
	Arg Asn Phe Gly Pro Trp Ala Lys Pro Leu Trp Thr Ala Phe Asn Asp			
	250	255	260	
	gaa gtc tgg gcc gag tta aat tca taaacttttg ccgtaattac ggt			930
	Glu Val Trp Ala Glu Leu Asn Ser			
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Ala	Ser Val Ile Ser Asp Gly Ala Val His Phe Tyr Gly Asp Val Asp			
	20	25	30	
Arg	Val Phe Glu Leu Met Ser Val Thr Lys Leu Leu Ala Thr Tyr Gly			
	35	40	45	
Phe	Leu Val Ala Ile Glu Glu Gly Val Phe Glu Leu Asp Ser Pro Met			
	50	55	60	

Gly Pro Glu Gly Ser Thr Val Arg His Leu Leu Ser His Ala Ser Gly
 65 70 75 80
 Val Ala Phe Asp Lys Pro Val Ala Glu Lys Gly Val Gly Glu Arg Arg
 85 90 95
 Ile Tyr Ser Ser Ala Gly Met Asp Ile Leu Ala Asp Ala Val Ala Ala
 100 105 110
 Glu Ala Glu Met Pro Phe Ala Glu Tyr Leu Arg Glu Ala Val Phe Glu
 115 120 125
 Pro Leu Gly Met Glu Asn Ser Glu Leu Trp Gly Ser Ala Gly His Glu
 130 135 140
 Ala Arg Ser Thr Val Ala Asp Leu Thr Lys Phe Gly Gln Glu Leu Thr
 145 150 155 160
 Ala Pro Thr Leu Ile Ser Pro Glu Thr Leu Ala Glu Ala Phe Gln Val
 165 170 175
 Gln Phe Pro Glu Leu Ile Gly Thr Val Pro Gly Tyr Gly Met Gln Lys
 180 185 190
 Pro Cys Pro Trp Gly Leu Gly Phe Glu Ile Lys Gly Gln Lys Ser Pro
 195 200 205
 His Trp Thr Gly Asp Leu Met Pro Glu Asn Thr Ala Gly His Phe Gly
 210 215 220
 Gln Ser Gly Thr Phe Phe Trp Thr Val Pro Gly Ser Gly Gln Val Gly
 225 230 235 240
 Val Val Leu Thr Asp Arg Asn Phe Gly Pro Trp Ala Lys Pro Leu Trp
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 Thr Ala Phe Asn Asp Glu Val Trp Ala Glu Leu Asn Ser
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<210> 643

<211> 930

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(907)

<223> FRXA01471

<400> 643

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 Met Gln Ser Phe Lys
 1 5

acg ctt gaa tct tgg cct gtc gac aat gtt tgc gcc agt gtc atc tcc 163
 Thr Leu Glu Ser Trp Pro Val Asp Asn Val Ser Ala Ser Val Ile Ser
 10 15 20

gac ggc gcc gtg cac ttt tac ggc gac gtc gat cgt gtt ttt gaa ctc Asp Gly Ala Val His Phe Tyr Gly Asp Val Asp Arg Val Phe Glu Leu	211
25 30 35	
atg agt gtg aca aaa ctc ctg gcc acc tac ggt ttc ctt gtt gcc atc Met Ser Val Thr Lys Leu Leu Ala Thr Tyr Gly Phe Leu Val Ala Ile	259
40 45 50	
gaa gaa ggt gtt ttt gag ctc gat tca ccg atg ggt cct gaa gga tcc Glu Glu Gly Val Phe Glu Leu Asp Ser Pro Met Gly Pro Glu Gly Ser	307
55 60 65	
aca gtg agg cat ctg ctc tca cat gct tcc ggc gtg gca ttc gat aag Thr Val Arg His Leu Leu Ser His Ala Ser Gly Val Ala Phe Asp Lys	355
70 75 80 85	
ccg gta gcg gaa aag gga gtg ggg gag cgc cgc att tac tcc tct gct Pro Val Ala Glu Lys Gly Val Gly Glu Arg Arg Ile Tyr Ser Ser Ala	403
90 95 100	
ggc atg gac atc ttg gcg gat gct gtt gcc gct gaa gct gaa atg ccg Gly Met Asp Ile Leu Ala Asp Ala Val Ala Ala Glu Ala Glu Met Pro	451
105 110 115	
ttt gca gag tat ctc cgc gag gct gtg ttc gag cct ttg gga atg gag Phe Ala Glu Tyr Leu Arg Glu Ala Val Phe Glu Pro Leu Gly Met Glu	499
120 125 130	
aac tct gaa cta tgg ggt tct gcg ggc cac gag gcg cgc agc aca gtg Asn Ser Glu Leu Trp Gly Ser Ala Gly His Glu Ala Arg Ser Thr Val	547
135 140 145	
gct gat ctg acc aag ttc ggc caa gag ctc acc gca cca act ctg atc Ala Asp Leu Thr Lys Phe Gly Gln Glu Leu Thr Ala Pro Thr Leu Ile	595
150 155 160 165	
tca cca gaa acc ctt gca gag gct ttc cag gtg caa ttc ccg gaa ctg Ser Pro Glu Thr Leu Ala Glu Ala Phe Gln Val Gln Phe Pro Glu Leu	643
170 175 180	
att ggc acc gtc ccc ggt tat ggc atg cag aag ccg tgt ccg tgg gga Ile Gly Thr Val Pro Gly Tyr Gly Met Gln Lys Pro Cys Pro Trp Gly	691
185 190 195	
ttg ggc ttt gaa att aag gga cag aag tcg ccg cac tgg aca ggt gac Leu Gly Phe Glu Ile Lys Gly Gln Lys Ser Pro His Trp Thr Gly Asp	739
200 205 210	
ttg atg ccg gag aac act gct gga cac ttt gga cag tcg gga aca ttc Leu Met Pro Glu Asn Thr Ala Gly His Phe Gly Gln Ser Gly Thr Phe	787
215 220 225	
ttt tgg act gtt cca ggc tca ggt caa gtc ggg gtt gtt ttg act gac Phe Trp Thr Val Pro Gly Ser Gly Gln Val Gly Val Val Leu Thr Asp	835
230 235 240 245	
cga aat ttc ggt cct tgg gct aaa ccg ttg tgg act gcc ttc aat gac Arg Asn Phe Gly Pro Trp Ala Lys Pro Leu Trp Thr Ala Phe Asn Asp	883
250 255 260	
gaa gtc tgg gcc gag tta aat tca taaacttttg ccgtaattac ggt	930

Glu Val Trp Ala Glu Leu Asn Ser
265

<210> 644

<211> 269

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 644

Met Gln Ser Phe Lys Thr Leu Glu Ser Trp Pro Val Asp Asn Val Ser
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20 25 30

Arg Val Phe Glu Leu Met Ser Val Thr Lys Leu Leu Ala Thr Tyr Gly
35 40 45

Phe Leu Val Ala Ile Glu Glu Gly Val Phe Glu Leu Asp Ser Pro Met
50 55 60

Gly Pro Glu Gly Ser Thr Val Arg His Leu Leu Ser His Ala Ser Gly
65 70 75 80

Val Ala Phe Asp Lys Pro Val Ala Glu Lys Gly Val Gly Glu Arg Arg
85 90 95

Ile Tyr Ser Ser Ala Gly Met Asp Ile Leu Ala Asp Ala Val Ala Ala
100 105 110

Glu Ala Glu Met Pro Phe Ala Glu Tyr Leu Arg Glu Ala Val Phe Glu
115 120 125

Pro Leu Gly Met Glu Asn Ser Glu Leu Trp Gly Ser Ala Gly His Glu
130 135 140

Ala Arg Ser Thr Val Ala Asp Leu Thr Lys Phe Gly Gln Glu Leu Thr
145 150 155 160

Ala Pro Thr Leu Ile Ser Pro Glu Thr Leu Ala Glu Ala Phe Gln Val
165 170 175

Gln Phe Pro Glu Leu Ile Gly Thr Val Pro Gly Tyr Gly Met Gln Lys
180 185 190

Pro Cys Pro Trp Gly Leu Gly Phe Glu Ile Lys Gly Gln Lys Ser Pro
195 200 205

His Trp Thr Gly Asp Leu Met Pro Glu Asn Thr Ala Gly His Phe Gly
210 215 220

Gln Ser Gly Thr Phe Phe Trp Thr Val Pro Gly Ser Gly Gln Val Gly
225 230 235 240

Val Val Leu Thr Asp Arg Asn Phe Gly Pro Trp Ala Lys Pro Leu Trp
245 250 255

Thr Ala Phe Asn Asp Glu Val Trp Ala Glu Leu Asn Ser
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<220>
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<222> (101)..(340)
<223> RXN01479
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20 25 30

Met Ile Asn Ser Pro Ala Thr Lys Ser Ala Val Asn Ala Arg Lys
35 40 45

Ala Ile Ala Asn Lys Leu Asp Pro Gln Pro Arg Met Lys Glu Val Lys
50 55 60

Asn Leu Arg Thr Ala Asp Gly His Glu Val Leu Glu Gln Asp Gln Asp
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 <211> 351
 <212> DNA
 <213> Corynebacterium glutamicum

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 Val Ile Gly Ala Ala
 1 5
 gca ggc tac gtg ctt ggc aca aag gcc ggc cgc aag cgt tac cac cag 163
 Ala Gly Tyr Val Leu Gly Thr Lys Ala Gly Arg Lys Arg Tyr His Gln
 10 15 20
 atc aaa aag gga tat gag gca gcg att aac tcc cct gcc acc aaa tct 211
 Ile Lys Lys Gly Tyr Glu Ala Ala Ile Asn Ser Pro Ala Thr Lys Ser
 25 30 35
 gca gta aac gcc gcc cgc aaa gcc att gcc aac aag ctg gat cgg cag 259
 Ala Val Asn Ala Ala Arg Lys Ala Ile Ala Asn Lys Leu Asp Pro Gln
 40 45 50
 ccc cgc atg aag gaa gta aaa aac ctg cgg act gcg gac ggg cat gaa 307
 Pro Arg Met Lys Glu Val Lys Asn Leu Arg Thr Ala Asp Gly His Glu
 55 60 65
 gtc ctc gag caa gac cag gac taaattaccc tctaaacgcc cgg 351
 Val Leu Glu Gln Asp Gln Asp
 70 75

<210> 648
 <211> 76
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 648
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 20 25 30
 Pro Ala Thr Lys Ser Ala Val Asn Ala Ala Arg Lys Ala Ile Ala Asn
 35 40 45
 Lys Leu Asp Pro Gln Pro Arg Met Lys Glu Val Lys Asn Leu Arg Thr
 50 55 60

Ala Asp Gly His Glu Val Leu Glu Gln Asp Gln Asp
65 70 75

<210> 649

<211> 669

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(646)

<223> RXN01484

<400> 649

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cagaacgcct aataatcggc acaaaattga ttoaattttg gtg ttg ggc aca gct 115
Val Leu Gly Thr Ala
1 5

caa tat gat gga gtt cca tcg agg cag ttt gct gct cgt ttg agg cat 163
Gln Tyr Asp Gly Val Pro Ser Arg Gln Phe Ala Ala Arg Leu Arg His
10 15 20

gcc gcg aag ctg tgg cgt ctt cat gaa atc cag cat gta tat act gtc 211
Ala Ala Lys Leu Trp Arg Leu His Glu Ile Gln His Val Tyr Thr Val
25 30 35

ggc gga aaa ctt cct gcc gat cgt ttc acc gaa gca gaa gtc gcg cgg 259
Gly Gly Lys Leu Pro Gly Asp Arg Phe Thr Glu Ala Glu Val Ala Arg
40 45 50

gag tat ttg atc aaa gag gcc gtg gat ccg gat ctg att ttt gtc tct 307
Glu Tyr Leu Ile Lys Glu Gly Val Asp Pro Asp Leu Ile Phe Val Ser
55 60 65

gca gtt gcc aat gac act gtc tcc tcc tat gag gcg ctt gat ccg gaa 355
Ala Val Gly Asn Asp Thr Val Ser Ser Tyr Glu Ala Leu Asp Pro Glu
70 75 80 85

aag ctt ggt cgg gtg ctg att gtt act gat ccg aac cat tcg tat cgg 403
Lys Leu Gly Arg Val Leu Ile Val Thr Asp Pro Asn His Ser Tyr Arg
90 95 100

gcg gtg cgc atc gcg cga cgc atg gcc ttt gac gcg aaa cct tcc ccg 451
Ala Val Arg Ile Ala Arg Arg Met Gly Phe Asp Ala Lys Pro Ser Pro
105 110 115

aca acc tat agt ccc gcg aag ttt ccg tcg ata gtt tat ttt ctg acc 499
Thr Thr Tyr Ser Pro Ala Lys Phe Pro Ser Ile Val Tyr Phe Leu Thr
120 125 130

ttg tcc cat gag tgg gcc ggg gta gta gta cag gac gtg tcg cgg ctc 547
Leu Ser His Glu Trp Gly Gly Val Val Val Gln Asp Val Ser Arg Leu
135 140 145

ttg ggt gaa cgg gtg ccc gat aag gtg aag cat ctt tgc gcg caa tcc 595
Leu Gly Glu Arg Val Pro Asp Lys Val Lys His Leu Cys Ala Gln Ser
150 155 160 165

aag gtc tgc tgc gcc ctt cgc ggc gtg cac gcc atg agc aac ttc gga 643
 Lys Val Cys Cys Ala Leu Arg Gly Val His Ala Met Ser Asn Phe Gly
 170 175 180

ggc tga aaa agta gatgtacccc tat 669
 Gly

<210> 650
 <211> 182
 <212> FRT
 <213> Corynebacterium glutamicum

<400> 650
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 20 25 30

His Val Tyr Thr Val Gly Gly Lys Leu Pro Gly Asp Arg Phe Thr Glu
 35 40 45

Ala Glu Val Ala Arg Glu Tyr Leu Ile Lys Glu Gly Val Asp Pro Asp
 50 55 60

Leu Ile Phe Val Ser Ala Val Gly Asn Asp Thr Val Ser Ser Tyr Glu
 65 70 75 80

Ala Leu Asp Pro Glu Lys Leu Gly Arg Val Leu Ile Val Thr Asp Pro
 85 90 95

Asn His Ser Tyr Arg Ala Val Arg Ile Ala Arg Arg Met Gly Phe Asp
 100 105 110

Ala Lys Pro Ser Pro Thr Thr Tyr Ser Pro Ala Lys Phe Pro Ser Ile
 115 120 125

Val Tyr Phe Leu Thr Leu Ser His Glu Trp Gly Gly Val Val Val Gln
 130 135 140

Asp Val Ser Arg Leu Leu Gly Glu Arg Val Pro Asp Lys Val Lys His
 145 150 155 160

Leu Cys Ala Gln Ser Lys Val Cys Cys Ala Leu Arg Gly Val His Ala
 165 170 175

Met Ser Asn Phe Gly Gly
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<210> 651
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                                   Val Leu Gly Thr Ala
                                   1           5
caa tat gat gga gtt cca tgc agg cag ttt gct gct cgt ttg agg cat 163
Gln Tyr Asp Gly Val Pro Ser Arg Gln Phe Ala Ala Arg Leu Arg His
               10           15           20
gcc gcg aag ctg tgg cgt ctt cat gaa atc cag cat gta tat act gtc 211
Ala Ala Lys Leu Trp Arg Leu His Glu Ile Gln His Val Tyr Thr Val
               25           30           35
ggc gga aaa ctt cct ggc gat cgt ttc acc gaa gca gaa gtc gcg cgg 259
Gly Gly Lys Leu Pro Gly Asp Arg Phe Thr Glu Ala Glu Val Ala Arg
               40           45           50
gag tat ttg atc aaa gag ggc gtg gat ccg gat ctg att ttt gtc tct 307
Glu Tyr Leu Ile Lys Glu Gly Val Asp Pro Asp Leu Ile Phe Val Ser
               55           60           65
gca gtt ggc aat gac act gtc tcc tcc tat gag gcg ctt gat ccg gaa 355
Ala Val Gly Asn Asp Thr Val Ser Ser Tyr Glu Ala Leu Asp Pro Glu
               70           75           80           85
aag ctt ggt cgg gtg ctg att gtt act gat ccg aac cat tgc tat cgg 403
Lys Leu Gly Arg Val Leu Ile Val Thr Asp Pro Asn His Ser Tyr Arg
               90           95           100
gcg gtg cgc atc gcg cga cgc atg ggc ttt gac gcg aaa cct tcc ccg 451
Ala Val Arg Ile Ala Arg Arg Met Gly Phe Asp Ala Lys Pro Ser Pro
               105           110           115
aca acc tat agt ccc gcg aag ttt ccg tgc ata gtt tat ttt ctg acc 499
Thr Thr Tyr Ser Pro Ala Lys Phe Pro Ser Ile Val Tyr Phe Leu Thr
               120           125           130
ttg tcc cat gag tgg ggc ggg gta gta gta cag gac gtg tgc cgg ctc 547
Leu Ser His Glu Trp Gly Gly Val Val Val Gln Asp Val Ser Arg Leu
               135           140           145
ttg ggt gaa cgg gtg ccc gat aag gtg aag cat ctt tgc gcg caa tcc 595
Leu Gly Glu Arg Val Pro Asp Lys Val Lys His Leu Cys Ala Gln Ser
               150           155           160           165
aag gtc tgc tgc gcc ctt cgc gcc gtg cac gcc atg agc aac ttc gga 643
Lys Val Cys Cys Ala Leu Arg Gly Val His Ala Met Ser Asn Phe Gly
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Gly

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<212> PRT

<213> Corynebacterium glutamicum

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His Val Tyr Thr Val Gly Gly Lys Leu Pro Gly Asp Arg Phe Thr Glu
 35 40 45

Ala Glu Val Ala Arg Glu Tyr Leu Ile Lys Glu Gly Val Asp Pro Asp
 50 55 60

Leu Ile Phe Val Ser Ala Val Gly Asn Asp Thr Val Ser Ser Tyr Glu
 65 70 75 80

Ala Leu Asp Pro Glu Lys Leu Gly Arg Val Leu Ile Val Thr Asp Pro
 85 90 95

Asn His Ser Tyr Arg Ala Val Arg Ile Ala Arg Arg Met Gly Phe Asp
 100 105 110

Ala Lys Pro Ser Pro Thr Thr Tyr Ser Pro Ala Lys Phe Pro Ser Ile
 115 120 125

Val Tyr Phe Leu Thr Leu Ser His Glu Trp Gly Gly Val Val Val Gln
 130 135 140

Asp Val Ser Arg Leu Leu Gly Glu Arg Val Pro Asp Lys Val Lys His
 145 150 155 160

Leu Cys Ala Gln Ser Lys Val Cys Cys Ala Leu Arg Gly Val His Ala
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Met Ser Asn Phe Gly Gly
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<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2152)

<223> RXN01485

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ttaactagtg tgccagctgg actcgtctaa ggtgggggacc atg aac ttt agt ttg 115
 Met Asn Phe Ser Leu
 1 5

gtg cat ctt cgg gaa aac gtc cgc cgt gta tcg gtc act gtg gca att 163
 Val His Leu Arg Glu Asn Val Arg Arg Val Ser Val Thr Val Ala Ile
 10 15 20

gga gct ggc gcg ctc ctt atc agt gga cca ttt ttt act gct cac act 211

Gly	Ala	Gly	Ala	Leu	Leu	Ile	Ser	Gly	Pro	Phe	Phe	Thr	Ala	His	Thr	
			25					30					35			
gca	gaa	gcc	aca	gaa	aca	tat	gtc	ttg	gct	gaa	tca	cca	gaa	ttt	tac	259
Ala	Glu	Ala	Thr	Glu	Thr	Tyr	Val	Leu	Ala	Glu	Ser	Pro	Glu	Phe	Tyr	
		40					45					50				
caa	gac	aat	gtc	act	gac	tac	acc	ggc	cag	att	tcc	tcg	tcc	gat	atc	307
Gln	Asp	Asn	Val	Thr	Asp	Tyr	Thr	Gly	Gln	Ile	Ser	Ser	Ser	Asp	Ile	
		55				60					65					
acc	aac	att	cag	gct	gcc	atc	gat	gat	gta	aag	gca	tct	gaa	caa	aag	355
Thr	Asn	Ile	Gln	Ala	Ala	Ile	Asp	Asp	Val	Lys	Ala	Ser	Glu	Gln	Lys	
		70			75					80					85	
gtt	att	ttc	gtt	gtt	ttc	cta	agc	tct	ttc	gac	gga	gtt	gac	cct	gaa	403
Val	Ile	Phe	Val	Val	Phe	Leu	Ser	Ser	Phe	Asp	Gly	Val	Asp	Pro	Glu	
				90					95					100		
acg	tg	acg	cag	caa	gca	ctc	caa	gcc	aac	ggc	ggc	gga	aac	gtc	ttg	451
Thr	Trp	Thr	Gln	Gln	Ala	Leu	Gln	Ala	Asn	Gly	Gly	Gly	Asn	Val	Leu	
			105				110						115			
att	tat	gca	ctc	gct	ccc	gag	gaa	cgg	cag	tac	ggc	atc	caa	ggt	ggt	499
Ile	Tyr	Ala	Leu	Ala	Pro	Glu	Glu	Arg	Gln	Tyr	Gly	Ile	Gln	Gly	Gly	
		120				125					130					
act	caa	tg	acc	gac	gct	gaa	ctc	gac	gcc	gcc	aac	aac	gct	gct	ttc	547
Thr	Gln	Trp	Thr	Asp	Ala	Glu	Leu	Asp	Ala	Ala	Asn	Asn	Ala	Ala	Phe	
		135			140						145					
cag	gca	ctt	tcc	caa	gaa	gat	tg	gca	ggc	tct	gca	cta	gcg	ctg	gca	595
Gln	Ala	Leu	Ser	Gln	Glu	Asp	Trp	Ala	Gly	Ser	Ala	Leu	Ala	Leu	Ala	
		150			155				160					165		
gaa	tca	gtt	ggt	tct	agt	tct	tcc	agc	tct	tcg	ggc	tcg	tcc	agc	tct	643
Glu	Ser	Val	Gly	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Ser	
			170					175						180		
tcc	gat	ttt	tcc	ggc	gct	tg	ttg	gct	gct	gcg	ggc	gtt	ggc	aca	gtg	691
Ser	Asp	Phe	Ser	Gly	Ala	Trp	Leu	Ala	Ala	Ala	Gly	Val	Gly	Thr	Val	
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gcc	gct	ggt	ggc	gga	att	tg	gcc	tat	tcc	cgc	agc	cgc	aag	aag	aaa	739
Ala	Ala	Gly	Gly	Gly	Ile	Trp	Ala	Tyr	Ser	Arg	Ser	Arg	Lys	Lys	Lys	
		200				205					210					
aca	agt	get	gca	acc	ttg	gaa	gat	gca	cgc	gaa	atc	gac	ccg	cgc	gat	787
Thr	Ser	Ala	Ala	Thr	Leu	Glu	Asp	Ala	Arg	Glu	Ile	Asp	Pro	Arg	Asp	
		215			220						225					
acc	aac	cgc	ctc	atg	cag	ctt	ccc	atg	gaa	act	ctc	gaa	cac	ctt	gcc	835
Thr	Asn	Arg	Leu	Met	Gln	Leu	Pro	Met	Glu	Thr	Leu	Glu	His	Leu	Ala	
		230			235				240					245		
caa	gaa	gag	ctc	acc	tcc	act	gat	gac	tcc	atc	cgt	cgc	gga	aaa	gaa	883
Gln	Glu	Glu	Leu	Thr	Ser	Thr	Asp	Asp	Ser	Ile	Arg	Arg	Gly	Lys	Glu	
			250					255						260		
gag	ctc	gct	atc	gct	acc	tcc	gag	ttc	gga	cca	gag	cgc	acc	cgc	agc	931
Glu	Leu	Ala	Ile	Ala	Thr	Ser	Glu	Phe	Gly	Pro	Glu	Arg	Thr	Arg	Ser	

265	270	275	
ttc aac cgc gcc atg aac cac tcc acc ggc acc ctg caa aaa gcc ttt	979		
Phe Asn Arg Ala Met Asn His Ser Thr Gly Thr Leu Gln Lys Ala Phe			
280	285	290	
gag att cag cag cgc ctc aac gat tct atc cca gaa tcc gaa gcc gaa	1027		
Glu Ile Gln Gln Arg Leu Asn Asp Ser Ile Pro Glu Ser Glu Ala Glu			
295	300	305	
cgt caa tcc atg ctg gta gaa atc att tca tcc tgt ggc caa gcc gac	1075		
Arg Gln Ser Met Leu Val Glu Ile Ile Ser Ser Cys Gly Gln Ala Asp			
310	315	320	325
gat gcc ctc gac gcc gaa gcc caa aac ttt gcc gat atg cgc aac ctg	1123		
Asp Ala Leu Asp Ala Glu Ala Gln Asn Phe Ala Asp Met Arg Asn Leu			
330	335	340	
ctg atc aac gcg gcc agc aaa ttg gat gct ctc acc caa aaa tcc gtc	1171		
Leu Ile Asn Ala Gly Ser Lys Leu Asp Ala Leu Thr Gln Lys Ser Val			
345	350	355	
gac ctg cgc acc cgc ctc ccc aag gcc caa gaa aca ctc gct ggc ctg	1219		
Asp Leu Arg Thr Arg Leu Pro Lys Ala Gln Glu Thr Leu Ala Gly Leu			
360	365	370	
cgc act cgc tac tca gca gag gtc ctt gaa agc atc gac gac aac gtc	1267		
Arg Thr Arg Tyr Ser Ala Glu Val Leu Glu Ser Ile Asp Asp Asn Val			
375	380	385	
gac ctc gcc agc gct tgc ctc gac gaa gca gaa gaa gtc ctg cca cag	1315		
Asp Leu Ala Ser Ala Ser Leu Asp Glu Ala Glu Glu Val Leu Pro Gln			
390	395	400	405
gcg tac gag ata gag tcc atg ccc gca gcc gag cag gcc ggg ctt atc	1363		
Ala Tyr Glu Ile Glu Ser Met Pro Ala Gly Glu Gln Gly Gly Leu Ile			
410	415	420	
gac gcg atc cgt cac atc gag cac gcc atc act acc gca gac aaa ctc	1411		
Asp Ala Ile Arg His Ile Glu His Ala Ile Thr Thr Ala Asp Lys Leu			
425	430	435	
ctc gcg gcc gtc gag cat gcc gat gaa aac atc tcc aca gcc aaa gca	1459		
Leu Ala Gly Val Glu His Ala Asp Glu Asn Ile Ser Thr Ala Lys Ala			
440	445	450	
aac gtt gcc gat ctg atc caa gaa atc tca gac gaa atc aac gaa gcc	1507		
Asn Val Ala Asp Leu Ile Gln Glu Ile Ser Asp Glu Ile Asn Glu Ala			
455	460	465	
ggc caa ctc aaa caa agc gca gga gcc gac ggt gcc cgt gcc gac tgg	1555		
Gly Gln Leu Lys Gln Ser Ala Gly Ala Asp Gly Ala Arg Ala Asp Trp			
470	475	480	485
gcc tcc ctc gac gat gct gtc cgc gca gcc agc gca gca cta atc acc	1603		
Ala Ser Leu Asp Asp Ala Val Arg Ala Ala Ser Ala Ala Leu Ile Thr			
490	495	500	
gca tca gca gac gcc gaa aag gat cgg ctc gga acc tac aca gaa ctt	1651		
Ala Ser Ala Asp Ala Glu Lys Asp Pro Leu Gly Thr Tyr Thr Glu Leu			
505	510	515	

gtc gat gtc gac tcc gcc ctc gac act caa ctt gac aca ctt cgc gcc 1699
 Val Asp Val Asp Ser Ala Leu Asp Thr Gln Leu Asp Thr Leu Arg Ala
 520 525 530

acc gca gct gat caa gcc cgc cag cta cgc gta ttc gac caa cag ctg 1747
 Thr Ala Ala Asp Gln Ala Arg Gln Leu Arg Val Phe Asp Gln Gln Leu
 535 540 545

caa tct gca aga agc caa atc caa aag gcc gaa gac ctc atc tcc acc 1795
 Gln Ser Ala Arg Ser Gln Ile Gln Lys Ala Glu Asp Leu Ile Ser Thr
 550 555 560 565

cgc ggt cgc atc gta aaa tcc gaa gcc cgc acc cac ctg gcc aac gca 1843
 Arg Gly Arg Ile Val Lys Ser Glu Ala Arg Thr His Leu Ala Asn Ala
 570 575 580

caa aag ctg tac gcc atg gca caa caa aac cgc acc cgc gac acc cgt 1891
 Gln Lys Leu Tyr Ala Met Ala Gln Gln Asn Arg Thr Arg Asp Thr Arg
 585 590 595

gca gga att gat tac gga cgt caa gca gca gtc gca gcc caa cgc gcc 1939
 Ala Gly Ile Asp Tyr Gly Arg Gln Ala Ala Val Ala Ala Gln Arg Ala
 600 605 610

agc aag tca gca caa aac gac atc acc acc tac aac aat cgc cac aat 1987
 Ser Lys Ser Ala Gln Asn Asp Ile Thr Thr Tyr Asn Asn Arg His Asn
 615 620 625

tcc ggt ggc gga acc acc ggt gcg att gtc acc ggc atg gtg atc aac 2035
 Ser Gly Gly Gly Thr Thr Gly Ala Ile Val Thr Gly Met Val Ile Asn
 630 635 640 645

tcg att ctc aac agc ggc cgc ggt ggc ggt ttc tgt gga ggc gga ggc 2083
 Ser Ile Leu Asn Ser Gly Arg Gly Gly Phe Cys Gly Gly Gly Gly
 650 655 660

ttt ggt gga ggc ggt ggc ggc ttc agc ggt ggt ggc ggt ggc gga gga 2131
 Phe Gly Gly Gly Gly Gly Phe Ser Gly Gly Gly Gly Gly Gly Gly
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<211> 684

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<213> *Corynebacterium glutamicum*

<400> 654

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 Phe Thr Ala His Thr Ala Glu Ala Thr Glu Thr Tyr Val Leu Ala Glu
 35 40 45

Ser Pro Glu Phe Tyr Gln Asp Asn Val Thr Asp Tyr Thr Gly Gln Ile
 50 55 60
 Ser Ser Ser Asp Ile Thr Asn Ile Gln Ala Ala Ile Asp Asp Val Lys
 65 70 75 80
 Ala Ser Glu Gln Lys Val Ile Phe Val Val Phe Leu Ser Ser Phe Asp
 85 90 95
 Gly Val Asp Pro Glu Thr Trp Thr Gln Gln Ala Leu Gln Ala Asn Gly
 100 105 110
 Gly Gly Asn Val Leu Ile Tyr Ala Leu Ala Pro Glu Glu Arg Gln Tyr
 115 120 125
 Gly Ile Gln Gly Gly Thr Gln Trp Thr Asp Ala Glu Leu Asp Ala Ala
 130 135 140
 Asn Asn Ala Ala Phe Gln Ala Leu Ser Gln Glu Asp Trp Ala Gly Ser
 145 150 155 160
 Ala Leu Ala Leu Ala Glu Ser Val Gly Ser Ser Ser Ser Ser Ser Ser
 165 170 175
 Gly Ser Ser Ser Ser Ser Asp Phe Ser Gly Ala Trp Leu Ala Ala Ala
 180 185 190
 Gly Val Gly Thr Val Ala Ala Gly Gly Gly Ile Trp Ala Tyr Ser Arg
 195 200 205
 Ser Arg Lys Lys Lys Thr Ser Ala Ala Thr Leu Glu Asp Ala Arg Glu
 210 215 220
 Ile Asp Pro Arg Asp Thr Asn Arg Leu Met Gln Leu Pro Met Glu Thr
 225 230 235 240
 Leu Glu His Leu Ala Gln Glu Glu Leu Thr Ser Thr Asp Asp Ser Ile
 245 250 255
 Arg Arg Gly Lys Glu Glu Leu Ala Ile Ala Thr Ser Glu Phe Gly Pro
 260 265 270
 Glu Arg Thr Arg Ser Phe Asn Arg Ala Met Asn His Ser Thr Gly Thr
 275 280 285
 Leu Gln Lys Ala Phe Glu Ile Gln Gln Arg Leu Asn Asp Ser Ile Pro
 290 295 300
 Glu Ser Glu Ala Glu Arg Gln Ser Met Leu Val Glu Ile Ile Ser Ser
 305 310 315 320
 Cys Gly Gln Ala Asp Asp Ala Leu Asp Ala Glu Ala Gln Asn Phe Ala
 325 330 335
 Asp Met Arg Asn Leu Leu Ile Asn Ala Gly Ser Lys Leu Asp Ala Leu
 340 345 350
 Thr Gln Lys Ser Val Asp Leu Arg Thr Arg Leu Pro Lys Ala Gln Glu
 355 360 365
 Thr Leu Ala Gly Leu Arg Thr Arg Tyr Ser Ala Glu Val Leu Glu Ser

370

375

380

Ile Asp Asp Asn Val Asp Leu Ala Ser Ala Ser Leu Asp Glu Ala Glu
 385 390 395 400

Glu Val Leu Pro Gln Ala Tyr Glu Ile Glu Ser Met Pro Ala Gly Glu
 405 410 415

Gln Gly Gly Leu Ile Asp Ala Ile Arg His Ile Glu His Ala Ile Thr
 420 425 430

Thr Ala Asp Lys Leu Leu Ala Gly Val Glu His Ala Asp Glu Asn Ile
 435 440 445

Ser Thr Ala Lys Ala Asn Val Ala Asp Leu Ile Gln Glu Ile Ser Asp
 450 455 460

Glu Ile Asn Glu Ala Gly Gln Leu Lys Gln Ser Ala Gly Ala Asp Gly
 465 470 475 480

Ala Arg Ala Asp Trp Ala Ser Leu Asp Asp Ala Val Arg Ala Ala Ser
 485 490 495

Ala Ala Leu Ile Thr Ala Ser Ala Asp Ala Glu Lys Asp Pro Leu Gly
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Thr Tyr Thr Glu Leu Val Asp Val Asp Ser Ala Leu Asp Thr Gln Leu
 515 520 525

Asp Thr Leu Arg Ala Thr Ala Ala Asp Gln Ala Arg Gln Leu Arg Val
 530 535 540

Phe Asp Gln Gln Leu Gln Ser Ala Arg Ser Gln Ile Gln Lys Ala Glu
 545 550 555 560

Asp Leu Ile Ser Thr Arg Gly Arg Ile Val Lys Ser Glu Ala Arg Thr
 565 570 575

His Leu Ala Asn Ala Gln Lys Leu Tyr Ala Met Ala Gln Gln Asn Arg
 580 585 590

Thr Arg Asp Thr Arg Ala Gly Ile Asp Tyr Gly Arg Gln Ala Ala Val
 595 600 605

Ala Ala Gln Arg Ala Ser Lys Ser Ala Gln Asn Asp Ile Thr Thr Tyr
 610 615 620

Asn Asn Arg His Asn Ser Gly Gly Gly Thr Thr Gly Ala Ile Val Thr
 625 630 635 640

Gly Met Val Ile Asn Ser Ile Leu Asn Ser Gly Arg Gly Gly Gly Phe
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Cys Gly Gly Gly Gly Phe Gly Gly Gly Gly Gly Phe Ser Gly Gly
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<211> 2175

<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (101)..(2152)

<223> FRXA01485

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				1				5	

gtg	cat	ott	egg	gaa	aac	gtc	cgc	cgt	gta	tcg	gtc	act	gtg	gca	att	163
Val	His	Leu	Arg	Glu	Asn	Val	Arg	Arg	Val	Ser	Val	Thr	Val	Ala	Ile	
			10						15					20		

gga	gct	ggc	gcg	ctc	ott	atc	agt	gga	cca	ttt	ttt	act	gct	cac	act	211
Gly	Ala	Gly	Ala	Leu	Leu	Ile	Ser	Gly	Pro	Phe	Phe	Thr	Ala	His	Thr	
			25					30					35			

gca	gaa	gcc	aca	gaa	aca	tat	gtc	ttg	gct	gaa	tca	cca	gaa	ttt	tac	259
Ala	Glu	Ala	Thr	Glu	Thr	Tyr	Val	Leu	Ala	Glu	Ser	Pro	Glu	Phe	Tyr	
		40					45					50				

caa	gac	aat	gtc	act	gac	tac	acc	ggc	cag	att	tcc	tcg	tcc	gat	atc	307
Gln	Asp	Asn	Val	Thr	Asp	Tyr	Thr	Gly	Gln	Ile	Ser	Ser	Ser	Asp	Ile	
		55				60					65					

acc	aac	att	cag	gct	gcc	atc	gat	gat	gta	aag	gca	tct	gaa	caa	aag	355
Thr	Asn	Ile	Gln	Ala	Ala	Ile	Asp	Asp	Val	Lys	Ala	Ser	Glu	Gln	Lys	
	70				75				80						85	

gtt	att	ttc	gtt	gtt	ttc	cta	agc	tct	ttc	gac	gga	gtt	gac	cct	gaa	403
Val	Ile	Phe	Val	Val	Phe	Leu	Ser	Ser	Phe	Asp	Gly	Val	Asp	Pro	Glu	
			90						95					100		

acg	tggt	acg	cag	caa	gca	ctc	caa	gcc	aac	ggc	ggc	gga	aac	gtc	ttg	451
Thr	Trp	Thr	Gln	Gln	Ala	Leu	Gln	Ala	Asn	Gly	Gly	Gly	Asn	Val	Leu	
			105					110					115			

att	tat	gca	ctc	gct	ccc	gag	gaa	cgg	cag	tac	ggc	atc	caa	ggt	ggt	499
Ile	Tyr	Ala	Leu	Ala	Pro	Glu	Glu	Arg	Gln	Tyr	Gly	Ile	Gln	Gly	Gly	
		120					125					130				

act	caa	tggt	acc	gac	gct	gaa	ctc	gac	gcc	gcc	aac	aac	gct	gct	ttc	547
Thr	Gln	Trp	Thr	Asp	Ala	Glu	Leu	Asp	Ala	Ala	Asn	Asn	Ala	Ala	Phe	
		135				140					145					

cag	gca	ott	tcc	caa	gaa	gat	tggt	gca	ggc	tct	gca	cta	gcg	ctg	gca	595
Gln	Ala	Leu	Ser	Gln	Glu	Asp	Trp	Ala	Gly	Ser	Ala	Leu	Ala	Leu	Ala	
		150			155					160				165		

gaa	tca	gtt	ggt	tct	agt	tct	tcc	agc	tct	tcg	ggc	tcg	tcc	agc	tct	643
Glu	Ser	Val	Gly	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Ser	
			170					175						180		

tcc	gat	ttt	tcc	ggc	gct	tggt	ttg	gct	gct	gcg	ggc	gtt	ggc	aca	gtg	691
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Ser	Asp	Phe	Ser	Gly	Ala	Trp	Leu	Ala	Ala	Ala	Gly	Val	Gly	Thr	Val	
			185					190					195			
gcc	gct	ggt	ggc	gga	att	tgg	gcc	tat	tcc	cgc	agc	cgc	aag	aag	aaa	739
Ala	Ala	Gly	Gly	Gly	Ile	Trp	Ala	Tyr	Ser	Arg	Ser	Arg	Lys	Lys	Lys	
		200					205					210				
aca	agt	gct	gca	acc	ttg	gaa	gat	gca	cgc	gaa	atc	gac	ccg	cgc	gat	787
Thr	Ser	Ala	Ala	Thr	Leu	Glu	Asp	Ala	Arg	Glu	Ile	Asp	Pro	Arg	Asp	
		215				220					225					
acc	aac	cgc	ctc	atg	cag	ctt	ccc	atg	gaa	act	ctc	gaa	cac	ctt	gcc	835
Thr	Asn	Arg	Leu	Met	Gln	Leu	Pro	Met	Glu	Thr	Leu	Glu	His	Leu	Ala	
		230			235					240				245		
caa	gaa	gag	ctc	acc	tcc	act	gat	gac	tcc	atc	cgt	cgc	gga	aaa	gaa	883
Gln	Glu	Glu	Leu	Thr	Ser	Thr	Asp	Asp	Ser	Ile	Arg	Arg	Gly	Lys	Glu	
			250					255						260		
gag	ctc	gct	atc	gct	acc	tcc	gag	ttc	gga	cca	gag	cgc	acc	cgc	agc	931
Glu	Leu	Ala	Ile	Ala	Thr	Ser	Glu	Phe	Gly	Pro	Glu	Arg	Thr	Arg	Ser	
			265					270					275			
ttc	aac	cgc	gcc	atg	aac	cac	tcc	acc	ggc	acc	ctg	caa	aaa	gcc	ttt	979
Phe	Asn	Arg	Ala	Met	Asn	His	Ser	Thr	Gly	Thr	Leu	Gln	Lys	Ala	Phe	
		280					285					290				
gag	att	cag	cag	cgc	ctc	aac	gat	tct	atc	cca	gaa	tcc	gaa	gcc	gaa	1027
Glu	Ile	Gln	Gln	Arg	Leu	Asn	Asp	Ser	Ile	Pro	Glu	Ser	Glu	Ala	Glu	
		295				300					305					
cgt	caa	tcc	atg	ctg	gta	gaa	atc	att	tca	tcc	tgt	ggc	caa	gcc	gac	1075
Arg	Gln	Ser	Met	Leu	Val	Glu	Ile	Ile	Ser	Ser	Cys	Gly	Gln	Ala	Asp	
		310			315					320				325		
gat	gcc	ctc	gac	gcc	gaa	gcc	caa	aac	ttt	gcc	gat	atg	cgc	aac	ctg	1123
Asp	Ala	Leu	Asp	Ala	Glu	Ala	Gln	Asn	Phe	Ala	Asp	Met	Arg	Asn	Leu	
			330					335						340		
ctg	atc	aac	gcg	ggc	agc	aaa	ttg	gat	gct	ctc	acc	caa	aaa	tcc	gtc	1171
Leu	Ile	Asn	Ala	Gly	Ser	Lys	Leu	Asp	Ala	Leu	Thr	Gln	Lys	Ser	Val	
			345				350						355			
gac	ctg	cgc	acc	cgc	ctc	ccc	aag	gcc	caa	gaa	aca	ctc	gct	ggc	ctg	1219
Asp	Leu	Arg	Thr	Arg	Leu	Pro	Lys	Ala	Gln	Glu	Thr	Leu	Ala	Gly	Leu	
		360				365					370					
cgc	act	cgc	tac	tca	gca	gag	gtc	ctt	gaa	agc	atc	gac	gac	aac	gtc	1267
Arg	Thr	Arg	Tyr	Ser	Ala	Glu	Val	Leu	Glu	Ser	Ile	Asp	Asp	Asn	Val	
		375				380					385					
gac	ctc	gcc	agc	gct	tcg	ctc	gac	gaa	gca	gaa	gaa	gtc	ctg	cca	cag	1315
Asp	Leu	Ala	Ser	Ala	Ser	Leu	Asp	Glu	Ala	Glu	Glu	Val	Leu	Pro	Gln	
		390			395				400					405		
gcg	tac	gag	ata	gag	tcc	atg	ccc	gca	ggc	gag	cag	ggc	ggg	ctt	atc	1363
Ala	Tyr	Glu	Ile	Glu	Ser	Met	Pro	Ala	Gly	Glu	Gln	Gly	Gly	Leu	Ile	
			410					415					420			
gac	gcg	atc	cgt	cac	atc	gag	cac	gcc	atc	act	acc	gca	gac	aaa	ctc	1411
Asp	Ala	Ile	Arg	His	Ile	Glu	His	Ala	Ile	Thr	Thr	Ala	Asp	Lys	Leu	

	425	430	435	
	ctc gcg ggc gtc gag cat gcc gat gaa aac atc tcc aca gcc aaa gca			1459
	Leu Ala Gly Val Glu His Ala Asp Glu Asn Ile Ser Thr Ala Lys Ala			
	440	445	450	
	aac gtt gcc gat ctg atc caa gaa atc tca gac gaa atc aac gaa gcc			1507
	Asn Val Ala Asp Leu Ile Gln Glu Ile Ser Asp Gly Ala Ile Asn Glu Ala			
	455	460	465	
	ggc caa ctc aaa caa agc gca gga gcc gac ggt gcc cgt gcc gac tgg			1555
	Gly Gln Leu Lys Gln Ser Ala Gly Ala Asp Gly Ala Arg Ala Asp Trp			
	470	475	480	485
	gcc tcc ctc gac gat gct gtc cgc gca gcc agc gca gca cta atc acc			1603
	Ala Ser Leu Asp Asp Ala Val Arg Ala Ala Ser Ala Ala Leu Ile Thr			
	490	495	500	
	gca tca gca gac gcc gaa aag gat cgc ctc gga acc tac aca gaa ctt			1651
	Ala Ser Ala Asp Ala Glu Lys Asp Pro Leu Gly Thr Tyr Thr Glu Leu			
	505	510	515	
	gtc gat gtc gac tcc gcc ctc gac act caa ctt gac aca ctt cgc gcc			1699
	Val Asp Val Asp Ser Ala Leu Asp Thr Gln Leu Asp Thr Leu Arg Ala			
	520	525	530	
	acc gca gct gat caa gcc cgc cag cta cgc gta ttc gac caa cag ctg			1747
	Thr Ala Ala Asp Gln Ala Arg Gln Leu Arg Val Phe Asp Gln Gln Leu			
	535	540	545	
	caa tct gca aga agc caa atc caa aag gcc gaa gac ctc atc tcc acc			1795
	Gln Ser Ala Arg Ser Gln Ile Gln Lys Ala Glu Asp Leu Ile Ser Thr			
	550	555	560	565
	cgc ggt cgc atc gta aaa tcc gaa gcc cgc acc cac ctg gcc aac gca			1843
	Arg Gly Arg Ile Val Lys Ser Glu Ala Arg Thr His Leu Ala Asn Ala			
	570	575	580	
	caa aag ctg tac gcc atg gca caa caa aac cgc acc cgc gac acc cgt			1891
	Gln Lys Leu Tyr Ala Met Ala Gln Gln Asn Arg Thr Arg Asp Thr Arg			
	585	590	595	
	gca gga att gat tac gga cgt caa gca gca gtc gca gcc caa cgc gcc			1939
	Ala Gly Ile Asp Tyr Gly Arg Gln Ala Ala Val Ala Ala Gln Arg Ala			
	600	605	610	
	agc aag tca gca caa aac gac atc acc acc tac aac aat cgc cac aat			1987
	Ser Lys Ser Ser Ala Gln Asn Asp Ile Thr Thr Tyr Asn Asn Arg His Asn			
	615	620	625	
	tcc ggt ggc gga acc acc ggt gcg att gtc acc ggc atg gtg atc aac			2035
	Ser Gly Gly Gly Thr Thr Gly Ala Ile Val Thr Gly Met Val Ile Asn			
	630	635	640	645
	tcg att ctc aac agc ggc cgc ggt ggc ggt ttc tgt gga ggc gga ggc			2083
	Ser Ile Leu Asn Ser Gly Arg Gly Gly Gly Phe Cys Gly Gly Gly Gly			
	650	655	660	
	ttt ggt gga ggc ggt ggc ggc ttc agc ggt ggt ggc ggt ggc gga gga			2131
	Phe Gly Gly Gly Gly Gly Phe Ser Gly Gly Gly Gly Gly Gly Gly			
	665	670	675	

ggg ttc cgc gga ggc cgc ttc tagcctgaaa cgagcaaaac caa 2175
 Gly Phe Arg Gly Gly Arg Phe
 680

<210> 656

<211> 684

<212> PRT

<213> Corynebacterium glutamicum

<400> 656

Met Asn Phe Ser Leu Val His Leu Arg Glu Asn Val Arg Arg Val Ser
 1 5 10 15

Val Thr Val Ala Ile Gly Ala Gly Ala Leu Leu Ile Ser Gly Pro Phe
 20 25 30

Phe Thr Ala His Thr Ala Glu Ala Thr Glu Thr Tyr Val Leu Ala Glu
 35 40 45

Ser Pro Glu Phe Tyr Gln Asp Asn Val Thr Asp Tyr Thr Gly Gln Ile
 50 55 60

Ser Ser Ser Asp Ile Thr Asn Ile Gln Ala Ala Ile Asp Asp Val Lys
 65 70 75 80

Ala Ser Glu Gln Lys Val Ile Phe Val Val Phe Leu Ser Ser Phe Asp
 85 90 95

Gly Val Asp Pro Glu Thr Trp Thr Gln Gln Ala Leu Gln Ala Asn Gly
 100 105 110

Gly Gly Asn Val Leu Ile Tyr Ala Leu Ala Pro Glu Glu Arg Gln Tyr
 115 120 125

Gly Ile Gln Gly Gly Thr Gln Trp Thr Asp Ala Glu Leu Asp Ala Ala
 130 135 140

Asn Asn Ala Ala Phe Gln Ala Leu Ser Gln Glu Asp Trp Ala Gly Ser
 145 150 155 160

Ala Leu Ala Leu Ala Glu Ser Val Gly Ser Ser Ser Ser Ser Ser
 165 170 175

Gly Ser Ser Ser Ser Asp Phe Ser Gly Ala Trp Leu Ala Ala Ala
 180 185 190

Gly Val Gly Thr Val Ala Ala Gly Gly Gly Ile Trp Ala Tyr Ser Arg
 195 200 205

Ser Arg Lys Lys Lys Thr Ser Ala Ala Thr Leu Glu Asp Ala Arg Glu
 210 215 220

Ile Asp Pro Arg Asp Thr Asn Arg Leu Met Gln Leu Pro Met Glu Thr
 225 230 235 240

Leu Glu His Leu Ala Gln Glu Glu Leu Thr Ser Thr Asp Asp Ser Ile
 245 250 255

Arg Arg Gly Lys Glu Glu Leu Ala Ile Ala Thr Ser Glu Phe Gly Pro

260	265	270
Glu Arg Thr Arg Ser Phe Asn Arg Ala Met Asn His Ser Thr Gly Thr		
275	280	285
Leu Gln Lys Ala Phe Glu Ile Gln Gln Arg Leu Asn Asp Ser Ile Pro		
290	295	300
Glu Ser Glu Ala Glu Arg Gln Ser Met Leu Val Glu Ile Ile Ser Ser		
305	310	315
Cys Gly Gln Ala Asp Asp Ala Leu Asp Ala Glu Ala Gln Asn Phe Ala		
325	330	335
Asp Met Arg Asn Leu Leu Ile Asn Ala Gly Ser Lys Leu Asp Ala Leu		
340	345	350
Thr Gln Lys Ser Val Asp Leu Arg Thr Arg Leu Pro Lys Ala Gln Glu		
355	360	365
Thr Leu Ala Gly Leu Arg Thr Arg Tyr Ser Ala Glu Val Leu Glu Ser		
370	375	380
Ile Asp Asp Asn Val Asp Leu Ala Ser Ala Ser Leu Asp Glu Ala Glu		
385	390	395
Glu Val Leu Pro Gln Ala Tyr Glu Ile Glu Ser Met Pro Ala Gly Glu		
405	410	415
Gln Gly Gly Leu Ile Asp Ala Ile Arg His Ile Glu His Ala Ile Thr		
420	425	430
Thr Ala Asp Lys Leu Leu Ala Gly Val Glu His Ala Asp Glu Asn Ile		
435	440	445
Ser Thr Ala Lys Ala Asn Val Ala Asp Leu Ile Gln Glu Ile Ser Asp		
450	455	460
Glu Ile Asn Glu Ala Gly Gln Leu Lys Gln Ser Ala Gly Ala Asp Gly		
465	470	475
Ala Arg Ala Asp Trp Ala Ser Leu Asp Asp Ala Val Arg Ala Ala Ser		
485	490	495
Ala Ala Leu Ile Thr Ala Ser Ala Asp Ala Glu Lys Asp Pro Leu Gly		
500	505	510
Thr Tyr Thr Glu Leu Val Asp Val Asp Ser Ala Leu Asp Thr Gln Leu		
515	520	525
Asp Thr Leu Arg Ala Thr Ala Ala Asp Gln Ala Arg Gln Leu Arg Val		
530	535	540
Phe Asp Gln Gln Leu Gln Ser Ala Arg Ser Gln Ile Gln Lys Ala Glu		
545	550	555
Asp Leu Ile Ser Thr Arg Gly Arg Ile Val Lys Ser Glu Ala Arg Thr		
565	570	575
His Leu Ala Asn Ala Gln Lys Leu Tyr Ala Met Ala Gln Gln Asn Arg		
580	585	590

Thr Arg Asp Thr Arg Ala Gly Ile Asp Tyr Gly Arg Gln Ala Ala Val
 595 600 605

Ala Ala Gln Arg Ala Ser Lys Ser Ala Gln Asn Asp Ile Thr Thr Tyr
 610 615 620

Asn Asn Arg His Asn Ser Gly Gly Gly Thr Thr Gly Ala Ile Val Thr
 625 630 635 640

Gly Met Val Ile Asn Ser Ile Leu Asn Ser Gly Arg Gly Gly Gly Phe
 645 650 655

Cys Gly Gly Gly Gly Phe Gly Gly Gly Gly Gly Phe Ser Gly Gly
 660 665 670

Gly Gly Gly Gly Gly Phe Arg Gly Gly Arg Phe
 675 680

<210> 657

<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> RXN01492

<400> 657

tgaagtgggc gcgttagcct cggcgcgtgg caaaccacat ttgctggact gcaggcataa 60

tggacaaaaga ctttagcaa caactatgtg gaggtgacag gtg acc aca act ctg 115
 Val Thr Thr Thr Leu 5
 1

tgg gcg gtt tct gac ctc cat gca gcg gtg aaa gct aac gct gat cca 163
 Trp Ala Val Ser Asp Leu His Ala Ala Val Lys Ala Asn Ala Asp Pro 20
 10 15

att gag aat att cag cct aag gat ccg tct gac tgg ttg att gtt gca 211
 Ile Glu Asn Ile Gln Pro Lys Asp Pro Ser Asp Trp Leu Ile Val Ala 35
 25 30

ggt gac gtg gcg gaa cgt acc gaa ttg gtg ctg gaa att ttg gca cgt 259
 Gly Asp Val Ala Glu Arg Thr Glu Leu Val Leu Glu Ile Leu Ala Arg 50
 40 45

ttg cgc agg cgc ttt gcc aag gtg atc tgg gtt ccg ggt aac cat gag 307
 Leu Arg Arg Arg Phe Ala Lys Val Ile Trp Val Pro Gly Asn His Glu 65
 55 60

ttg ttt tct cgc tcc gcg gac cgc tat cag ggg cgc gat aag tac tct 355
 Leu Phe Ser Arg Ser Ala Asp Arg Tyr Gln Gly Arg Asp Lys Tyr Ser 85
 70 75 80

gaa ctc gtt gaa ggc tgc cgc aag att gat gtg ttg act ccg gag gac 403
 Glu Leu Val Glu Gly Cys Arg Lys Ile Asp Val Leu Thr Pro Glu Asp 100
 90 95

cct tac tta acc ttt ggt ggg gtt act atc gtt cgg ttg ttt aca ctc 451
Pro Tyr Leu Thr Phe Gly Gly Val Thr Ile Val Pro Leu Phe Thr Leu
105 110 115

tat gac tac tcg ttc cgt cga cct ggt ttc acc gtg gag cag gct gtg 499
Tyr Asp Tyr Ser Phe Arg Arg Gly Phe Thr Val Glu Gln Ala Val
120 125 130

caa gcg gcg cgg gat cgt caa gtg atg atg act gat gag ttt tct att 547
Gln Ala Ala Arg Asp Arg Gln Val Met Met Thr Asp Glu Phe Ser Ile
135 140 145

gcg cct ttt gtt gat atc cga gcg tgg tgc tgg gat cgc tta gcc tat 595
Ala Pro Phe Val Asp Ile Arg Ala Trp Cys Trp Asp Arg Leu Ala Tyr
150 155 160 165

tcc att aag cgt ttg agc aag atc aac ggg cca aca att ttg att aac 643
Ser Ile Lys Arg Leu Ser Lys Ile Asn Gly Pro Thr Ile Leu Ile Asn
170 175 180

cac tgg cgg ctg gtg gtg gaa ccg act tat cag atg cgc tgg cag gaa 691
His Trp Pro Leu Val Val Glu Pro Thr Tyr Gln Met Arg Trp Gln Glu
185 190 195

ctt gca ttg tgg tgc ggt act cgc cac acc agg gga tgg gcc gaa cgc 739
Leu Ala Leu Trp Cys Gly Thr Arg His Thr Arg Gly Trp Ala Glu Arg
200 205 210

tac aac gcg gaa gcc gtt att tac ggt cat ctg cat atg ccc gga ata 787
Tyr Asn Ala Glu Ala Val Ile Tyr Gly His Leu His Met Pro Gly Ile
215 220 225

acc aac gtc aac ggt gtg aaa cac att gaa gtg tcg ttg ggt tat ccg 835
Thr Asn Val Asn Gly Val Lys His Ile Glu Val Ser Leu Gly Tyr Pro
230 235 240 245

cgc gaa tgg gag cat tgg tct ggg cag cat gtg tgg cca tat cca gtg 883
Arg Glu Trp Glu His Trp Ser Gly Gln His Val Trp Pro Tyr Pro Val
250 255 260

atg gag gtg gac aat gct gga tgagtccttg tttccaaatt cgg 927
Met Glu Val Asp Asn Ala Gly
265

<210> 658

<211> 268

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 658

Val Thr Thr Thr Leu Trp Ala Val Ser Asp Leu His Ala Val Lys
1 5 10 15

Ala Asn Ala Asp Pro Ile Glu Asn Ile Gln Pro Lys Asp Pro Ser Asp
20 25 30

Trp Leu Ile Val Ala Gly Asp Val Ala Glu Arg Thr Glu Leu Val Leu
35 40 45

Glu Ile Leu Ala Arg Leu Arg Arg Arg Phe Ala Lys Val Ile Trp Val

50					55					60				
Pro 65	Gly	Asn	His	Leu 70	Phe	Ser	Arg	Ser	Ala 75	Asp	Arg	Tyr	Gln	Gly 80
Arg	Asp	Lys	Tyr 85	Glu	Leu	Val	Glu	Gly 90	Cys	Arg	Lys	Ile	Asp 95	Val
Leu	Thr	Pro 100	Asp	Pro	Tyr	Leu	Thr 105	Phe	Gly	Gly	Val	Thr 110	Ile	Val
Pro	Leu	Phe 115	Thr	Leu	Tyr	Asp	Tyr 120	Ser	Phe	Arg	Arg	Pro 125	Gly	Phe
Val	Glu 130	Gln	Ala	Val	Gln	Ala 135	Ala	Arg	Asp	Arg 140	Gln	Val	Met	Thr
Asp 145	Glu	Phe	Ser	Ile 150	Ala	Pro	Phe	Val	Asp	Ile 155	Arg	Ala	Trp	Cys
Asp	Arg	Leu	Ala 165	Tyr	Ser	Ile	Lys	Arg	Leu 170	Ser	Lys	Ile	Asn	Gly
Thr	Ile	Leu 180	Ile	Asn	His	Trp	Pro	Leu 185	Val	Val	Glu	Pro 190	Thr	Gln
Met	Arg	Trp 195	Gln	Glu	Leu	Ala 200	Leu	Trp	Cys	Gly	Thr	Arg 205	His	Thr
Gly	Trp 210	Ala	Glu	Arg	Tyr	Asn 215	Ala	Glu	Ala	Val	Ile 220	Tyr	Gly	His
His 225	Met	Pro	Gly	Ile 230	Thr	Asn	Val	Asn	Gly 235	Val	Lys	His	Ile	Glu
Ser	Leu	Gly	Tyr 245	Pro	Arg	Glu	Trp	Glu 250	His	Trp	Ser	Gly	Gln	His
Trp	Pro	Tyr 260	Val	Met	Glu	Val	Asp 265	Asn	Ala	Gly				

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<210> 659
<211> 927
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(904)
<223> FRXA01492
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<400> 659
tgaagtgggc gcgtagcgtt cggcgcggtg caaacccat ttgctggact gcaggcataa 60
tggacaaaaa cttttagcaa caactatgtg gaggtgacag gtg acc aca act ctg 115
                                     Val Thr Thr Thr Leu
                                     1         5
tgg gcg gtt tct gac ctc cat gca gcg gtg aaa gct aac gct gat cca
Trp Ala Val Ser Asp Leu His Ala Ala Val Lys Ala Asn Ala Asp Pro 163

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115

163

	10	15	20	
att gag aat att cag cct aag gat ccg tct gac tgg ttg att gtt gca				211
Ile Glu Asn Ile Gln Pro Lys Asp Pro Ser Asp Trp Leu Ile Val Ala	25	30	35	
ggg gac gtg gcg gaa cgt acc gaa ttg gtg ctg gaa att ttg gca cgt				259
Gly Asp Val Ala Glu Arg Thr Glu Leu Val Leu Glu Ile Leu Ala Arg	40	45	50	
ttg cgc agg cgc ttt gcc aag gtg atc tgg gtt ccg ggt aac cat gag				307
Leu Arg Arg Arg Phe Ala Lys Val Ile Trp Val Pro Gly Asn His Glu	55	60	65	
ttg ttt tct cgc tcc gcg gac cgc tat cag ggg cgc gat aag tac tct				355
Leu Phe Ser Arg Ser Ala Asp Arg Tyr Gln Gly Arg Asp Lys Tyr Ser	70	75	80	85
gaa ctc gtt gaa ggc tgc cgc aag att gat gtg ttg act ccg gag gac				403
Glu Leu Val Glu Gly Cys Arg Lys Ile Asp Val Leu Thr Pro Glu Asp	90	95	100	
cct tac tta acc ttt ggt ggg gtt act atc gtt ccg ttg ttt aca ctc				451
Pro Tyr Leu Thr Phe Gly Gly Val Thr Ile Val Pro Leu Phe Thr Leu	105	110	115	
tat gac tac tcg ttc cgt cga cct ggt ttc acc gtg gag cag gct gtg				499
Tyr Asp Tyr Ser Phe Arg Arg Pro Gly Phe Thr Val Glu Gln Ala Val	120	125	130	
caa gcg gcg ccg gat cgt caa gtg atg atg act gat gag ttt tct att				547
Gln Ala Ala Arg Asp Arg Gln Val Met Met Thr Asp Glu Phe Ser Ile	135	140	145	
gcg cct ttt gtt gat atc cga gcg tgg tgc tgg gat cgc tta gcc tat				595
Ala Pro Phe Val Asp Ile Arg Ala Trp Cys Trp Asp Arg Leu Ala Tyr	150	155	160	165
tcc att aag cgt ttg agc aag atc aac ggg cca aca att ttg att aac				643
Ser Ile Lys Arg Leu Ser Lys Ile Asn Gly Pro Thr Ile Leu Ile Asn	170	175	180	
cac tgg ccg ctg gtg gtg gaa ccg act tat cag atg cgc tgg cag gaa				691
His Trp Pro Leu Val Val Glu Pro Thr Tyr Gln Met Arg Trp Gln Glu	185	190	195	
ctt gca ttg tgg tgc ggt act cgc cac acc agg gga tgg gcc gaa cgc				739
Leu Ala Leu Trp Cys Gly Thr Arg His Thr Arg Gly Trp Ala Glu Arg	200	205	210	
tac aac gcg gaa gcc gtt att tac ggt cat ctg cat atg ccc gga ata				787
Tyr Asn Ala Glu Ala Val Ile Tyr Gly His Leu His Met Pro Gly Ile	215	220	225	
acc aac gtc aac ggt gtg aaa cac att gaa gtg tcg ttg ggt tat ccg				835
Thr Asn Val Asn Gly Val Lys His Ile Glu Val Ser Leu Gly Tyr Pro	230	235	240	245
cgc gaa tgg gag cat tgg tct ggg cag cat gtg tgg cca tat cca gtg				883
Arg Glu Trp Glu His Trp Ser Gly Gln His Val Trp Pro Tyr Pro Val	250	255	260	

atg gag gtg gac aat gct gga tgagtctttg ttccaaatt cgg
 Met Glu Val Asp Asn Ala Gly
 265

927

<210> 660

<211> 268

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 660

Val Thr Thr Thr Leu Trp Ala Val Ser Asp Leu His Ala Ala Val Lys
 1 5 10 15

Ala Asn Ala Asp Pro Ile Glu Asn Ile Gln Pro Lys Asp Pro Ser Asp
 20 25 30

Trp Leu Ile Val Ala Gly Asp Val Ala Glu Arg Thr Glu Leu Val Leu
 35 40 45

Glu Ile Leu Ala Arg Leu Arg Arg Arg Phe Ala Lys Val Ile Trp Val
 50 55 60

Pro Gly Asn His Glu Leu Phe Ser Arg Ser Ala Asp Arg Tyr Gln Gly
 65 70 75 80

Arg Asp Lys Tyr Ser Glu Leu Val Glu Gly Cys Arg Lys Ile Asp Val
 85 90 95

Leu Thr Pro Glu Asp Pro Tyr Leu Thr Phe Gly Gly Val Thr Ile Val
 100 105 110

Pro Leu Phe Thr Leu Tyr Asp Tyr Ser Phe Arg Arg Pro Gly Phe Thr
 115 120 125

Val Glu Gln Ala Val Gln Ala Ala Arg Asp Arg Gln Val Met Met Thr
 130 135 140

Asp Glu Phe Ser Ile Ala Pro Phe Val Asp Ile Arg Ala Trp Cys Trp
 145 150 155 160

Asp Arg Leu Ala Tyr Ser Ile Lys Arg Leu Ser Lys Ile Asn Gly Pro
 165 170 175

Thr Ile Leu Ile Asn His Trp Pro Leu Val Val Glu Pro Thr Tyr Gln
 180 185 190

Met Arg Trp Gln Glu Leu Ala Leu Trp Cys Gly Thr Arg His Thr Arg
 195 200 205

Gly Trp Ala Glu Arg Tyr Asn Ala Glu Ala Val Ile Tyr Gly His Leu
 210 215 220

His Met Pro Gly Ile Thr Asn Val Asn Gly Val Lys His Ile Glu Val
 225 230 235 240

Ser Leu Gly Tyr Pro Arg Glu Trp Glu His Trp Ser Gly Gln His Val
 245 250 255

Trp Pro Tyr Pro Val Met Glu Val Asp Asn Ala Gly

260

265

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<210> 661
<211> 597
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(574)
<223> RXN01518
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<400> 661
agcagaacct gatgccgtcc tgcacggcac gaccattgca gaacatgtgg ataattttga 60

tcccacagac attgaagggtg tcaccaagat ttaaggagtc gtg gct ttc atg cag 115
Val Ala Phe Met Gln
1 5

aaa acg tca gcg ggt tgg ttg atc gca acg gga ggt ttc ctc gcc gct 163
Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly Gly Phe Leu Ala Ala
10 15 20

gtg tcc gcc att ttg acg tgg cgt ttt tat gga tcc atg acc tct att 211
Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly Ser Met Thr Ser Ile
25 30 35

tcc atc acg gta tcc atc act ttt tgg ttg ttg gcc gtg gtg tgt ggt 259
Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu Ala Val Val Cys Gly
40 45 50

ttc gca ggt gtg aag gtc caa ggt cgc ctc gat gag ggg ctg atc ggc 307
Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp Glu Gly Leu Ile Gly
55 60 65

cag gac aaa tcc caa atg aac ccc gtg acc att gcc tat ctg gcc atg 355
Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile Ala Tyr Leu Ala Met
70 75 80 85

ctg ggt cga gcg tgt gcg tgg ggt ggc gca att ttc ggc ggc gtt tat 403
Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile Phe Gly Gly Val Tyr
90 95 100

gtg gga att ggc agt tat gta atc cca cgc gcc ggt gag ttg tcc gca 451
Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala Gly Glu Leu Ser Ala
105 110 115

gca tgc aat gat ctt ccg gga gtt att gcc tgt gcg ctg ggc gga atc 499
Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys Ala Leu Gly Gly Ile
120 125 130

gca ctc tca gct gcc gga ctt tat tta gag cga agc tgt gag gct ccg 547
Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg Ser Cys Glu Ala Pro
135 140 145

cct ccc caa tct ggc gaa gcg atc agc tagattggaa ttcattgaatc 594
Pro Pro Gln Ser Gly Glu Ala Ile Ser
150 155

aaq 597

<210> 662

<211> 158

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 662

Val Ala Phe Met Gln Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly
 1 5 10 15

Gly Phe Leu Ala Ala Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly
 20 25 30

Ser Met Thr Ser Ile Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu
 35 40 45

Ala Val Val Cys Gly Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp
 50 55 60

Glu Gly Leu Ile Gly Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile
 65 70 75 80

Ala Tyr Leu Ala Met Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile
 85 90 95

Phe Gly Gly Val Tyr Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala
 100 105 110

Gly Glu Leu Ser Ala Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys
 115 120 125

Ala Leu Gly Gly Ile Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg
 130 135 140

Ser Cys Glu Ala Pro Pro Pro Gln Ser Gly Glu Ala Ile Ser
 145 150 155

<210> 663

<211> 597

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(574)

<223> FRXA01518

<400> 663

agcagaacct gatgcgctcc tgcacgacac gaccattgca gaacatgtgg ataactctga 60

tcccacagac attgaagggtg tcaccaagat ttaaggagtc gtg gct ttc atg cag 115
 Val Ala Phe Met Gln
 1 5

aaa acg tca gcg ggt tgg ttg atc gca acg gga ggt ttc ctc gcc gct 163
 Lys Thr Ser Ala Gly Trp Leu Ile Ala Thr Gly Gly Phe Leu Ala Ala
 10 15 20

gtg tcc gcc att ttg acg tgg cgt ttt tat gga tcc atg acc tct att 211

Val Ser Ala Ile Leu Thr Trp Arg Phe Tyr Gly Ser Met Thr Ser Ile
 25 30 35
 tcc atc acg gta tcc atc act ttt tgg ttg ttg gcc gtg gtg tgt ggt 259
 Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu Ala Val Val Cys Gly
 40 45 50
 ttc gca ggt gtg aag gtc caa ggt cgc ctc gat gag ggg ctg atc ggc 307
 Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp Glu Gly Leu Ile Gly
 55 60 65
 cag gac aaa tcc caa atg aac ccc gtg acc att gcc tat ctg gcc atg 355
 Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile Ala Tyr Leu Ala Met
 70 75 80 85
 ctg ggt cga gcg tgt gcg tgg ggt ggc gca att ttc gcc gcc gtt tat 403
 Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala lle Phe Gly Gly Val Tyr
 90 95 100
 gtg gga att ggc agt tat gta atc cca cgc gcc ggt gag ttg tcc gca 451
 Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala Gly Glu Leu Ser Ala
 105 110 115
 gca tgc aat gat ctt ccg gga gtt att gcc tgt gcg ctg gcc gga atc 499
 Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys Ala Leu Gly Gly Ile
 120 125 130
 gca ctc tca gct gcc gga ctt tat tta gag cga agc tgt gag gct ccg 547
 Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg Ser Cys Glu Ala Pro
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 cct ccc caa tct ggc gaa gcg atc agc tagattgaa ttcattgaatc 594
 Pro Pro Gln Ser Gly Glu Ala Ile Ser
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 aag 597
 <210> 664
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 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 664
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 Ser Met Thr Ser Ile Ser Ile Thr Val Ser Ile Thr Phe Trp Leu Leu
 35 40 45
 Ala Val Val Cys Gly Phe Ala Gly Val Lys Val Gln Gly Arg Leu Asp
 50 55 60
 Glu Gly Leu Ile Gly Gln Asp Lys Ser Gln Met Asn Pro Val Thr Ile
 65 70 75 80
 Ala Tyr Leu Ala Met Leu Gly Arg Ala Cys Ala Trp Gly Gly Ala Ile
 85 90 95

Phe Gly Gly Val Tyr Val Gly Ile Gly Ser Tyr Val Ile Pro Arg Ala
100 105 110

Gly Glu Leu Ser Ala Ala Ser Asn Asp Leu Pro Gly Val Ile Ala Cys
115 120 125

Ala Leu Gly Gly Ile Ala Leu Ser Ala Ala Gly Leu Tyr Leu Glu Arg
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Ser Cys Glu Ala Pro Pro Pro Gln Ser Gly Glu Ala Ile Ser
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<210> 665

<211> 1727

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (46)..(1704)

<223> RXN01549

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Phe Ile Glu Pro Asn Asp Ala Pro Asp Ala Pro Asp Asn Gly Asp Ser 20
5 10 15

gga agc tcg ggg ttt gtt gat gaa gca aaa gat aag acc cgc tca gct 153
Gly Ser Ser Gly Phe Val Asp Glu Ala Lys Asp Lys Thr Arg Ser Ala 35
25 30 35

gca caa ggc tta ggt tat ggc gca cta cgt gta ggt ttt ggt act gca 201
Ala Gln Gly Leu Gly Tyr Gly Ala Leu Arg Val Gly Phe Gly Thr Ala 50
40 45 50

gca ctt gca gcc aat ggt gct cgc tct atg ggt aat ttg gct aaa aac 249
Ala Leu Ala Ala Asn Gly Ala Arg Ser Met Gly Asn Leu Ala Lys Asn 65
55 60 65

ctg tgg aca cga atg atg ggg ctt gcc ctg tct gcc ggt act ggt atc 297
Leu Trp Thr Arg Met Met Gly Leu Ala Leu Ser Ala Gly Thr Gly Ile 75
70 75 80

tct gct gcc aca ggt ggc atg atc act gca cgt gta ggc gca atg ctg 345
Ser Ala Ala Thr Gly Gly Met Ile Thr Ala Arg Val Gly Ala Met Leu 95
85 90 95 100

gca ggt aca ggc tcg gtg ttg tcg tcg gtg acg act att gcg ttg att 393
Ala Gly Thr Gly Ser Val Leu Ser Ser Val Thr Thr Ile Ala Leu Ile 115
105 110 115

gtg tcg atg att gtg gtg ccg gca ggt cga aaa gac ggc att atc gag 441
Val Ser Met Ile Val Val Pro Ala Gly Arg Lys Asp Gly Ile Ile Glu 130
120 125 130

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Leu Cys Glu Pro Pro Val Thr Ala Asn Pro Phe Thr Ile Asp Ala Gly	
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gat atg act gag aac gcg aag ttg gtg tac ggt gcg ctg tcg tat ctt	537
Asp Met Thr Glu Asn Ala Lys Leu Val Tyr Gly Ala Leu Ser Tyr Leu	
150 155 160	
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Gly Met Asn Asp Gln Asn Ile Ala Gly Val Leu Gly Asn Phe Glu Thr	
165 170 175 180	
gaa tca ggt atc gac ccg act gcg gtg gag ggt att ttt gat gaa cca	633
Glu Ser Gly Ile Asp Pro Thr Ala Val Glu Gly Ile Phe Asp Glu Pro	
185 190 195	
aat acc atc ggt cct ccg aag aga gct gcg tgg gat aag aac ttt gaa	681
Asn Thr Ile Gly Pro Arg Lys Arg Ala Ala Trp Asp Lys Asn Phe Glu	
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cct cag ccg atg ggt att ggg ctt ggg cag tgg aca gca ggg cgc aca	729
Pro Gln Pro Met Gly Ile Gly Leu Gly Gln Trp Thr Ala Gly Arg Thr	
215 220 225	
cag atg ttg cta gat ttt gcc gcc gat aga aac cga gac tgg cat tac	777
Gln Met Leu Leu Asp Phe Ala Ala Asp Arg Asn Arg Asp Trp His Tyr	
230 235 240	
atc gac gtg cag ctt gca ttt gct att agt ggc gat aat gaa agc gat	825
Ile Asp Val Gln Leu Ala Phe Ala Ile Ser Gly Asp Asn Glu Ser Asp	
245 250 255 260	
gcg aag gtt ttt ctg gaa atg gtt gat aat aaa aac tcc agt agc aat	873
Arg Lys Val Phe Leu Glu Met Val Asp Asn Lys Asn Ser Ser Ser Asn	
265 270 275	
agc ccc acc gca gcg tcc gag tac ttc ctg cgt gag tgg gag cgc ccg	921
Ser Pro Thr Ala Ala Ser Glu Tyr Phe Leu Arg Glu Trp Glu Arg Pro	
280 285 290	
gca gat gtc gca ggt aat gca ccc att cgt gca gag caa gca tct aag	969
Ala Asp Val Ala Gly Asn Ala Pro Ile Arg Ala Glu Gln Ala Ser Lys	
295 300 305	
tgg tac gcg cag atg ggt ggt tgg caa aag aac tca acc ttg ggt gag	1017
Trp Tyr Ala Gln Met Gly Trp Gln Lys Asn Ser Thr Leu Gly Glu	
310 315 320	
tct gtg atc gct atg gct gat ggt gca gca gca aaa tcc acg gcg cgt	1065
Ser Val Ile Ala Met Ala Asp Gly Ala Ala Ala Lys Ser Thr Ala Arg	
325 330 335 340	
gat gag cag gat gct ctt aat gat tgt cct gaa gag gac cgc acc tca	1113
Asp Glu Gln Asp Ala Leu Asn Asp Cys Pro Glu Glu Asp Arg Thr Ser	
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Gly Gly Asn Thr Ser Ala Ala Glu Ala Met Val Thr Ile Ser His Pro	
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tat ctg gct gat tct cgt ggc aat gac ggt act gat att tac cgc tat	1209

Tyr Leu Ala Asp Ser Arg Gly Asn Asp Gly Thr Asp Ile Tyr Arg Tyr
 375 380 385
 atc cat gat gaa gtg ctc acc ggt gat ccg tat tac gca tcc tgt gac 1257
 Ile His Asp Glu Val Leu Thr Gly Asp Pro Tyr Tyr Ala Ser Cys Asp
 390 395 400
 cgt ggc gtt gct acc gct att cgc tgg tgc ggc acg gat gat acg ttc 1305
 Arg Gly Val Ala Thr Ala Ile Arg Trp Ser Gly Thr Asp Asp Thr Phe
 405 410 415 420
 cca gca ggt cca aca gca gca cag tat gaa tac gtt gtg ggc aca gga 1353
 Pro Ala Gly Pro Thr Ala Ala Gln Tyr Glu Tyr Val Val Gly Thr Gly
 425 430 435
 tcg ggc cgt tgg gag gaa atc ggc aat ctt gcc acc atg tca gag aac 1401
 Ser Gly Arg Trp Glu Glu Ile Gly Asn Leu Ala Thr Met Ser Glu Asn
 440 445 450
 gat ttg tta cct ggc gat gtg ctt ctt ggt gca ccg aat cac gtt gcg 1449
 Asp Leu Leu Pro Gly Asp Val Leu Leu Gly Ala Pro Asn His Val Ala
 455 460 465
 atg tat gtc agc aat gag gtt gtt gtg gac atg ttg ggc cct ggt aat 1497
 Met Tyr Val Ser Asn Glu Val Val Val Asp Met Leu Gly Pro Gly Asn
 470 475 480
 gca gag cct aat gca gct att ggt cat gca tgc ttg aat gac cgc tca 1545
 Ala Glu Pro Asn Ala Ala Ile Gly His Ala Ser Leu Asn Asp Arg Ser
 485 490 495 500
 cct ggt ctg gat acc ttg agt ctg gat gga tgg ggc gtg aac ttc aag 1593
 Pro Gly Leu Asp Thr Leu Ser Leu Asp Gly Trp Gly Val Asn Phe Lys
 505 510 515
 gtg ttc cgc aac acc cag gct gag aca aac tca gtg ttc tct ggt gta 1641
 Val Phe Arg Asn Thr Gln Ala Glu Thr Asn Ser Val Phe Ser Gly Val
 520 525 530
 cag att ccg gct ggt aaa gaa att ggc gaa atg act aac cca act cga 1689
 Gln Ile Pro Ala Gly Lys Glu Ile Gly Glu Met Thr Asn Pro Thr Arg
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 act act cct gca gga taagtttttt tcatcgctgg gtt 1727
 Thr Thr Pro Ala Gly
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 <211> 553
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 666
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 Asn Gly Asp Ser Gly Ser Ser Gly Phe Val Asp Glu Ala Lys Asp Lys
 20 25 30
 Thr Arg Ser Ala Ala Gln Gly Leu Gly Tyr Gly Ala Leu Arg Val Gly

35					40					45						
Phe	Gly	Thr	Ala	Ala	Leu	Ala	Ala	Asn	Gly	Ala	Arg	Ser	Met	Gly	Asn	
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Leu	Ala	Lys	Asn	Leu	Trp	Thr	Arg	Met	Met	Gly	Leu	Ala	Leu	Ser	Ala	
65					70					75					80	
Gly	Thr	Gly	Ile	Ser	Ala	Ala	Thr	Gly	Gly	Met	Ile	Thr	Ala	Arg	Val	
85					90					95					100	
Gly	Ala	Met	Leu	Ala	Gly	Thr	Gly	Ser	Val	Leu	Ser	Ser	Val	Thr	Thr	
100					105					110					115	
Ile	Ala	Leu	Ile	Val	Ser	Met	Ile	Val	Val	Pro	Ala	Gly	Arg	Lys	Asp	
115					120					125					130	
Gly	Ile	Ile	Glu	Leu	Cys	Glu	Pro	Pro	Val	Thr	Ala	Asn	Pro	Phe	Thr	
130					135					140					145	
Ile	Asp	Ala	Gly	Asp	Met	Thr	Glu	Asn	Ala	Lys	Leu	Val	Tyr	Gly	Ala	
145					150					155					160	
Leu	Ser	Tyr	Leu	Gly	Met	Asn	Asp	Gln	Asn	Ile	Ala	Gly	Val	Leu	Gly	
165					170					175					180	
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180					185					190					195	
Phe	Asp	Glu	Pro	Asn	Thr	Ile	Gly	Pro	Arg	Lys	Arg	Ala	Ala	Trp	Asp	
195					200					205					210	
Lys	Asn	Phe	Glu	Pro	Gln	Pro	Met	Gly	Ile	Gly	Leu	Gly	Gln	Trp	Thr	
210					215					220					225	
Ala	Gly	Arg	Thr	Gln	Met	Leu	Leu	Asp	Phe	Ala	Ala	Asp	Arg	Asn	Arg	
225					230					235					240	
Asp	Trp	His	Tyr	Ile	Asp	Val	Gln	Leu	Ala	Phe	Ala	Ile	Ser	Gly	Asp	
245					250					255					260	
Asn	Glu	Ser	Asp	Arg	Lys	Val	Phe	Leu	Glu	Met	Val	Asp	Asn	Lys	Asn	
260					265					270					275	
Ser	Ser	Ser	Asn	Ser	Pro	Thr	Ala	Ala	Ser	Glu	Tyr	Phe	Leu	Arg	Glu	
275					280					285					290	
Trp	Glu	Arg	Pro	Ala	Asp	Val	Ala	Gly	Asn	Ala	Pro	Ile	Arg	Ala	Glu	
290					295					300					305	
Gln	Ala	Ser	Lys	Trp	Tyr	Ala	Gln	Met	Gly	Gly	Trp	Gln	Lys	Asn	Ser	
310					315					320					325	
Thr	Leu	Gly	Glu	Ser	Val	Ile	Ala	Met	Ala	Asp	Gly	Ala	Ala	Ala	Lys	
325					330					335					340	
Ser	Thr	Ala	Arg	Asp	Glu	Gln	Asp	Ala	Leu	Asn	Asp	Cys	Pro	Glu	Glu	
340					345					350					355	
Asp	Arg	Thr	Ser	Gly	Gly	Asn	Thr	Ser	Ala	Ala	Glu	Ala	Met	Val	Thr	
355					360					365					370	

Ile Ser His Pro Tyr Leu Ala Asp Ser Arg Gly Asn Asp Gly Thr Asp
370 375 380

Ile Tyr Arg Tyr Ile His Asp Glu Val Leu Thr Gly Asp Pro Tyr Tyr
385 390 395 400

Ala Ser Cys Asp Arg Gly Val Ala Thr Ala Ile Arg Trp Ser Gly Thr
405 410 415

Asp Asp Thr Phe Pro Ala Gly Pro Thr Ala Ala Gln Tyr Glu Tyr Val
420 425 430

Val Gly Thr Gly Ser Gly Arg Trp Glu Glu Ile Gly Asn Leu Ala Thr
435 440 445

Met Ser Glu Asn Asp Leu Leu Pro Gly Asp Val Leu Leu Gly Ala Pro
450 455 460

Asn His Val Ala Met Tyr Val Ser Asn Glu Val Val Val Asp Met Leu
465 470 475 480

Gly Pro Gly Asn Ala Glu Pro Asn Ala Ala Ile Gly His Ala Ser Leu
485 490 495

Asn Asp Arg Ser Pro Gly Leu Asp Thr Leu Ser Leu Asp Gly Trp Gly
500 505 510

Val Asn Phe Lys Val Phe Arg Asn Thr Gln Ala Glu Thr Asn Ser Val
515 520 525

Phe Ser Gly Val Gln Ile Pro Ala Gly Lys Glu Ile Gly Glu Met Thr
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Asn Pro Thr Arg Thr Thr Pro Ala Gly
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<210> 667

<211> 942

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (59)..(919)

<223> FRXA01549

<400> 667

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Val Asp Asn Lys Asn Ser Ser Ser Asn Ser Pro Thr Ala Ala Ser Glu
5 10 15

tac ttc ctg cgt gag tgg gag cgc ccg gca gat gtc gca ggt aat gca 157
Tyr Phe Leu Arg Glu Trp Glu Arg Pro Ala Asp Val Ala Gly Asn Ala
20 25 30

ccc att cgt gca gag caa gca tct aag tgg tac gcg cag atg ggt ggt 205
 Pro Ile Arg Ala Glu Gln Ala Ser Lys Trp Tyr Ala Gln Met Gly Gly
 35 40 45

tgg caa aag aac tca acc ttg ggt gag tct gtg atc gct atg gct gat 253
 Trp Gln Lys Asn Ser Thr Leu Gly Glu Ser Val Ile Ala Met Ala Asp
 50 55 60 65

ggt gca gca gca aaa tcc acg gcg cgt gat gag cag gat gct ctt aat 301
 Gly Ala Ala Ala Lys Ser Thr Ala Arg Asp Glu Gln Asp Ala Leu Asn
 70 75 80

gat tgt cct gaa gag gac cgc acc tca ggt gga aat acg tcc gct gca 349
 Asp Cys Pro Glu Glu Asp Arg Thr Ser Gly Gly Asn Thr Ser Ala Ala
 85 90 95

gaa gca atg gtg act att tca cat cct tat ctg gct gat tct cgt ggc 397
 Glu Ala Met Val Thr Ile Ser His Pro Tyr Leu Ala Asp Ser Arg Gly
 100 105 110

aat gac ggt act gat att tac cgc tat atc cat gat gaa gtg ctc acc 445
 Asn Asp Gly Thr Asp Ile Tyr Arg Tyr Ile His Asp Glu Val Leu Thr
 115 120 125

ggt gat ccg tat tac gca tcc tgt gac cgt ggc gtt gct acc gct att 493
 Gly Asp Pro Tyr Tyr Ala Ser Cys Asp Arg Gly Val Ala Thr Ala Ile
 130 135 140 145

cgc tgg tgc ggc acg gat gat acg ttc cca gca ggt cca aca gca gca 541
 Arg Trp Ser Gly Thr Asp Asp Thr Phe Pro Ala Gly Pro Thr Ala Ala
 150 155 160

cag tat gaa tac gtt gtg ggc aca gga tgc ggc cgt tgg gag gaa atc 589
 Gln Tyr Glu Tyr Val Val Gly Thr Gly Ser Gly Arg Trp Glu Glu Ile
 165 170 175

ggc aat ctt gcc acc atg tca gag aac gat ttg tta cct gcc gat gtg 637
 Gly Asn Leu Ala Thr Met Ser Glu Asn Asp Leu Leu Pro Gly Asp Val
 180 185 190

ctt ctt ggt gca ccg aat cac gtt gcg atg tat gtc agc aat gag gtt 685
 Leu Leu Gly Ala Pro Asn His Val Ala Met Tyr Val Ser Asn Glu Val
 195 200 205

gtt gtg gac atg ttg ggc cct ggt aat gca gag cct aat gca gct att 733
 Val Val Asp Met Leu Gly Pro Gly Asn Ala Glu Pro Asn Ala Ala Ile
 210 215 220 225

ggt cat gca tgc ttg aat gac cgc tca cct ggt ctg gat acc ttg agt 781
 Gly His Ala Ser Leu Asn Asp Arg Ser Pro Gly Leu Asp Thr Leu Ser
 230 235 240

ctg gat gga tgg ggc gtg aac ttc aag gtg ttc cgc aac acc cag gct 829
 Leu Asp Gly Trp Gly Val Asn Phe Lys Val Phe Arg Asn Thr Gln Ala
 245 250 255

gag aca aac tca gtg ttc tct ggt gta cag att ccg gct ggt aaa gaa 877
 Glu Thr Asn Ser Val Phe Ser Gly Val Gln Ile Pro Ala Gly Lys Glu
 260 265 270

att ggc gaa atg act aac cca act cga act act cct gca gga 919

Ile Gly Glu Met Thr Asn Pro Thr Arg Thr Thr Pro Ala Gly
 275 280 285

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942

<210> 668

<211> 287

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 668

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 20 25 30

Ala Pro Ile Arg Ala Glu Gln Ala Ser Lys Trp Tyr Ala Gln Met Gly
 35 40 45

Gly Trp Gln Lys Asn Ser Thr Leu Gly Glu Ser Val Ile Ala Met Ala
 50 55 60

Asp Gly Ala Ala Ala Lys Ser Thr Ala Arg Asp Glu Gln Asp Ala Leu
 65 70 75 80

Asn Asp Cys Pro Glu Asp Arg Thr Ser Gly Gly Asn Thr Ser Ala
 85 90 95

Ala Glu Ala Met Val Thr Ile Ser His Pro Tyr Leu Ala Asp Ser Arg
 100 105 110

Gly Asn Asp Gly Thr Asp Ile Tyr Arg Tyr Ile His Asp Glu Val Leu
 115 120 125

Thr Gly Asp Pro Tyr Tyr Ala Ser Cys Asp Arg Gly Val Ala Thr Ala
 130 135 140

Ile Arg Trp Ser Gly Thr Asp Asp Thr Phe Pro Ala Gly Pro Thr Ala
 145 150 155 160

Ala Gln Tyr Glu Tyr Val Val Gly Thr Gly Ser Gly Arg Trp Glu Glu
 165 170 175

Ile Gly Asn Leu Ala Thr Met Ser Glu Asn Asp Leu Leu Pro Gly Asp
 180 185 190

Val Leu Leu Gly Ala Pro Asn His Val Ala Met Tyr Val Ser Asn Glu
 195 200 205

Val Val Val Asp Met Leu Gly Pro Gly Asn Ala Glu Pro Asn Ala Ala
 210 215 220

Ile Gly His Ala Ser Leu Asn Asp Arg Ser Pro Gly Leu Asp Thr Leu
 225 230 235 240

Ser Leu Asp Gly Trp Gly Val Asn Phe Lys Val Phe Arg Asn Thr Gln
 245 250 255

Ala Glu Thr Asn Ser Val Phe Ser Gly Val Gln Ile Pro Ala Gly Lys

260

265

270

Glu Ile Gly Glu Met Thr Asn Pro Thr Arg Thr Thr Pro Ala Gly
 275 280 285

<210> 669

<211> 363

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (46)..(363)

<223> FRXA02011

<400> 669

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 Phe Ile Glu Pro Asn Asp Ala Pro Asp Ala Pro Asp Asn Gly Asp Ser
 5 10 15 20

gga agc tcg ggg ttt gtt gat gaa gca aaa gat aag acc cgc tca gct 153
 Gly Ser Ser Gly Phe Val Asp Glu Ala Lys Asp Lys Thr Arg Ser Ala
 25 30 35

gca caa ggc tta ggt tat ggc gca cta cgt gta ggt ttt ggt act gca 201
 Ala Gln Gly Leu Gly Tyr Gly Ala Leu Arg Val Gly Phe Gly Thr Ala
 40 45 50

gca ctt gca gcc aat ggt gct cgc tct atg ggt aat ttg gct aaa aac 249
 Ala Leu Ala Ala Asn Gly Ala Arg Ser Met Gly Asn Leu Ala Lys Asn
 55 60 65

ctg tgg aca cca atg atg ggg ctt gcc ctg tct gcc ggt act ggt atc 297
 Leu Trp Thr Pro Met Met Gly Leu Ala Leu Ser Ala Gly Thr Gly Ile
 70 75 80

tct gct gcc aca ggt ggc atg atc act gca cgt gta ggc gca atg ctg 345
 Ser Ala Ala Thr Gly Gly Met Ile Thr Ala Arg Val Gly Ala Met Leu
 85 90 95 100

gca ggt aca ggc tcg gcg 363
 Ala Gly Thr Gly Ser Ala
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<210> 670

<211> 106

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 670

Val Ala Asn Asp Phe Ile Glu Pro Asn Asp Ala Pro Asp Ala Pro Asp
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Asn Gly Asp Ser Gly Ser Ser Gly Phe Val Asp Glu Ala Lys Asp Lys
 20 25 30

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Thr Arg Ser Ala Ala Gln Gly Leu Gly Tyr Gly Ala Leu Arg Val Gly
    35                      40                      45

Phe Gly Thr Ala Ala Leu Ala Ala Asn Gly Ala Arg Ser Met Gly Asn
    50                      55                      60

Leu Ala Lys Asn Leu Trp Thr Pro Met Met Gly Leu Ala Leu Ser Ala
    65                      70                      75                      80

Gly Thr Gly Ile Ser Ala Ala Thr Gly Gly Met Ile Thr Ala Arg Val
    85                      90                      95

Gly Ala Met Leu Ala Gly Thr Gly Ser Ala
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<210> 671

<211> 939

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(916)

<223> RXN01557

<400> 671

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                               Val Arg Ser Ser Asn
                               1                      5

ccc gtt ttt agt tcc ctt aag gaa act caa cgt cca caa ggc cag aac 163
Pro Val Phe Ser Ser Leu Lys Glu Thr Gln Arg Pro Gln Gly Gln Asn
                               10                      15                      20

cca tac ggt ggt tac gac aac ttc ggt ggt gtc tac cag caa aac gta 211
Pro Tyr Gly Gly Tyr Asp Asn Phe Gly Gly Val Tyr Gln Gln Asn Val
                               25                      30                      35

gct cca cag aag gcg gag cgc cca atg act gtg gat gat gtg atc acc 259
Ala Pro Gln Lys Ala Glu Arg Pro Met Thr Val Asp Asp Val Ile Thr
                               40                      45                      50

aag act ggt atc act ctc gcg gtt att atc gtt ttt gca ttg gtc acc 307
Lys Thr Gly Ile Thr Leu Ala Val Ile Ile Val Phe Ala Leu Val Thr
                               55                      60                      65

ttt ggc gtg tgg ttg gtt agc ccc gcc ctc gga atg atc ttg acc ctt 355
Phe Gly Val Trp Leu Val Ser Pro Gly Leu Gly Met Ile Leu Thr Leu
    70                      75                      80                      85

gtt ggt gcc atc ggt ggt ttc atc acc gtt ctg gtc agc acc ttc gcc 403
Val Gly Ala Ile Gly Gly Phe Ile Thr Val Leu Val Ser Thr Phe Gly
    90                      95                      100

aag aag tac gga tct gcg gca gtc act ttg att tac gca gta ttc gaa 451
Lys Lys Tyr Gly Ser Ala Ala Val Thr Leu Ile Tyr Ala Val Phe Glu
    105                      110                      115

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ggc ctc ttc gtc ggc gga att tcc ctt ctg ctg tcc ggc ttc aca gtt 499
Gly Leu Phe Val Gly Gly Ile Ser Leu Leu Leu Ser Gly Phe Thr Val
120 125 130

ggt aac gcc aac gca ggt ggc ctc att ggc cag gca gtc ctt ggc acc 547
Gly Asn Ala Asn Ala Gly Gly Leu Ile Gly Gln Ala Val Leu Gly Thr
135 140 145

atc ggt gta ttc att ggc atg ctg ttt gta tac aag act ggc gct atc 595
Ile Gly Val Phe Ile Gly Met Leu Phe Val Tyr Thr Gly Ala Ile
150 155 160 165

aag gtc act cct aag ttc aac cgc atc ctc acc ggc atg atg gtt ggc 643
Lys Val Thr Pro Lys Phe Asn Arg Ile Leu Thr Gly Met Met Val Gly
170 175 180

gtc ctg gtt ctt gtc ctg ggc aac gtt gta tgg gca ctg ttc act ggt 691
Val Leu Val Leu Val Leu Gly Asn Val Val Trp Ala Leu Phe Thr Gly
185 190 195

ggc gca agc cca ctg cgt gac ggt gga atc atc gcg att atc ttc tcc 739
Gly Ala Ser Pro Leu Arg Asp Gly Gly Ile Ile Ala Ile Ile Phe Ser
200 205 210

ctc ttc tgc atc ggc ctg gca gca ttc agc ttc ctc tcc gac ttc gat 787
Leu Phe Cys Ile Gly Leu Ala Ala Phe Ser Phe Leu Ser Asp Phe Asp
215 220 225

gca gct gac cgc ctc gtc cgc gaa ggt gca cct tcc aag atg gca tgg 835
Ala Ala Asp Arg Leu Val Arg Glu Gly Ala Pro Ser Lys Met Ala Trp
230 235 240 245

ggc gtt gcg ctt ggt ctt gca gtg acc ttg gtc tgg ctc tac acc gaa 883
Gly Val Ala Leu Gly Leu Ala Val Thr Leu Val Trp Leu Tyr Thr Glu
250 255 260

atc cta cgt ctg ctt agc tac ttc caa aac cgc tagtttacgc agcacaagac 936
Ile Leu Arg Leu Leu Ser Tyr Phe Gln Asn Arg
265 270

ccc 939

<210> 672
<211> 272
<212> PRT
<213> Corynebacterium glutamicum

<400> 672
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20 25 30

Tyr Gln Gln Asn Val Ala Pro Gln Lys Ala Glu Arg Pro Met Thr Val
35 40 45

Asp Asp Val Ile Thr Lys Thr Gly Ile Thr Leu Ala Val Ile Ile Val
50 55 60

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Phe Ala Leu Val Thr Phe Gly Val Trp Leu Val Ser Pro Gly Leu Gly
 65              70              75              80

Met Ile Leu Thr Leu Val Gly Ala Ile Gly Gly Phe Ile Thr Val Leu
      85              90              95

Val Ser Thr Phe Gly Lys Lys Tyr Gly Ser Ala Ala Val Thr Leu Ile
      100             105             110

Tyr Ala Val Phe Glu Gly Leu Phe Val Gly Gly Ile Ser Leu Leu Leu
      115             120             125

Ser Gly Phe Thr Val Gly Asn Ala Asn Ala Gly Gly Leu Ile Gly Gln
      130             135             140

Ala Val Leu Gly Thr Ile Gly Val Phe Ile Gly Met Leu Phe Val Tyr
      145             150             155             160

Lys Thr Gly Ala Ile Lys Val Thr Pro Lys Phe Asn Arg Ile Leu Thr
      165             170             175

Gly Met Met Val Gly Val Leu Val Leu Val Leu Gly Asn Val Val Trp
      180             185             190

Ala Leu Phe Thr Gly Gly Ala Ser Pro Leu Arg Asp Gly Gly Ile Ile
      195             200             205

Ala Ile Ile Phe Ser Leu Phe Cys Ile Gly Leu Ala Ala Phe Ser Phe
      210             215             220

Leu Ser Asp Phe Asp Ala Ala Asp Arg Leu Val Arg Glu Gly Ala Pro
      225             230             235             240

Ser Lys Met Ala Trp Gly Val Ala Leu Gly Leu Ala Val Thr Leu Val
      245             250             255

Trp Leu Tyr Thr Glu Ile Leu Arg Leu Leu Ser Tyr Phe Gln Asn Arg
      260             265             270

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<210> 673

<211> 939

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(916)

<223> FRXA01557

<400> 673

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gattgacgac gaaaaatcaa ttgaaaggat cggggactcc gtg cga agc agc aat 115
Val Arg Ser Ser Asn

1

5

ccc gtt ttt agt tcc ctt aag gaa act caa cgt cca caa ggc cag aac 163
 Pro Val Phe Ser Ser Leu Lys Glu Thr Gln Arg Pro Gln Gly Gln Asn
 10 15 20

cca tac ggt ggt tac gac aac ttc ggt ggt gtc tac cag caa aac gta 211
 Pro Tyr Gly Gly Tyr Asp Asn Phe Gly Gly Val Tyr Gln Gln Asn Val
 25 30 35

gct cca cag aag gcg gag cgc cca atg act gtg gat gat gtg atc acc 259
 Ala Pro Gln Lys Ala Glu Arg Pro Met Thr Val Asp Asp Val Ile Thr
 40 45 50

aag act ggt atc act ctc gcg gtt att atc gtt ttt gca ttg gtc acc 307
 Lys Thr Gly Ile Thr Leu Ala Val Ile Ile Val Phe Ala Leu Val Thr
 55 60 65

ttt ggc gtg tgg ttg gtt agc ccc ggc ctc gga atg atc ttg acc ctt 355
 Phe Gly Val Trp Leu Val Ser Pro Gly Leu Gly Met Ile Leu Thr Leu
 70 75 80 85

gtt ggt gcc atc ggt ggt ttc atc acc gtt ctg gtc agc acc ttc ggc 403
 Val Gly Ala Ile Gly Gly Phe Ile Thr Val Leu Val Ser Thr Phe Gly
 90 95 100

aag aag tac gga tct gcg gca gtc act ttg att tac gca gta ttc gaa 451
 Lys Lys Tyr Gly Ser Ala Ala Val Thr Leu Ile Tyr Ala Val Phe Glu
 105 110 115

ggc ctc ttc gtc ggc gga att tcc ctt ctg ctg tcc ggc ttc aca gtt 499
 Gly Leu Phe Val Gly Gly Ile Ser Leu Leu Leu Ser Gly Phe Thr Val
 120 125 130

ggt aac gcc aac gca ggt ggc ctc att ggc cag gca gtc ctt ggc acc 547
 Gly Asn Ala Asn Ala Gly Gly Leu Ile Gly Gln Ala Val Leu Gly Thr
 135 140 145

atc ggt gta ttc att ggc atg ctg ttt gta tac aag act ggc gct atc 595
 Ile Gly Val Phe Ile Gly Met Leu Phe Val Tyr Lys Thr Gly Ala Ile
 150 155 160 165

aag gtc act cct aag ttc aac cgc atc ctc acc ggc atg atg gtt ggc 643
 Lys Val Thr Pro Lys Phe Asn Arg Ile Leu Thr Gly Met Met Val Gly
 170 175 180

gtc ctg gtt ctt gtc ctg ggc aac gtt gta tgg gca ctg ttc act ggt 691
 Val Leu Val Leu Val Leu Gly Asn Val Val Trp Ala Leu Phe Thr Gly
 185 190 195

ggc gca agc cca ctg cgt gac ggt gga atc atc gcg att atc ttc tcc 739
 Gly Ala Ser Pro Leu Arg Asp Gly Gly Ile Ile Ala Ile Ile Phe Ser
 200 205 210

ctc ttc tgc atc ggc ctg gca gca ttc agc ttc ctc tcc gac ttc gat 787
 Leu Phe Cys Ile Gly Leu Ala Ala Phe Ser Phe Leu Ser Asp Phe Asp
 215 220 225

gca gct gac cgc ctc gtc cgc gaa ggt gca cct tcc aag atg gca tgg 835
 Ala Ala Asp Arg Leu Val Arg Glu Gly Ala Pro Ser Lys Met Ala Trp
 230 235 240 245

ggc gtt gcg ctt ggt ctt gca gtg acc ttg gtc tgg ctc tac acc gaa 883

Gly Val Ala Leu Gly Leu Ala Val Thr Leu Val Trp Leu Tyr Thr Glu
 250 255 260

atc cta cgt ctg ctt agc tac ttc caa aac cgc tagtttacgc agcacaagac 936
 Ile Leu Arg Leu Leu Ser Tyr Phe Gln Asn Arg
 265 270

ccc

939

<210> 674

<211> 272

<212> PRT

<213> Corynebacterium glutamicum

<400> 674

Val Arg Ser Ser Asn Pro Val Phe Ser Ser Leu Lys Glu Thr Gln Arg
 1 5 10 15

Pro Gln Gly Gln Asn Pro Tyr Gly Gly Tyr Asp Asn Phe Gly Gly Val
 20 25 30

Tyr Gln Gln Asn Val Ala Pro Gln Lys Ala Glu Arg Pro Met Thr Val
 35 40 45

Asp Asp Val Ile Thr Lys Thr Gly Ile Thr Leu Ala Val Ile Ile Val
 50 55 60

Phe Ala Leu Val Thr Phe Gly Val Trp Leu Val Ser Pro Gly Leu Gly
 65 70 75 80

Met Ile Leu Thr Leu Val Gly Ala Ile Gly Gly Phe Ile Thr Val Leu
 85 90 95

Val Ser Thr Phe Gly Lys Lys Tyr Gly Ser Ala Ala Val Thr Leu Ile
 100 105 110

Tyr Ala Val Phe Glu Gly Leu Phe Val Gly Gly Ile Ser Leu Leu Leu
 115 120 125

Ser Gly Phe Thr Val Gly Asn Ala Asn Ala Gly Gly Leu Ile Gly Gln
 130 135 140

Ala Val Leu Gly Thr Ile Gly Val Phe Ile Gly Met Leu Phe Val Tyr
 145 150 155 160

Lys Thr Gly Ala Ile Lys Val Thr Pro Lys Phe Asn Arg Ile Leu Thr
 165 170 175

Gly Met Met Val Gly Val Leu Val Leu Val Leu Gly Asn Val Val Trp
 180 185 190

Ala Leu Phe Thr Gly Gly Ala Ser Pro Leu Arg Asp Gly Gly Ile Ile
 195 200 205

Ala Ile Ile Phe Ser Leu Phe Cys Ile Gly Leu Ala Ala Phe Ser Phe
 210 215 220

Leu Ser Asp Phe Asp Ala Ala Asp Arg Leu Val Arg Glu Gly Ala Pro
 225 230 235 240

Ser Lys Met Ala Trp Gly Val Ala Leu Gly Leu Ala Val Thr Leu Val
 245 250 255

Trp Leu Tyr Thr Glu Ile Leu Arg Leu Leu Ser Tyr Phe Gln Asn Arg
 260 265 270

<210> 675

<211> 1158

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1135)

<223> RXN01574

<400> 675

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aagggtgggca acgagtcggg gagagtatga ggaatatattg atg agc aac aaa cgc 115
 Met Ser Asn Lys Arg
 1 5

atc ggt gta gtg atc gtt tcc tac gga cac gaa caa gat gtt gcc aac 163
 Ile Gly Val Val Ile Val Ser Tyr Gly His Glu Gln Asp Val Ala Asn
 10 15 20

ctg gta gac aca ttt gca gat cag ctg aaa act ggt gac cgc gta gtt 211
 Leu Val Asp Thr Phe Ala Asp Gln Leu Lys Thr Gly Asp Arg Val Val
 25 30 35

gtc gtg gac aac cgc aaa cct tgg gtg tta aaa gac gcc gtg ggg gag 259
 Val Val Asp Asn Arg Lys Pro Trp Val Leu Lys Asp Ala Val Gly Glu
 40 45 50

cgc ctg gaa aaa cac ggc gca gag atc atc aac cac gac aac ggt ggt 307
 Arg Leu Glu Lys His Gly Ala Glu Ile Ile Asn His Asp Asn Gly Gly
 55 60 65

ttc gcc gct ggc tgc aac gtg ggc gca gcg cac atc gtg gat gac gtt 355
 Phe Ala Ala Gly Cys Asn Val Gly Ala Ala His Ile Val Asp Asp Val
 70 75 80 85

gac ctg ctg ttc ttc ctc aac ccc gac aca gtg atc gac gat ccc acc 403
 Asp Leu Leu Phe Phe Leu Asn Pro Asp Thr Val Ile Asp Asp Pro Thr
 90 95 100

ctg ttc aat tcg ctg aga cgc gtc gat gaa cag tgg gca gca ttc atg 451
 Leu Phe Asn Ser Leu Arg Arg Val Asp Glu Gln Trp Ala Ala Phe Met
 105 110 115

cgg tac ctg ctg ctt cct gac agc acc att aac tcc gca ggc aac gcc 499
 Pro Tyr Leu Leu Leu Pro Asp Ser Thr Ile Asn Ser Ala Gly Asn Ala
 120 125 130

ctg cat att tcc gga ctg tcg tgg gtg act ggt ctg gat gaa aaa cca 547
 Leu His Ile Ser Gly Leu Ser Trp Val Thr Gly Leu Asp Glu Lys Pro

135	140	145	
gtt gaa ggc tca tct gaa gtt acc gat att tcc att gcc tct ggc gcc Val Glu Gly Ser Ser Glu Val Thr Asp Ile Ser Ile Ala Ser Gly Ala 150 155 160 165			595
tgc ctt gcc gtg cgc gtg gac tgg tgg aaa cgc ctc ggt gcc atg gaa Cys Leu Ala Val Phe Arg Val Asp Trp Trp Lys Arg Leu Gly Gly Met Glu 170 175 180			643
gaa ctg tat ttc atg tac cac gaa gac act gac ttc tcc gcc cgc ttg Glu Leu Tyr Phe Met Tyr His Glu Asp Thr Asp Phe Ser Ala Arg Leu 185 190 195			691
ctg ctg gcc ggc ggt cga att ggt ctc ctg cat tcc gcg tat gtc acc Leu Leu Ala Gly Gly Arg Ile Gly Leu Leu His Ser Ala Tyr Val Thr 200 205 210			739
cac cat tac gac tac gcc aag ggt gac tac aag tgg att tac atc gaa His His Tyr Asp Tyr Ala Lys Gly Asp Tyr Lys Trp Ile Tyr Ile Glu 215 220 225			787
cga aac cga cac gtt ttg ctg ctc agc gtg ctg ccg ctt cca ttg ctg Arg Asn Arg His Val Leu Leu Ser Val Leu Pro Leu Pro Leu Leu 230 235 240 245			835
ttc gtg ctg atc ccg cag atc ctc ggt gtg aac ctg gga ctg tgg gcg Phe Val Leu Ile Pro Gln Ile Leu Gly Val Asn Leu Gly Leu Trp Ala 250 255 260			883
att gcc gca aag gaa aag agg gtc gga ctc aag gtg aag tcc ctt cgc Ile Ala Ala Lys Glu Lys Arg Val Gly Leu Lys Val Lys Ser Leu Arg 265 270 275			931
ctc ctg atc cgc gat cta cca gcg att ttc aaa ctg cgt agg agc acg Leu Leu Ile Arg Asp Leu Pro Ala Ile Phe Lys Leu Arg Arg Ser Thr 280 285 290			979
cag gag ctt gcc gaa ctc aca cca tgc caa tat ctg gca aaa atg gaa Gln Glu Leu Ala Glu Leu Thr Pro Ser Gln Tyr Leu Ala Lys Met Glu 295 300 305			1027
tgg cgc cta gac aat ccc aac cta ggc aac att gga tcc aac aag att Trp Arg Leu Asp Asn Pro Asn Leu Gly Asn Ile Gly Ser Asn Lys Ile 310 315 320 325			1075
gtt gcg act gga tat aag acc tat tac aag ttg tgt atg agt atc ctg Val Ala Thr Gly Tyr Lys Thr Tyr Tyr Lys Leu Cys Met Ser Ile Leu 330 335 340			1123
aaa ttg ctc gct taacacccca taaagagggt gaa Lys Leu Leu Ala 345			1158

<210> 676

<211> 345

<212> PRT

<213> Corynebacterium glutamicum

<400> 676

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 Gln Asp Val Ala Asn Leu Val Asp Thr Phe Ala Asp Gln Leu Lys Thr
 20 25 30
 Gly Asp Arg Val Val Val Val Asp Asn Arg Lys Pro Trp Val Leu Lys
 35 40 45
 Asp Ala Val Gly Glu Arg Leu Glu Lys His Gly Ala Glu Ile Ile Asn
 50 55 60
 His Asp Asn Gly Gly Phe Ala Ala Gly Cys Asn Val Gly Ala Ala His
 65 70 75 80
 Ile Val Asp Asp Val Asp Leu Leu Phe Phe Leu Asn Pro Asp Thr Val
 85 90 95
 Ile Asp Asp Pro Thr Leu Phe Asn Ser Leu Arg Arg Val Asp Glu Gln
 100 105 110
 Trp Ala Ala Phe Met Pro Tyr Leu Leu Leu Pro Asp Ser Thr Ile Asn
 115 120 125
 Ser Ala Gly Asn Ala Leu His Ile Ser Gly Leu Ser Trp Val Thr Gly
 130 135 140
 Leu Asp Glu Lys Pro Val Glu Gly Ser Ser Glu Val Thr Asp Ile Ser
 145 150 155 160
 Ile Ala Ser Gly Ala Cys Leu Ala Val Arg Val Asp Trp Trp Lys Arg
 165 170 175
 Leu Gly Gly Met Glu Glu Leu Tyr Phe Met Tyr His Glu Asp Thr Asp
 180 185 190
 Phe Ser Ala Arg Leu Leu Leu Ala Gly Gly Arg Ile Gly Leu Leu His
 195 200 205
 Ser Ala Tyr Val Thr His His Tyr Asp Tyr Ala Lys Gly Asp Tyr Lys
 210 215 220
 Trp Ile Tyr Ile Glu Arg Asn Arg His Val Leu Leu Leu Ser Val Leu
 225 230 235 240
 Pro Leu Pro Leu Leu Phe Val Leu Ile Pro Gln Ile Leu Gly Val Asn
 245 250 255
 Leu Gly Leu Trp Ala Ile Ala Ala Lys Glu Lys Arg Val Gly Leu Lys
 260 265 270
 Val Lys Ser Leu Arg Leu Leu Ile Arg Asp Leu Pro Ala Ile Phe Lys
 275 280 285
 Leu Arg Arg Ser Thr Gln Glu Leu Ala Glu Leu Thr Pro Ser Gln Tyr
 290 295 300
 Leu Ala Lys Met Glu Trp Arg Leu Asp Asn Pro Asn Leu Gly Asn Ile
 305 310 315 320
 Gly Ser Asn Lys Ile Val Ala Thr Gly Tyr Lys Thr Tyr Tyr Lys Leu

325

330

335

Cys Met Ser Ile Leu Lys Leu Leu Ala
340 345

<210> 677

<211> 1158

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}..(1135)

<223> PRXA01574

<400> 677

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aaggtgggca acgagtcggt gagagtatga ggaatatattg atg agc aac aaa cgc 115
Met Ser Asn Lys Arg
1 5

atc ggt gta gtg atc gtt tcc tac gga cac gaa caa gat gtt gcc aac 163
Ile Gly Val Val Ile Val Ser Tyr Gly His Glu Gln Asp Val Ala Asn
10 15 20

ctg gta gac aca ttt gca gat cag ctg aaa act ggt gac cgc gta gtt 211
Leu Val Asp Thr Phe Ala Asp Gln Leu Lys Thr Gly Asp Arg Val Val
25 30 35

gtc gtg gac aac cgc aaa cct tgg gtg tta aaa gac gcc gtg ggg gag 259
Val Val Asp Asn Arg Lys Pro Trp Val Leu Lys Asp Ala Val Gly Glu
40 45 50

cgc ctg gaa aaa cac ggc gca gag atc atc aac cac gac aac ggt ggt 307
Arg Leu Glu Lys His Gly Ala Glu Ile Ile Asn His Asp Asn Gly Gly
55 60 65

ttc gcc gct ggc tgc aac gtg ggc gca gcg cac atc gtg gat gac gtt 355
Phe Ala Ala Gly Cys Asn Val Gly Ala Ala His Ile Val Asp Asp Val
70 75 80 85

gac ctg ctg ttc ttc ctc aac ccc gac aca gtg atc gac gat ccc acc 403
Asp Leu Leu Phe Phe Leu Asn Pro Asp Thr Val Ile Asp Asp Pro Thr
90 95 100

ctg ttc aat tcg ctg aga cgc gtc gat gaa cag tgg gca gca ttc atg 451
Leu Phe Asn Ser Leu Arg Arg Val Asp Glu Gln Trp Ala Ala Phe Met
105 110 115

ccg tac ctg ctg ctt cct gac agc acc att aac tcc gca ggc aac gcc 499
Pro Tyr Leu Leu Leu Pro Asp Ser Thr Ile Asn Ser Ala Gly Asn Ala
120 125 130

ctg cat att tcc gga ctg tcg tgg gtg act ggt ctg gat gaa aaa cca 547
Leu His Ile Ser Gly Leu Ser Trp Val Thr Gly Leu Asp Glu Lys Pro
135 140 145

gtt gaa ggc tca tct gaa gtt acc gat att tcc att gcc tct ggc gcc 595
Val Glu Gly Ser Ser Glu Val Thr Asp Ile Ser Ile Ala Ser Gly Ala

150	155	160	165	
tgc ctt gcc gtg cgc	gtg gac tgg tgg aaa cgc	ctc ggt ggc atg gaa	643	
Cys Leu Ala Val Arg	Val Asp Trp Trp Lys Arg	Leu Gly Gly Met Glu		
	170	175	180	
gaa ctg tat ttc atg	tac cac gaa gac act gac	ttc tcc gcc cgc ttg	691	
Glu Leu Tyr Phe Met	Tyr His Glu Asp Thr Asp	Phe Ser Ala Arg Leu		
	185	190	195	
ctg ctg gcc ggc ggt	cga att ggt ctc ctg	cat tcc gcg tat gtc acc	739	
Leu Leu Ala Gly Gly	Arg Ile Gly Leu Leu	His Ser Ala Tyr Val Thr		
	200	205	210	
cac cat tac gac tac	gcc aag ggt gac tac aag	tgg att tac atc gaa	787	
His His Tyr Asp Tyr	Ala Lys Gly Asp Tyr Lys	Trp Ile Tyr Ile Glu		
	215	220	225	
cga aac cga cac gtt	ttg ctg ctc agc gtg ctg	ccg ctt cca ttg ctg	835	
Arg Asn Arg His Val	Leu Leu Leu Ser Val	Leu Pro Leu Pro Leu Leu		
	230	235	240	245
ttc gtg ctg atc ccg	cag atc ctc ggt gtg aac	ctg gga ctg tgg gcg	883	
Phe Val Leu Ile Pro	Gln Ile Leu Gly Val Asn	Leu Gly Leu Trp Ala		
	250	255	260	
att gcc gca aag gaa	aag agg gtc gga ctc aag	gtg aag tcc ctt cgc	931	
Ile Ala Ala Lys Glu	Lys Arg Val Gly Leu Lys	Val Lys Ser Leu Arg		
	265	270	275	
ctc ctg atc cgc gat	cta cca gcg att ttc aaa	ctg cgt agg agc acg	979	
Leu Leu Ile Arg Asp	Leu Pro Ala Ile Phe	Lys Leu Arg Arg Ser Thr		
	280	285	290	
cag gag ctt gcc gaa	ctc aca cca tcg caa tat	ctg gca aaa atg gaa	1027	
Gln Glu Leu Ala Glu	Leu Thr Pro Ser Gln Tyr	Leu Ala Lys Met Glu		
	295	300	305	
tgg cgc cta gac aat	ccc aac cta ggc aac att	gga tcc aac aag att	1075	
Trp Arg Leu Asp Asn	Pro Asn Leu Gly Asn Ile	Gly Ser Asn Lys Ile		
	310	315	320	325
gtt gcg act gga tat	aag acc tat tac aag	ttg tgt atg agt atc ctg	1123	
Val Ala Thr Gly Tyr	Lys Thr Tyr Tyr Lys	Leu Cys Met Ser Ile Leu		
	330	335	340	
aaa ttg ctc gct taacacccca	taaagagggt gaa		1158	
Lys Leu Leu Ala				
	345			

<210> 678

<211> 345

<212> PRT

<213> Corynebacterium glutamicum

<400> 678

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10

15

Gln Asp Val Ala Asn Leu Val Asp Thr Phe Ala Asp Gln Leu Lys Thr

		20						25					30
Gly	Asp	Arg	Val	Val	Val	Val	Asp	Asn	Arg	Lys	Pro	Trp	Val
		35						40				45	Leu
Asp	Ala	Val	Gly	Glu	Arg	Leu	Glu	Lys	His	Gly	Ala	Glu	Ile
	50					55					60	Ile	Asn
His	Asp	Asn	Gly	Gly	Phe	Ala	Ala	Gly	Cys	Asn	Val	Gly	Ala
	65				70				75			Ala	His
Ile	Val	Asp	Asp	Val	Asp	Leu	Leu	Phe	Phe	Leu	Asn	Pro	Asp
			85						90				95
Ile	Asp	Asp	Pro	Thr	Leu	Phe	Asn	Ser	Leu	Arg	Arg	Val	Asp
			100					105					110
Trp	Ala	Ala	Phe	Met	Pro	Tyr	Leu	Leu	Leu	Pro	Asp	Ser	Thr
		115					120					125	Ile
Ser	Ala	Gly	Asn	Ala	Leu	His	Ile	Ser	Gly	Leu	Ser	Trp	Val
	130					135						140	Thr
Leu	Asp	Glu	Lys	Pro	Val	Glu	Gly	Ser	Ser	Glu	Val	Thr	Asp
	145				150					155			Ile
Ile	Ala	Ser	Gly	Ala	Cys	Leu	Ala	Val	Arg	Val	Asp	Trp	Trp
			165						170				Lys
Leu	Gly	Gly	Met	Glu	Glu	Leu	Tyr	Phe	Met	Tyr	His	Glu	Asp
			180					185					190
Phe	Ser	Ala	Arg	Leu	Leu	Leu	Ala	Gly	Gly	Arg	Ile	Gly	Leu
		195					200					205	Leu
Ser	Ala	Tyr	Val	Thr	His	His	Tyr	Asp	Tyr	Ala	Lys	Gly	Asp
	210				215						220		Tyr
Trp	Ile	Tyr	Ile	Glu	Arg	Asn	Arg	His	Val	Leu	Leu	Ser	Val
	225				230					235			240
Pro	Leu	Pro	Leu	Leu	Phe	Val	Leu	Ile	Pro	Gln	Ile	Leu	Gly
			245						250				255
Leu	Gly	Leu	Trp	Ala	Ile	Ala	Ala	Lys	Glu	Lys	Arg	Val	Gly
		260					265						270
Val	Lys	Ser	Leu	Arg	Leu	Leu	Ile	Arg	Asp	Leu	Pro	Ala	Ile
	275						280					285	Phe
Leu	Arg	Arg	Ser	Thr	Gln	Glu	Leu	Ala	Glu	Leu	Thr	Pro	Ser
	290					295					300		Gln
Leu	Ala	Lys	Met	Glu	Trp	Arg	Leu	Asp	Asn	Pro	Asn	Leu	Gly
	305				310				315				320
Gly	Ser	Asn	Lys	Ile	Val	Ala	Thr	Gly	Tyr	Lys	Thr	Tyr	Tyr
			325						330				Lys
													335
Cys	Met	Ser	Ile	Leu	Lys	Leu	Leu	Ala					
			340					345					

<210> 679
 <211> 1143
 <212> DNA
 <213> *Corynebacterium glutamicum*
 <220>
 <221> CDS
 <222> (101)..(1120)
 <223> RXN01589
 <400> 679
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 gctttaattc aaaaattgta agctgttagg aggtccacaa atg gta gaa caa ata 115
 Met Val Glu Gln Ile
 1 5
 aaa gat aaa cta gga cgt ccc atc cgt gac tta cgg tta tct gtg aca 163
 Lys Asp Lys Leu Gly Arg Pro Ile Arg Asp Leu Arg Leu Ser Val Thr
 10 15 20
 gat cgg tgt aac ttt agg tgt gat tat tgc atg cct aaa gag gta ttt 211
 Asp Arg Cys Asn Phe Arg Cys Asp Tyr Cys Met Pro Lys Glu Val Phe
 25 30 35
 gga gat gat ttc gta ttt tta cct aaa aat gaa ctg tta acg ttt gat 259
 Gly Asp Asp Phe Val Phe Leu Pro Lys Asn Glu Leu Thr Phe Asp
 40 45 50
 gaa atg gct aga atc gct aag gta tat gca gaa tta ggt gta aaa aaa 307
 Glu Met Ala Arg Ile Ala Lys Val Tyr Ala Glu Leu Gly Val Lys Lys
 55 60 65
 ata cgc att aca ggt gga gaa cca ttg atg cga cgc gat tta gat gta 355
 Ile Arg Ile Thr Gly Gly Glu Pro Leu Met Arg Arg Asp Leu Asp Val
 70 75 80 85
 ctt ata gct aaa tta aat caa atc gat ggt att gaa gat att ggt ttg 403
 Leu Ile Ala Lys Leu Asn Gln Ile Asp Gly Ile Glu Asp Ile Gly Leu
 90 95 100
 act aca aat ggt ttg tta tta aaa aag cat gga caa aag tta tat gat 451
 Thr Thr Asn Gly Leu Leu Leu Lys Lys His Gly Gln Lys Leu Tyr Asp
 105 110 115
 get ggg cta cgc aga att aat gtc agt ttg gat gct att gat gat acg 499
 Ala Gly Leu Arg Arg Ile Asn Val Ser Leu Asp Ala Ile Asp Asp Thr
 120 125 130
 cta ttt caa tca atc aat aat cgt aat att aaa gcg act acg att tta 547
 Leu Phe Gln Ser Ile Asn Asn Arg Asn Ile Lys Ala Thr Thr Ile Leu
 135 140 145
 gaa caa att gat tac gcg acg tct att ggt ttg aat gta aaa gta aat 595
 Glu Gln Ile Asp Tyr Ala Thr Ser Ile Gly Leu Asn Val Lys Val Asn
 150 155 160 165
 gtt gtt ata caa aaa ggt att aac gat gat caa atc ata cca atg ctt 643
 Val Val Ile Gln Lys Gly Ile Asn Asp Asp Gln Ile Ile Pro Met Leu

	170	175	180	
	gaa tat ttt aaa gat aaa cat ata gag att cga ttt ata gaa ttt atg			691
	Glu Tyr Phe Lys Asp Lys His Ile Glu Ile Arg Phe Ile Glu Phe Met			
	185	190	195	
	gat gtt ggt aat gat aat gga tgg gat ttc agt aaa gtt gta act aaa			739
	Asp Val Gly Asn Asp Asn Gly Trp Asp Phe Ser Lys Val Val Thr Lys			
	200	205	210	
	gat gaa atg ctt aca atg ata gag cag cac ttt gaa atc gat cct gta			787
	Asp Glu Met Leu Thr Met Ile Glu Gln His Phe Glu Ile Asp Pro Val			
	215	220	225	
	gaa cca aaa tat ttt ggg gaa gta gca aaa tat tat cgc cat aag gat			835
	Glu Pro Lys Tyr Phe Gly Glu Val Ala Lys Tyr Tyr Arg His Lys Asp			
	230	235	240	245
	aat ggt gtt caa ttt ggt ttg att aca agt gtt tca caa tca ttt tgt			883
	Asn Gly Val Gln Phe Gly Leu Ile Thr Ser Val Ser Gln Ser Phe Cys			
	250	255	260	
	tct aca tgt aca cgc gca agg ctg tca tca gat ggg aag ttt tac gga			931
	Ser Thr Cys Thr Arg Ala Arg Leu Ser Ser Asp Gly Lys Phe Tyr Gly			
	265	270	275	
	tgt tta ttt gca act gtc gat gga ttt aac gtt aaa cgc ttt att cgt			979
	Cys Leu Phe Ala Thr Val Asp Gly Phe Asn Val Lys Ala Phe Ile Arg			
	280	285	290	
	tct ggc gtg acc gac gaa gaa tta aaa gaa caa ttt aaa gct tta tgg			1027
	Ser Gly Val Thr Asp Glu Glu Leu Lys Glu Gln Phe Lys Ala Leu Trp			
	295	300	305	
	caa ata aga gat gat cga tat tca gat gag aga act gct caa aca gtt			1075
	Gln Ile Arg Asp Asp Arg Tyr Ser Asp Glu Arg Thr Ala Gln Thr Val			
	310	315	320	325
	gcc aat cgt caa cgt aaa aag ata aac atg aat tat att ggt ggt			1120
	Ala Asn Arg Gln Arg Lys Lys Ile Asn Met Asn Tyr Ile Gly Gly			
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	taatgtgtag ggaccactac ata			1143
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	<211> 340			
	<212> PRT			
	<213> <i>Corynebacterium glutamicum</i>			
	<400> 680			
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	Arg Leu Ser Val Thr Asp Arg Cys Asn Phe Arg Cys Asp Tyr Cys Met			
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	Pro Lys Glu Val Phe Gly Asp Asp Phe Val Phe Leu Pro Lys Asn Glu			
	35	40	45	
	Leu Leu Thr Phe Asp Glu Met Ala Arg Ile Ala Lys Val Tyr Ala Glu			

50					55					60					
Leu	Gly	Val	Lys	Lys	Ile	Arg	Ile	Thr	Gly	Gly	Glu	Pro	Leu	Met	Arg
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Arg	Asp	Leu	Asp	Val	Leu	Ile	Ala	Lys	Leu	Asn	Gln	Ile	Asp	Gly	Ile
				85					90					95	
Glu	Asp	Ile	Gly	Leu	Thr	Thr	Asn	Gly	Leu	Leu	Leu	Lys	Lys	His	Gly
			100					105					110		
Gln	Lys	Leu	Tyr	Asp	Ala	Gly	Leu	Arg	Arg	Ile	Asn	Val	Ser	Leu	Asp
			115				120					125			
Ala	Ile	Asp	Asp	Thr	Leu	Phe	Gln	Ser	Ile	Asn	Asn	Arg	Asn	Ile	Lys
				130			135					140			
Ala	Thr	Thr	Ile	Leu	Glu	Gln	Ile	Asp	Tyr	Ala	Thr	Ser	Ile	Gly	Leu
				145			150					155			160
Asn	Val	Lys	Val	Asn	Val	Val	Ile	Gln	Lys	Gly	Ile	Asn	Asp	Asp	Gln
				165					170					175	
Ile	Ile	Pro	Met	Leu	Glu	Tyr	Phe	Lys	Asp	Lys	His	Ile	Glu	Ile	Arg
			180					185					190		
Phe	Ile	Glu	Phe	Met	Asp	Val	Gly	Asn	Asp	Asn	Gly	Trp	Asp	Phe	Ser
			195				200					205			
Lys	Val	Val	Thr	Lys	Asp	Glu	Met	Leu	Thr	Met	Ile	Glu	Gln	His	Phe
			210				215					220			
Glu	Ile	Asp	Pro	Val	Glu	Pro	Lys	Tyr	Phe	Gly	Glu	Val	Ala	Lys	Tyr
				225			230				235				240
Tyr	Arg	His	Lys	Asp	Asn	Gly	Val	Gln	Phe	Gly	Leu	Ile	Thr	Ser	Val
				245					250					255	
Ser	Gln	Ser	Phe	Cys	Ser	Thr	Cys	Thr	Arg	Ala	Arg	Leu	Ser	Ser	Asp
				260				265					270		
Gly	Lys	Phe	Tyr	Gly	Cys	Leu	Phe	Ala	Thr	Val	Asp	Gly	Phe	Asn	Val
				275			280					285			
Lys	Ala	Phe	Ile	Arg	Ser	Gly	Val	Thr	Asp	Glu	Glu	Leu	Lys	Glu	Gln
				290			295				300				
Phe	Lys	Ala	Leu	Trp	Gln	Ile	Arg	Asp	Asp	Arg	Tyr	Ser	Asp	Glu	Arg
				305			310				315				320
Thr	Ala	Gln	Thr	Val	Ala	Asn	Arg	Gln	Arg	Lys	Lys	Ile	Asn	Met	Asn
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Tyr	Ile	Gly	Gly												
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<210> 681

<211> 1425

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1402)

<223> RXN01592

<400> 681

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				Met	Ala	Asp	Asn	Phe	
				1				5	

gac	cgc	tct	cgt	gac	aac	gat	cgc	tca	agc	gac	cgc	act	cct	cgt	gga	163
Asp	Arg	Ser	Arg	Asp	Asn	Asp	Arg	Ser	Ser	Asp	Arg	Thr	Pro	Arg	Gly	
			10						15					20		

gac	cgc	ggc	gat	cgc	ggg	ggc	tac	cga	aac	tcc	cgc	ggc	aac	gat	gac	211
Asp	Arg	Gly	Asp	Arg	Gly	Gly	Tyr	Arg	Asn	Ser	Arg	Gly	Asn	Asp	Asp	
			25				30						35			

cgc	gga	aac	tac	cgt	caa	aac	cga	gat	ggg	gaa	tca	cga	gat	cgc	ggc	259
Arg	Gly	Asn	Tyr	Arg	Gln	Asn	Arg	Asp	Gly	Glu	Ser	Arg	Asp	Arg	Gly	
			40				45					50				

gga	tac	ctc	ggg	gac	cgt	cgc	gac	aac	cgc	tca	ggg	gaa	tat	cgt	caa	307
Gly	Tyr	Leu	Gly	Asp	Arg	Arg	Asp	Asn	Arg	Ser	Gly	Glu	Tyr	Arg	Gln	
			55				60					65				

cgt	gac	gat	agg	cgt	gac	gat	cgt	agg	gac	aac	cga	agc	gat	gac	cgc	355
Arg	Asp	Asp	Arg	Arg	Asp	Asp	Arg	Arg	Asp	Arg	Arg	Ser	Asp	Asp	Arg	
					75					80					85	

cgc	ggg	ggg	tac	cgc	tcc	gat	cgc	aac	ttt	gac	gat	cgc	aac	agc	aac	403
Arg	Gly	Gly	Tyr	Arg	Ser	Asp	Arg	Asn	Phe	Asp	Asp	Arg	Asn	Ser	Asn	
				90					95					100		

atg	cgt	gat	gat	cgt	cgc	ggc	ggc	gac	cgt	tca	tac	agc	cgt	aat	gat	451
Met	Arg	Asp	Asp	Arg	Arg	Gly	Gly	Asp	Arg	Ser	Tyr	Ser	Arg	Asn	Asp	
			105					110					115			

cgc	tcc	gat	cgt	ggc	tat	cgt	agc	aat	gac	cgc	tac	gac	cgt	aat	gat	499
Arg	Ser	Asp	Arg	Gly	Tyr	Arg	Ser	Asn	Asp	Arg	Tyr	Asp	Arg	Asn	Asp	
			120				125					130				

cgt	cgc	gat	gac	aac	agg	gac	acc	agg	ggg	ggc	gat	cgc	gga	gac	cgt	547
Arg	Arg	Asp	Asp	Asn	Arg	Asp	Thr	Arg	Gly	Gly	Asp	Arg	Gly	Asp	Arg	
			135			140					145					

cgc	tac	gac	agg	cgc	gat	gac	cga	cgt	gat	gat	cgt	cgc	gat	gat	cgt	595
Arg	Tyr	Asp	Arg	Arg	Asp	Asp	Arg	Arg	Asp	Asp	Arg	Arg	Asp	Asp	Arg	
					155					160					165	

cgt	ggc	gga	cag	ggc	cag	ggg	cgt	cca	ggg	gga	gat	cgt	cga	cat	gag	643
Arg	Gly	Gly	Gln	Gly	Gln	Gly	Arg	Pro	Gly	Gly	Asp	Arg	Arg	His	Ala	
				170					175					180		

aac	cgt	gca	ggg	gca	ggg	cgc	gat	cag	cag	cgt	gat	tgg	ctg	cat	cca	691
Asn	Arg	Ala	Gly	Ala	Gly	Arg	Asp	Gln	Gln	Arg	Asp	Ser	Leu	His	Pro	
			185				190						195			

cag cgc gct ggt ttc cgt gaa gag cgc ttg aac act cgt ctc aat gag 739
 Gln Arg Ala Gly Phe Arg Glu Glu Arg Leu Asn Thr Arg Leu Asn Glu
 200 205 210

cct gat ttg ccg ggc gat att gat atc aag gac ttg gat cct ttg gtc 787
 Pro Asp Leu Pro Gly Asp Ile Asp Ile Lys Asp Leu Asp Pro Leu Val
 215 220 225

ctg cag gat ttg aag gtt ttg tct aag gac aac gca gat gcc gtc gca 835
 Leu Gln Asp Leu Lys Val Leu Ser Lys Asp Asn Ala Asp Ala Val Ala
 230 235 240 245

aag cat atg atc atg gct gcg acc tgg ctg gcc gac gat cct caa ttg 883
 Lys His Met Ile Met Ala Ala Thr Trp Leu Ala Asp Asp Pro Gln Leu
 250 255 260

gca ctg cgc cac gcc cgt gct gcg aag gat cgc gcg gga cgc gtc tcc 931
 Ala Leu Arg His Ala Arg Ala Ala Lys Asp Arg Ala Gly Arg Val Ser
 265 270 275

gtc gtg cgt gag acg aac gcc att gct gct tac cat gct ggt gag tgg 979
 Val Val Arg Glu Thr Asn Gly Ile Ala Ala Tyr His Ala Gly Glu Trp
 280 285 290

aag gaa gct ctt tcg gag ctt cgt gct gcg cgc cgc atg tcg ggt ggt 1027
 Lys Glu Ala Leu Ser Glu Leu Arg Ala Ala Arg Arg Met Ser Gly Gly
 295 300 305

cct ggt ttg att gct gtg atg gct gac tgt gag cgt gcc ttg ggt cgt 1075
 Pro Gly Leu Ile Ala Val Met Ala Asp Cys Glu Arg Gly Leu Gly Arg
 310 315 320 325

cct gag aag gcg att gag ctg gct cga gaa gag gat ttg agc tct ttg 1123
 Pro Glu Lys Ala Ile Glu Leu Ala Arg Glu Glu Asp Leu Ser Ser Leu
 330 335 340

gat cag gat aac ctg atc gag tta gcg att gtt gtt gct gga gca cgc 1171
 Asp Gln Asp Asn Leu Ile Glu Leu Ala Ile Val Val Ala Gly Ala Arg
 345 350 355

cat gat ttg ggt cag cat gac tct gcg att gtg gaa ttg cag aag gtt 1219
 His Asp Leu Gly Gln His Asp Ser Ala Ile Val Glu Leu Lys Val
 360 365 370

aat cca agc ttg aag agc acc ggt ttc acc cat tct cgt ttg tct tac 1267
 Asn Pro Ser Leu Lys Ser Thr Gly Phe Thr His Ser Arg Leu Ser Tyr
 375 380 385

gct tac gcc gat gcg ctt gtt ttg gct ggt cgt gcc gat gaa gca cgt 1315
 Ala Tyr Ala Asp Ala Leu Val Leu Ala Gly Arg Gly Asp Glu Ala Arg
 390 395 400 405

gag tgg ttc cag cac gct gcc acc ttg gat gag gac gcc tac ctc gat 1363
 Glu Trp Phe Gln His Ala Ala Thr Leu Asp Glu Asp Gly Tyr Leu Asp
 410 415 420

gca gag gag cgt atc gag cag ctc gat aat ggg aac aac tagactattg 1412
 Ala Glu Glu Arg Ile Glu Gln Leu Asp Asn Gly Asn Asn
 425 430

gtctagagtg taa 1425

<210> 682

<211> 434

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 682

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35 40 45Ser Arg Asp Arg Gly Gly Tyr Leu Gly Asp Arg Arg Asp Asn Arg Ser
50 55 60Gly Glu Tyr Arg Gln Arg Asp Asp Arg Arg Asp Asp Arg Arg Asp Asn
65 70 75 80Arg Ser Asp Asp Arg Arg Gly Gly Tyr Arg Ser Asp Arg Asn Phe Asp
85 90 95Asp Arg Asn Ser Asn Met Arg Asp Asp Arg Arg Gly Gly Asp Arg Ser
100 105 110Tyr Ser Arg Asn Asp Arg Ser Asp Arg Gly Tyr Arg Ser Asn Asp Arg
115 120 125Tyr Asp Arg Asn Asp Arg Arg Asp Asp Asn Arg Asp Thr Arg Gly Gly
130 135 140Asp Arg Gly Asp Arg Arg Tyr Asp Arg Arg Asp Asp Arg Arg Asp Asp
145 150 155 160Arg Arg Asp Asp Arg Arg Gly Gly Gln Gly Gln Gly Arg Pro Gly Gly
165 170 175Asp Arg Arg His Ala Asn Arg Ala Gly Ala Gly Arg Asp Gln Gln Arg
180 185 190Asp Ser Leu His Pro Gln Arg Ala Gly Phe Arg Glu Glu Arg Leu Asn
195 200 205Thr Arg Leu Asn Glu Pro Asp Leu Pro Gly Asp Ile Asp Ile Lys Asp
210 215 220Leu Asp Pro Leu Val Leu Gln Asp Leu Lys Val Leu Ser Lys Asp Asn
225 230 235 240Ala Asp Ala Val Ala Lys His Met Ile Met Ala Ala Thr Trp Leu Ala
245 250 255Asp Asp Pro Gln Leu Ala Leu Arg His Ala Arg Ala Ala Lys Asp Arg
260 265 270Ala Gly Arg Val Ser Val Val Arg Glu Thr Asn Gly Ile Ala Ala Tyr
275 280 285

His Ala Gly Glu Trp Lys Glu Ala Leu Ser Glu Leu Arg Ala Ala Arg
290 295 300

Arg Met Ser Gly Gly Pro Gly Leu Ile Ala Val Met Ala Asp Cys Glu
305 310 315

Arg Gly Leu Gly Arg Pro Glu Lys Ala Ile Glu Leu Ala Arg Glu Glu
325 330 335

Asp Leu Ser Ser Leu Asp Gln Asp Asn Leu Ile Glu Leu Ala Ile Val
340 345 350

Val Ala Gly Ala Arg His Asp Leu Gly Gln His Asp Ser Ala Ile Val
355 360 365

Glu Leu Gln Lys Val Asn Pro Ser Leu Lys Ser Thr Gly Phe Thr His
370 375 380

Ser Arg Leu Ser Tyr Ala Tyr Ala Asp Ala Leu Val Leu Ala Gly Arg
385 390 395 400

Gly Asp Glu Ala Arg Glu Trp Phe Gln His Ala Ala Thr Leu Asp Glu
405 410 415

Asp Gly Tyr Leu Asp Ala Glu Glu Arg Ile Glu Gln Leu Asp Asn Gly
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Asn Asn

<210> 683

<211> 1316

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1293)

<223> FRXA01592

<400> 683

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cgt gga gac cgc ggc gat cgc ggt ggc tac cga aac tcc cgc ggc aac 96
Arg Gly Asp Arg Gly Asp Arg Gly Gly Tyr Arg Asn Ser Ser Arg Gly Asn
20 25 30

gat gac cgc gga aac tac cgt caa aac cga gat ggt gaa tca cga gat 144
Asp Asp Arg Gly Asn Tyr Arg Gln Asn Arg Asp Gly Glu Ser Arg Asp
35 40 45

cgc ggc gga tac ctc ggt gac cgt cgc gac aac cgc tca ggt gaa tat 192
Arg Gly Gly Tyr Leu Gly Asp Arg Arg Asp Asn Arg Ser Gly Glu Tyr
50 55 60

cgt caa cgt gac gat agg cgt gac gat cgt agg gac aac cga agc gat 240
Arg Gln Arg Asp Asp Arg Arg Asp Asp Arg Arg Asp Asn Arg Ser Asp

65	70	75	80	
gac cgc cgc ggt ggt tac cgc tcc gat cgc aac ttt gac gat cgc aac				288
Asp Arg Arg Gly Gly Tyr Arg Ser Asp Arg Asn Phe Asp Asp Arg Asn	85	90	95	
agc aac atg cgt gat gat cgt cgc ggc ggc gac cgt tca tac agc cgt				336
Ser Asn Met Arg Asp Asp Arg Arg Gly Gly Asp Arg Ser Tyr Ser Arg	100	105	110	
aat gat cgc tcc gat cgt ggc tat cgt agc aat gac cgc tac gac cgt				384
Asn Asp Arg Ser Asp Arg Gly Tyr Arg Ser Asn Asp Arg Tyr Asp Arg	115	120	125	
aat gat cgt cgc gat gac aac agg gac acc agg ggt ggc gat cgc gga				432
Asn Asp Arg Arg Asp Asp Asn Arg Asp Thr Arg Gly Gly Asp Arg Gly	130	135	140	
gac cgt cgc tac gac agg cgc gat gac cga cgt gat gat cgt cgc gat				480
Asp Arg Arg Tyr Asp Arg Asp Asp Arg Asp Asp Asp Arg Arg Asp	145	150	155	160
gat cgt cgt ggc gga cag ggc cag ggg cgt cca ggt gga gat cgt cga				528
Asp Arg Arg Gly Gly Gln Gly Gln Gly Arg Pro Gly Gly Asp Arg Arg	165	170	175	
cat gcg aac cgt gca ggt gca ggt cgc gat cag cag cgt gat tgc ctg				576
His Ala Asn Arg Ala Gly Ala Gly Arg Asp Gln Gln Arg Asp Ser Leu	180	185	190	
cat cca cag cgc gct ggt ttc cgt gaa gag cgc ttg aac act cgt ctc				624
His Pro Gln Arg Ala Gly Phe Arg Glu Glu Arg Leu Asn Thr Arg Leu	195	200	205	
aat gag cct gat ttg ccg ggc gat att gat atc aag gac ttg gat cct				672
Asn Glu Pro Asp Leu Pro Gly Asp Ile Asp Ile Lys Asp Leu Asp Pro	210	215	220	
ttg gtc ctg cag gat ttg aag gtt ttg tct aag gac aac gca gat gcc				720
Leu Val Leu Gln Asp Leu Lys Val Leu Ser Lys Asp Asn Ala Asp Ala	225	230	235	240
gtc gca aag cat atg atc atg gct gcg acc tgg ctg gcc gac gat cct				768
Val Ala Lys His Met Ile Met Ala Ala Thr Trp Leu Ala Asp Asp Pro	245	250	255	
caa ttg gca ctg cgc cac gcc cgt gct gcg aag gat cgc gcg gga cgc				816
Gln Leu Ala Leu Arg His Ala Arg Ala Ala Lys Asp Arg Ala Gly Arg	260	265	270	
gtg tcc gtc gtg cgt gag acg aac ggc att gct gct tac cat gct ggt				864
Val Ser Val Val Arg Glu Thr Asn Gly Ile Ala Ala Tyr His Ala Gly	275	280	285	
gag tgg aag gaa gct ctt tcg gag ctt cgt gct gcg cgc cgc atg tcg				912
Glu Trp Lys Glu Ala Leu Ser Glu Leu Arg Ala Ala Arg Arg Met Ser	290	295	300	
ggt ggt cct ggt ttg att gct gtg atg gct gac tgt gag cgt ggc ttg				960
Gly Gly Pro Gly Leu Ile Ala Val Met Ala Asp Cys Glu Arg Gly Leu	305	310	315	320

ggt cgt cct gag aag gcg att gag ctg gct cga gaa gag gat ttg agc 1008
 Gly Arg Pro Glu Lys Ala Ile Glu Leu Ala Arg Glu Glu Asp Leu Ser
 325 330 335

tct ttg gat cag gat aac ctg atc gag tta gcg att gtt gtt gct gga 1056
 Ser Leu Asp Gln Asp Asn Leu Ile Glu Leu Ala Ile Val Val Ala Gly
 340 345 350

gca cgc cat gat ttg ggt cag cat gac tct gcg att gtg gaa ttg cag 1104
 Ala Arg His Asp Leu Gly Gln His Asp Ser Ala Ile Val Glu Leu Gln
 355 360 365

aag gtt aat cca agc ttg aag agc acc ggt ttc acc cat tct cgt ttg 1152
 Lys Val Asn Pro Ser Leu Lys Ser Thr Gly Phe Thr His Ser Arg Leu
 370 375 380

tct tac gct tac gcc gat gcg ctt gtt ttg gct ggt cgt gcc gat gaa 1200
 Ser Tyr Ala Tyr Ala Asp Ala Leu Val Leu Ala Gly Arg Gly Asp Glu
 385 390 395 400

gca cgt gag tgg ttc cag cac gct gcc acc ttg gat gag gac gcc tac 1248
 Ala Arg Glu Trp Phe Gln His Ala Ala Thr Leu Asp Glu Asp Gly Tyr
 405 410 415

ctc gat gca gag gag cgt atc gag cag ctc gat aat ggg aac aac 1293
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 420 425 430

tagactattg gtctagagtg taa 1316

<210> 684

<211> 431

<212> PRT

<213> Corynebacterium glutamicum

<400> 684

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Asp Asp Arg Gly Asn Tyr Arg Gln Asn Arg Asp Gly Glu Ser Arg Asp
 35 40 45

Arg Gly Gly Tyr Leu Gly Asp Arg Arg Asp Asn Arg Ser Gly Glu Tyr
 50 55 60

Arg Gln Arg Asp Asp Arg Arg Asp Asp Arg Arg Asp Asn Arg Ser Asp
 65 70 75 80

Asp Arg Arg Gly Gly Tyr Arg Ser Asp Arg Asn Phe Asp Asp Arg Asn
 85 90 95

Ser Asn Met Arg Asp Asp Arg Arg Gly Gly Asp Arg Ser Tyr Ser Arg
 100 105 110

Asn Asp Arg Ser Asp Arg Gly Tyr Arg Ser Asn Asp Arg Tyr Asp Arg
 115 120 125

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Asn Asp Arg Arg Asp Asp Asn Arg Asp Thr Arg Gly Gly Asp Arg Gly
 130                               135                               140

Asp Arg Arg Tyr Asp Arg Arg Asp Arg Arg Asp Asp Arg Arg Asp
145                               150                               155                               160

Asp Arg Arg Gly Gly Gln Gly Gln Gly Arg Pro Gly Gly Asp Arg Arg
                               165                               170                               175

His Ala Asn Arg Ala Gly Ala Gly Arg Asp Gln Gln Arg Asp Ser Leu
 180                               185                               190

His Pro Gln Arg Ala Gly Phe Arg Glu Glu Arg Leu Asn Thr Arg Leu
 195                               200                               205

Asn Glu Pro Asp Leu Pro Gly Asp Ile Asp Ile Lys Asp Leu Asp Pro
 210                               215                               220

Leu Val Leu Gln Asp Leu Lys Val Leu Ser Lys Asp Asn Ala Asp Ala
225                               230                               235                               240

Val Ala Lys His Met Ile Met Ala Ala Thr Trp Leu Ala Asp Asp Pro
245                               250                               255

Gln Leu Ala Leu Arg His Ala Arg Ala Ala Lys Asp Arg Ala Gly Arg
260                               265                               270

Val Ser Val Val Arg Glu Thr Asn Gly Ile Ala Ala Tyr His Ala Gly
275                               280                               285

Glu Trp Lys Glu Ala Leu Ser Glu Leu Arg Ala Ala Arg Arg Met Ser
290                               295                               300

Gly Gly Pro Gly Leu Ile Ala Val Met Ala Asp Cys Glu Arg Gly Leu
305                               310                               315                               320

Gly Arg Pro Glu Lys Ala Ile Glu Leu Ala Arg Glu Glu Asp Leu Ser
325                               330                               335

Ser Leu Asp Gln Asp Asn Leu Ile Glu Leu Ala Ile Val Val Ala Gly
340                               345                               350

Ala Arg His Asp Leu Gly Gln His Asp Ser Ala Ile Val Glu Leu Gln
355                               360                               365

Lys Val Asn Pro Ser Leu Lys Ser Thr Gly Phe Thr His Ser Arg Leu
370                               375                               380

Ser Tyr Ala Tyr Ala Asp Ala Leu Val Leu Ala Gly Arg Gly Asp Glu
385                               390                               395                               400

Ala Arg Glu Trp Phe Gln His Ala Ala Thr Leu Asp Glu Asp Gly Tyr
405                               410                               415

Leu Asp Ala Glu Glu Arg Ile Glu Gln Leu Asp Asn Gly Asn Asn
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<210> 685

<211> 1305

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1282)

<223> RXN01597

<400> 685

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 Met Ser Leu Phe Asn
 1 5

cgc aaa gcc gac ctg ccc gcc ctg caa ggt gcc acc cga atc tgc acc 163
 Arg Lys Ala Asp Leu Pro Gly Leu Gln Gly Ala Thr Arg Ile Cys Thr
 10 15 20

ccg cag gcc aaa ggg cta aag cgc ctg tcc gaa gcc gat ctc gca atc 211
 Pro Gln Gly Lys Gly Leu Lys Arg Leu Ser Glu Gly Asp Leu Ala Ile
 25 30 35

att gat gca cca gat cta tcc agg acc ttc gcc caa cga ttg cta gca 259
 Ile Asp Ala Pro Asp Leu Ser Arg Thr Phe Ala Gln Arg Leu Leu Ala
 40 45 50

gca aaa ccc gcc gca gtc ctc aac gtt tcc cgg ttc acc acc gga tcg 307
 Ala Lys Pro Ala Ala Val Leu Asn Val Ser Arg Phe Thr Thr Gly Ser
 55 60 65

gtg ccc aac ttt gga ccg caa atg ctt atc gac gcc gcc atc cag ctc 355
 Val Pro Asn Phe Gly Pro Gln Met Leu Ile Asp Gly Gly Ile Gln Leu
 70 75 80 85

gtg gaa gcc ttt gcc cag gag ctg ctc gac gcc acc aaa gac ggt aag 403
 Val Glu Gly Phe Gly Gln Glu Leu Leu Asp Gly Thr Lys Asp Gly Lys
 90 95 100

aaa ggt cgc ctg aca gaa gat gga cag ctc ttc tac gcc gaa cga ctg 451
 Lys Gly Arg Leu Thr Glu Asp Gly Gln Leu Phe Tyr Gly Glu Arg Leu
 105 110 115

atc tct aac gcc agt gtt ctc agt gga cct gcg gct gaa aat gca ttt 499
 Ile Ser Asn Gly Ser Val Leu Ser Gly Pro Ala Ala Glu Asn Ala Phe
 120 125 130

gca gac gcc cag caa tca ctg ctg gac cgc atg gaa gcc tat ttc gcc 547
 Ala Asp Ala Gln Gln Ser Leu Leu Asp Arg Met Glu Ala Tyr Phe Gly
 135 140 145

aac acc att cag ttc att cac tca gaa gca ccg ctc ctg atc gat gcc 595
 Asn Thr Ile Gln Phe Ile His Ser Glu Ala Pro Leu Leu Ile Asp Gly
 150 155 160 165

ctc gcc att ccc gat acc gga aat gcc att gaa gcc cgc aaa gtt ctc 643
 Leu Gly Ile Pro Asp Thr Gly Asn Ala Ile Glu Gly Arg Lys Val Leu
 170 175 180

att gcc tca cca ggg gat aac cac cgc agc agg ctc aaa gaa ctc cgc 691
 Ile Ala Ser Pro Gly Asp Asn His Arg Ser Arg Leu Lys Glu Leu Arg

	185		190		195	
	agc ttc atc cgc gaa tac gat	cca gta ctc atc ggt gtc gat ggg gca	739			
	Ser Phe Ile Arg Glu Tyr Asp	Pro Val Leu Ile Gly Val Asp Gly Ala				
	200	205	210			
	gca gac acc ttg gtg gaa ttg ggg tac aag ccc gcg ctg atc gtc ggc	787				
	Ala Asp Thr Leu Val Glu Leu Gly Tyr Lys Pro Ala Leu Ile Val Gly					
	215	220	225			
	aat ccc act ggt atc ggc gca gat gcg ctg cgc agt ggc gcc aac gta	835				
	Asn Pro Thr Gly Ile Gly Ala Asp Ala Leu Arg Ser Gly Ala Asn Val					
	230	235	240			
	att ttg cca gct gat cca gac ggc cac gct gtt ggt ctg gag cgc atc	883				
	Ile Leu Pro Ala Asp Pro Asp Gly His Ala Val Gly Leu Glu Arg Ile					
	250	255	260			
	cag gat ctt ggc atc ggt gcg atg acc ttc cca tcc tca gta aat tcc	931				
	Gln Asp Leu Gly Ile Gly Ala Met Thr Phe Pro Ser Ser Val Asn Ser					
	265	270	275			
	tcc acg gat ctg gcg ctc ctg ctt gcg gat ttc cac aac ccg cag atg	979				
	Ser Thr Asp Leu Ala Leu Leu Leu Ala Asp Phe His Asn Pro Gln Met					
	280	285	290			
	atc gtc aac gtc ggc ggt cct gtc acc ctt gat ggt gtt ttt gaa aac	1027				
	Ile Val Asn Val Gly Gly Pro Val Thr Leu Asp Gly Val Phe Glu Asn					
	295	300	305			
	cga gaa gat tcc gat ccc gcg gcg ctt ttg acg cgc gcc aag cta ggc	1075				
	Arg Glu Asp Ser Asp Pro Ala Ala Leu Leu Thr Arg Ala Lys Leu Gly					
	310	315	320			
	acc aag ctt gtc gac gga tcc gtc atc gca agt ctt tac aca gtg cgc	1123				
	Thr Lys Leu Val Asp Gly Ser Val Ile Ala Ser Leu Tyr Thr Val Arg					
	330	335	340			
	agc tcc agc aac ctt gga tgg atg tgg gca ctg tta gcc att ttg gtg	1171				
	Ser Ser Ser Asn Leu Gly Trp Met Trp Ala Leu Leu Ala Ile Leu Val					
	345	350	355			
	gtt ctt gca gtc gtg att gtt atc gct ggc acc gca gga tca ggc tct	1219				
	Val Leu Ala Val Val Ile Val Ile Ala Gly Thr Ala Gly Ser Gly Ser					
	360	365	370			
	ttt acc gac aac ctc att gac acc tgg aac agc ttc gcg ctg aca gtg	1267				
	Phe Thr Asp Asn Leu Ile Asp Thr Trp Asn Ser Phe Ala Leu Thr Val					
	375	380	385			
	cag ggt tgg ttc aaa taggaaggca acatggctaa acg	1305				
	Gln Gly Trp Phe Lys					
	390					

<210> 686

<211> 394

<212> PRT

<213> Corynebacterium glutamicum

<400> 686

Met Ser Leu Phe Asn Arg Lys Ala Asp Leu Pro Gly Leu Gln Gly Ala
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 Thr Arg Ile Cys Thr Pro Gln Gly Lys Gly Leu Lys Arg Leu Ser Glu
 20 25 30
 Gly Asp Leu Ala Ile Ile Asp Ala Pro Asp Leu Ser Arg Thr Phe Ala
 35 40 45
 Gln Arg Leu Leu Ala Ala Lys Pro Ala Ala Val Leu Asn Val Ser Arg
 50 55 60
 Phe Thr Thr Gly Ser Val Pro Asn Phe Gly Pro Gln Met Leu Ile Asp
 65 70 75 80
 Gly Gly Ile Gln Leu Val Glu Gly Phe Gly Gln Glu Leu Leu Asp Gly
 85 90 95
 Thr Lys Asp Gly Lys Lys Gly Arg Leu Thr Glu Asp Gly Gln Leu Phe
 100 105 110
 Tyr Gly Glu Arg Leu Ile Ser Asn Gly Ser Val Leu Ser Gly Pro Ala
 115 120 125
 Ala Glu Asn Ala Phe Ala Asp Ala Gln Gln Ser Leu Leu Asp Arg Met
 130 135 140
 Glu Ala Tyr Phe Gly Asn Thr Ile Gln Phe Ile His Ser Glu Ala Pro
 145 150 155 160
 Leu Leu Ile Asp Gly Leu Gly Ile Pro Asp Thr Gly Asn Ala Ile Glu
 165 170 175
 Gly Arg Lys Val Leu Ile Ala Ser Pro Gly Asp Asn His Arg Ser Arg
 180 185 190
 Leu Lys Glu Leu Arg Ser Phe Ile Arg Glu Tyr Asp Pro Val Leu Ile
 195 200 205
 Gly Val Asp Gly Ala Ala Asp Thr Leu Val Glu Leu Gly Tyr Lys Pro
 210 215 220
 Ala Leu Ile Val Gly Asn Pro Thr Gly Ile Gly Ala Asp Ala Leu Arg
 225 230 235 240
 Ser Gly Ala Asn Val Ile Leu Pro Ala Asp Pro Asp Gly His Ala Val
 245 250 255
 Gly Leu Glu Arg Ile Gln Asp Leu Gly Ile Gly Ala Met Thr Phe Pro
 260 265 270
 Ser Ser Val Asn Ser Ser Thr Asp Leu Ala Leu Leu Leu Ala Asp Phe
 275 280 285
 His Asn Pro Gln Met Ile Val Asn Val Gly Gly Pro Val Thr Leu Asp
 290 295 300
 Gly Val Phe Glu Asn Arg Glu Asp Ser Asp Pro Ala Ala Leu Leu Thr
 305 310 315 320
 Arg Ala Lys Leu Gly Thr Lys Leu Val Asp Gly Ser Val Ile Ala Ser

325								330					335			
Leu	Tyr	Thr	Val	Arg	Ser	Ser	Ser	Asn	Leu	Gly	Trp	Met	Trp	Ala	Leu	
340								345					350			
Leu	Ala	Ile	Leu	Val	Val	Leu	Ala	Val	Val	Ile	Val	Ile	Ala	Gly	Thr	
355								360					365			
Ala	Gly	Ser	Gly	Ser	Phe	Thr	Asp	Asn	Leu	Ile	Asp	Thr	Trp	Asn	Ser	
370								375					380			
Phe	Ala	Leu	Thr	Val	Gln	Gly	Trp	Phe	Lys							
385								390								

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<210> 687
<211> 1305
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1282)
<223> FRXA01597
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ctccacaaaa		ggttgagact	ttggtttcac aatgggctgc atg agt ctg ttc aac 115
			Met Ser Leu Phe Asn 5
cgc aaa gcc gac ctg ccc ggc ctg caa ggt gcc acc cga atc tgc acc 163	Arg Lys Ala Asp 10	Pro Gly Leu Gln Gly Ala Thr Arg Ile Cys Thr 20	
ccg cag ggc aaa ggg cta aag cgc ctg tcc gaa ggc gat ctc gca atc 211	Pro Gln Gly Lys Gly Leu Lys Arg Leu Ser Glu Gly Asp Leu Ala Ile 25		
att gat gca cca gat cta tcc agg acc ttc gcc caa cga ttg cta gca 259	Ile Asp Ala Pro Asp Leu Ser Arg Thr Phe Ala Gln Arg Leu Leu Ala 40		
gca aaa ccc gcc gca gtc ctc aac gtt tcc cgg ttc acc acc gga tgc 307	Ala Lys Pro Ala Ala Val Leu Asn Val Ser Arg Phe Thr Thr Gly Ser 55		
gtg ccc aac ttt gga ccc caa atg ctt atc gac ggc ggc atc cag ctc 355	Val Pro Asn Phe Gly Pro Gln Met Leu Ile Asp Gly Gly Ile Gln Leu 70 75 80 85		
gtg gaa ggc ttt ggc cag gag ctg ctc gac ggc acc aaa gac ggt aag 403	Val Glu Gly Phe Gly Gln Glu Leu Leu Asp Gly Thr Lys Asp Gly Lys 90 95 100		
aaa ggt cgc ctg aca gaa gat gga cag ctc ttc tac ggc gaa cga ctg 451	Lys Gly Arg Leu Thr Glu Asp Gly Gln Leu Phe Tyr Gly Glu Arg Leu 105 110 115		
atc tct aac ggc agt gtt ctc agt gga cct cgc gct gaa aat gca ttt 499			

Ile	Ser	Asn	Gly	Ser	Val	Leu	Ser	Gly	Pro	Ala	Ala	Glu	Asn	Ala	Phe	
		120						125					130			
gca	gac	gcc	cag	caa	tca	ctg	ctg	gac	cgc	atg	gaa	gcc	tat	ttc	ggc	547
Ala	Asp	Ala	Gln	Gln	Ser	Leu	Leu	Asp	Arg	Met	Glu	Ala	Tyr	Phe	Gly	
	135					140					145					
aac	acc	att	cag	ttc	att	cac	tca	gaa	gca	cgc	ctc	ctg	atc	gat	ggc	595
Asn	Thr	Ile	Gln	Phe	Ile	His	Ser	Glu	Ala	Pro	Leu	Leu	Ile	Asp	Gly	
	150				155				160					165		
ctc	ggc	att	ccc	gat	acc	gga	aat	gcc	att	gaa	ggc	cgc	aaa	gtt	ctc	643
Leu	Gly	Ile	Pro	Asp	Thr	Gly	Asn	Ala	Ile	Glu	Gly	Arg	Lys	Val	Leu	
			170					175						180		
att	gcc	tca	cca	ggg	gat	aac	cac	cgc	agc	agg	ctc	aaa	gaa	ctc	cgc	691
Ile	Ala	Ser	Pro	Gly	Asp	Asn	His	Arg	Ser	Arg	Leu	Lys	Glu	Leu	Arg	
			185					190					195			
agc	ttc	atc	cgc	gaa	tac	gat	cca	gta	ctc	atc	ggc	gtc	gat	ggg	gca	739
Ser	Phe	Ile	Arg	Glu	Tyr	Asp	Pro	Val	Leu	Ile	Gly	Val	Asp	Gly	Ala	
		200					205					210				
gca	gac	acc	ttg	gtg	gaa	ttg	ggg	tac	aag	ccc	cgc	ctg	atc	gtc	ggc	787
Ala	Asp	Thr	Leu	Val	Glu	Leu	Gly	Tyr	Lys	Pro	Ala	Leu	Ile	Val	Gly	
	215					220					225					
aat	ccc	act	ggc	atc	ggc	gca	gat	cgc	ctg	cgc	agt	ggc	gcc	aac	gta	835
Asn	Pro	Thr	Gly	Ile	Gly	Ala	Asp	Ala	Leu	Arg	Ser	Gly	Ala	Asn	Val	
	230				235					240				245		
att	ttg	cca	gct	gat	cca	gac	ggc	cac	gct	gtt	ggc	ctg	gag	cgc	atc	883
Ile	Leu	Pro	Ala	Asp	Pro	Asp	Gly	His	Ala	Val	Gly	Leu	Glu	Arg	Ile	
			250					255						260		
cag	gat	ctt	ggc	atc	ggc	cgc	atg	acc	ttc	cca	tcc	tca	gta	aat	tcc	931
Gln	Asp	Leu	Gly	Ile	Gly	Ala	Met	Thr	Phe	Pro	Ser	Ser	Val	Asn	Ser	
		265						270					275			
tcc	acg	gat	ctg	cgc	ctc	ctg	ctt	cgc	gat	ttc	cac	aac	cgc	cag	atg	979
Ser	Thr	Asp	Leu	Ala	Leu	Leu	Ala	Asp	Phe	His	Asn	Pro	Gln	Met		
		280					285					290				
atc	gtc	aac	gtc	ggc	ggc	oct	gtc	acc	ctt	gat	ggc	gtt	ttt	gaa	aac	1027
Ile	Val	Asn	Val	Gly	Gly	Pro	Val	Thr	Leu	Asp	Gly	Val	Phe	Glu	Asn	
	295					300					305					
cga	gaa	gat	tcc	gat	ccc	cgc	cgc	ctt	ttg	acg	cgc	gcc	aag	cta	ggc	1075
Arg	Glu	Asp	Ser	Asp	Pro	Ala	Ala	Leu	Leu	Thr	Arg	Ala	Lys	Leu	Gly	
	310				315					320				325		
acc	aag	ctt	gtc	gac	gga	tcc	gtc	atc	gca	agt	ctt	tac	aca	gtg	cgc	1123
Thr	Lys	Leu	Val	Asp	Gly	Ser	Val	Ile	Ala	Ser	Leu	Tyr	Thr	Val	Arg	
			330						335					340		
agc	tcc	agc	aac	ctt	gga	tgg	atg	tgg	gca	ctg	tta	gcc	att	ttg	gtg	1171
Ser	Ser	Ser	Asn	Leu	Gly	Trp	Met	Trp	Ala	Leu	Leu	Ala	Ile	Leu	Val	
			345					350					355			
gtt	ctt	gca	gtc	gtg	att	gtt	atc	gct	ggc	acc	gca	gga	tca	ggc	tct	1219
Val	Leu	Ala	Val	Val	Ile	Val	Ile	Ala	Gly	Thr	Ala	Gly	Ser	Gly	Ser	

360

365

370

ttt acc gac aac ctc att gac acc tgg aac agc ttc gcg ctg aca gtg 1267
 Phe Thr Asp Asn Leu Ile Asp Thr Trp Asn Ser Phe Ala Leu Thr Val
 375 380 385

cag ggt tgg ttc aaa taggaaggca acatggcctaa acg 1305
 Gln Gly Trp Phe Lys
 390

<210> 688

<211> 394

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 688

Met Ser Leu Phe Asn Arg Lys Ala Asp Leu Pro Gly Leu Gln Gly Ala
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Thr Arg Ile Cys Thr Pro Gln Gly Lys Gly Leu Lys Arg Leu Ser Glu
 20 25 30

Gly Asp Leu Ala Ile Ile Asp Ala Pro Asp Leu Ser Arg Thr Phe Ala
 35 40 45

Gln Arg Leu Leu Ala Ala Lys Pro Ala Ala Val Leu Asn Val Ser Arg
 50 55 60

Phe Thr Thr Gly Ser Val Pro Asn Phe Gly Pro Gln Met Leu Ile Asp
 65 70 75 80

Gly Gly Ile Gln Leu Val Glu Gly Phe Gly Gln Glu Leu Leu Asp Gly
 85 90 95

Thr Lys Asp Gly Lys Lys Gly Arg Leu Thr Glu Asp Gly Gln Leu Phe
 100 105 110

Tyr Gly Glu Arg Leu Ile Ser Asn Gly Ser Val Leu Ser Gly Pro Ala
 115 120 125

Ala Glu Asn Ala Phe Ala Asp Ala Gln Gln Ser Leu Leu Asp Arg Met
 130 135 140

Glu Ala Tyr Phe Gly Asn Thr Ile Gln Phe Ile His Ser Glu Ala Pro
 145 150 155 160

Leu Leu Ile Asp Gly Leu Gly Ile Pro Asp Thr Gly Asn Ala Ile Glu
 165 170 175

Gly Arg Lys Val Leu Ile Ala Ser Pro Gly Asp Asn His Arg Ser Arg
 180 185 190

Leu Lys Glu Leu Arg Ser Phe Ile Arg Glu Tyr Asp Pro Val Leu Ile
 195 200 205

Gly Val Asp Gly Ala Ala Asp Thr Leu Val Glu Leu Gly Tyr Lys Pro
 210 215 220

Ala Leu Ile Val Gly Asn Pro Thr Gly Ile Gly Ala Asp Ala Leu Arg
 225 230 235 240

Ser Gly Ala Asn Val Ile Leu Pro Ala Asp Pro Asp Gly His Ala Val
245 250 255

Gly Leu Glu Arg Ile Gln Asp Leu Gly Ile Gly Ala Met Thr Phe Pro
260 265 270

Ser Ser Val Asn Ser Ser Thr Asp Leu Ala Leu Leu Ala Asp Phe
275 280 285

His Asn Pro Gln Met Ile Val Asn Val Gly Gly Pro Val Thr Leu Asp
290 295 300

Gly Val Phe Glu Asn Arg Glu Asp Ser Asp Pro Ala Ala Leu Leu Thr
305 310 315 320

Arg Ala Lys Leu Gly Thr Lys Leu Val Asp Gly Ser Val Ile Ala Ser
325 330 335

Leu Tyr Thr Val Arg Ser Ser Ser Asn Leu Gly Trp Met Trp Ala Leu
340 345 350

Leu Ala Ile Leu Val Val Leu Ala Val Val Ile Val Ile Ala Gly Thr
355 360 365

Ala Gly Ser Gly Ser Phe Thr Asp Asn Leu Ile Asp Thr Trp Asn Ser
370 375 380

Phe Ala Leu Thr Val Gln Gly Trp Phe Lys
385 390

<210> 689

<211> 1086

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1063)

<223> RXN01598

<400> 689

cgctggcacc gcaggatcag gctctttttac cgacaacctc attgacacct ggaacagctt 60

cgcgctgaca gtgcagggtt ggttcaaata ggaaggcaac atg gct aaa cga cgt 115
Met Ala Lys Arg Arg
1 5

gga aga ggc gcc gca acc ttc gcc gca ctg gga ttt ggt gca gca gcc 163
Gly Arg Gly Ala Ala Thr Phe Ala Ala Leu Gly Phe Gly Ala Ala Ala
10 15 20

ggc att gcc ttt gga act tat gtg ctt gca ccc aac ctt cct gaa aac 211
Gly Ile Ala Phe Gly Thr Tyr Val Leu Ala Pro Asn Leu Pro Glu Asn
25 30 35

att gac cca aat gca cca aca tca gct gaa tta gtc gag gca gag acc 259
Ile Asp Pro Asn Ala Pro Thr Ser Ala Glu Leu Val Glu Ala Glu Thr
40 45 50

CGCGCTGACA GTGCAGGTT GGTTCAAATA GGAAGGCAAC ATG GCT AAA CGA CGT 115
Met Ala Lys Arg Arg 5

ttg gct gag gtt aat gcg gtg cag gcc gat caa gca gac agc atc att 307
 Leu Ala Glu Val Asn Ala Val Gln Ala Asp Gln Ala Asp Ser Ile Ile
 55 60 65

gac cac atc gtg gaa gac gtg gtg gct ggc aca ctg acc gat cgc ccc 355
 Asp His Ile Val Glu Asp Val Val Ala Gly Thr Leu Thr Asp Arg Pro 85
 70 75 80

gta ctg gtg atg cgc acc gct gac gct gaa gaa tca gac gtt gcc gat 403
 Val Leu Val Met Arg Thr Ala Asp Ala Glu Ser Asp Val Ala Asp
 90 95 100

gtg tca tgg ctg ttg cag caa gca gga gct att aat gct gga tcc att 451
 Val Ser Trp Leu Leu Gln Gln Ala Gly Ala Ile Asn Ala Gly Ser Ile
 105 110 115

aca ctt gag gag aat ttc ttc tcc caa gac ggc gcg gac cag ctg aaa 499
 Thr Leu Glu Glu Asn Phe Phe Ser Gln Asp Gly Ala Asp Gln Leu Lys
 120 125 130

tca atc gtg gca aat acg ttg cct gca ggc gct cag ctt tct gaa acc 547
 Ser Ile Val Ala Asn Thr Leu Pro Ala Gly Ala Gln Leu Ser Glu Thr
 135 140 145

caa ctg gat cca gga act cac gct ggc gag gca ctt ggt gcc gct ttg 595
 Gln Leu Asp Pro Gly Thr His Ala Gly Glu Ala Leu Gly Ala Ala Leu
 150 155 160 165

ctg ctc aac cct gaa act ggt gaa cca cta gcc agc act gca gag cgc 643
 Leu Leu Asn Pro Glu Thr Gly Glu Pro Leu Ala Ser Thr Ala Glu Arg
 170 175 180

gga cta ttg ctc aac gtg ctg cgc gac aac ggt tac atc tcg tac gaa 691
 Gly Leu Leu Leu Asn Val Leu Arg Asp Asn Gly Tyr Ile Ser Tyr Glu
 185 190 195

gac ggc acc att ttg cca ggc cag gtc atc gtg atg att act ggc gat 739
 Asp Gly Thr Ile Leu Pro Gly Gln Val Ile Val Met Ile Thr Gly Asp
 200 205 210

agc gac ggc tca ggt gat ggt gcc ttc gct gca gaa aca caa tcg ctg 787
 Ser Asp Gly Ser Gly Asp Gly Ala Phe Ala Ala Glu Thr Gln Ser Leu
 215 220 225

ttt gct cgc gca ctt gac gcc caa gga tca ggc gtg gtg gtt gca gga 835
 Phe Ala Arg Ala Leu Asp Ala Gln Gly Ser Gly Val Val Val Ala Gly
 230 235 240 245

cgt att cac act got gct gat act gga gtt att gga cgg ctt cgt gcc 883
 Arg Ile His Thr Ala Ala Asp Thr Gly Val Ile Gly Arg Leu Arg Ala
 250 255 260

aac cct gat gct gca gaa aac gtc tct aca att gat tcc gtg aat cgt 931
 Asn Pro Asp Ala Ala Glu Asn Val Ser Thr Ile Asp Ser Val Asn Arg
 265 270 275

act tgg ggc aag atg gct acc gtg cta tca gtt cgt gag gaa cta gcc 979
 Thr Trp Gly Lys Met Ala Thr Val Leu Ser Val Arg Glu Glu Leu Ala
 280 285 290

ggt agg tct gga gcg ttt ggt tcc gct gcc tcc gca gac gcg gca agt 1027

Gly Arg Ser Gly Ala Phe Gly Ser Ala Ala Ser Ala Asp Ala Ala Ser
 295 300 305

ccg tct ctc gat gga act gca gca gcg cca gcg cag taggttttcc 1073
 Pro Ser Leu Asp Gly Thr Ala Ala Ala Pro Ala Gln
 310 315 320

aagcctttaa aac 1086

<210> 690

<211> 321

<212> PRT

<213> Corynebacterium glutamicum

<400> 690

Met Ala Lys Arg Arg Gly Arg Gly Ala Ala Thr Phe Ala Ala Leu Gly
 1 5 10 15

Phe Gly Ala Ala Ala Gly Ile Ala Phe Gly Thr Tyr Val Leu Ala Pro
 20 25 30

Asn Leu Pro Glu Asn Ile Asp Pro Asn Ala Pro Thr Ser Ala Glu Leu
 35 40 45

Val Glu Ala Glu Thr Leu Ala Glu Val Asn Ala Val Gln Ala Asp Gln
 50 55 60

Ala Asp Ser Ile Ile Asp His Ile Val Glu Asp Val Val Ala Gly Thr
 65 70 75 80

Leu Thr Asp Arg Pro Val Leu Val Met Arg Thr Ala Asp Ala Glu Glu
 85 90 95

Ser Asp Val Ala Asp Val Ser Trp Leu Leu Gln Gln Ala Gly Ala Ile
 100 105 110

Asn Ala Gly Ser Ile Thr Leu Glu Glu Asn Phe Phe Ser Gln Asp Gly
 115 120 125

Ala Asp Gln Leu Lys Ser Ile Val Ala Asn Thr Leu Pro Ala Gly Ala
 130 135 140

Gln Leu Ser Glu Thr Gln Leu Asp Pro Gly Thr His Ala Gly Glu Ala
 145 150 155 160

Leu Gly Ala Ala Leu Leu Leu Asn Pro Glu Thr Gly Glu Pro Leu Ala
 165 170 175

Ser Thr Ala Glu Arg Gly Leu Leu Leu Asn Val Leu Arg Asp Asn Gly
 180 185 190

Tyr Ile Ser Tyr Glu Asp Gly Thr Ile Leu Pro Gly Gln Val Ile Val
 195 200 205

Met Ile Thr Gly Asp Ser Asp Gly Ser Gly Asp Gly Ala Phe Ala Ala
 210 215 220

Glu Thr Gln Ser Leu Phe Ala Arg Ala Leu Asp Ala Gln Gly Ser Gly
 225 230 235 240

Val Val Val Ala Gly Arg Ile His Thr Ala Ala Asp Thr Gly Val Ile
 245 250 255

Gly Arg Leu Arg Ala Asn Pro Asp Ala Ala Glu Asn Val Ser Thr Ile
 260 265 270

Asp Ser Val Asn Arg Thr Trp Gly Lys Met Ala Thr Val Leu Ser Val
 275 280 285

Arg Glu Glu Leu Ala Gly Arg Ser Gly Ala Phe Gly Ser Ala Ala Ser
 290 295 300

Ala Asp Ala Ala Ser Pro Ser Leu Asp Gly Thr Ala Ala Ala Pro Ala
 305 310 315 320

Gln

<210> 691
 <211> 1086
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1063)
 <223> FRXA01598

<400> 691
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cgcgctgaca gtgcagggtt ggttcaaata ggaaggcaac atg gct aaa cga cgt 115
 Met Ala Lys Arg Arg
 1 5

gga aga ggc gcc gca acc ttc gcc gca ctg gga ttt ggt gca gca gcc 163
 Gly Arg Gly Ala Ala Thr Phe Ala Ala Leu Gly Phe Gly Ala Ala Ala
 10 15 20

ggc att gcc ttt gga act tat gtg ctt gca ccc aac ctt cct gaa aac 211
 Gly Ile Ala Phe Gly Thr Tyr Val Leu Ala Pro Asn Leu Pro Glu Asn
 25 30 35

att gac cca aat gca cca aca tca gct gaa tta gtc gag gca gag acc 259
 Ile Asp Pro Asn Ala Pro Thr Ser Ala Glu Leu Val Glu Ala Glu Thr
 40 45 50

ttg gct gag gtt aat gcg gtg cag gcc gat caa gca gac agc atc att 307
 Leu Ala Glu Val Asn Ala Val Gln Ala Asp Gln Ala Asp Ser Ile Ile
 55 60 65

gac cac atc gtg gaa gac gtg gtg gct ggc aca ctg acc gat cgc ccc 355
 Asp His Ile Val Glu Asp Val Val Ala Gly Thr Leu Thr Asp Arg Pro
 70 75 80 85

gta ctg gtg atg cgc acc gct gac gct gaa gaa tca gac gtt gcc gat 403
 Val Leu Val Met Arg Thr Ala Asp Ala Glu Glu Ser Asp Val Ala Asp
 90 95 100

gtg tca tgg ctg ttg cag caa gca gga gct att aat gct gga tcc att 451

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Val Ser Trp Leu Leu Gln Gln Ala Gly Ala Ile Asn Ala Gly Ser Ile
      105      110      115

aca ctt gag gag aat ttc ttc tcc caa gac ggc gcg gac cag ctg aaa 499
Thr Leu Glu Glu Asn Phe Phe Ser Gln Asp Gly Ala Asp Gln Leu Lys
      120      125      130

tca atc gtg gca aat acg ttg cct gca ggc gct cag ctt tct gaa acc 547
Ser Ile Val Ala Asn Thr Leu Pro Ala Gly Ala Gln Leu Ser Glu Thr
      135      140      145

caa ctg gat cca gga act cac gct ggc gag gca ctt ggt gcc gct ttg 595
Gln Leu Asp Pro Gly Thr His Ala Gly Glu Ala Leu Ala Leu
      150      155      160      165

ctg ctc aac cct gaa act ggt gaa cca cta gcc agc act gca gag cgc 643
Leu Leu Asn Pro Gln Thr Gly Glu Pro Leu Ala Ser Thr Ala Glu Arg
      170      175      180

gga cta ttg ctc aac gtg ctg cgc gac aac ggt tac atc tcg tac gaa 691
Gly Leu Leu Leu Asn Val Leu Arg Asp Asn Gly Tyr Ile Ser Tyr Glu
      185      190      195

gac ggc acc att ttg cca ggc cag gtc atc gtg atg att act ggc gat 739
Asp Gly Thr Ile Leu Pro Gly Gln Val Ile Val Met Ile Thr Gly Asp
      200      205      210

agc gac ggc tca ggt gat ggt gcc ttc gct gca gaa aca caa tcg ctg 787
Ser Asp Gly Ser Gly Asp Gly Ala Phe Ala Ala Glu Thr Gln Ser Leu
      215      220      225

ttt gct cgc gca ctt gac gcc caa gga tca ggc gtg gtg gtt gca gga 835
Phe Ala Arg Ala Leu Asp Ala Gln Gly Ser Gly Val Val Val Ala Gly
      230      235      240      245

cgt att cac act gct gct gat act gga gtt att gga cgg ctt cgt gcc 883
Arg Ile His Thr Ala Ala Asp Thr Gly Val Ile Gly Arg Leu Arg Ala
      250      255      260

aac cct gat gct gca gaa aac gtc tct aca att gat tcc gtg aat cgt 931
Asn Pro Asp Ala Ala Glu Asn Val Ser Thr Ile Asp Ser Val Asn Arg
      265      270      275

act tgg ggc aag atg gct acc gtg cta tca gtt cgt gag gaa cta gcc 979
Thr Trp Gly Lys Met Ala Thr Val Leu Ser Val Arg Glu Glu Leu Ala
      280      285      290

ggt agg tct gga gcg ttt ggt tcc gct gcc tcc gca gac gcg gca agt 1027
Gly Arg Ser Gly Ala Phe Gly Ser Ala Ala Ser Ala Asp Ala Ala Ser
      295      300      305

ccg tct ctc gat gga act gca gca gcg cca gcg cag taggttttcc 1073
Pro Ser Leu Asp Gly Thr Ala Ala Ala Pro Ala Gln
      310      315      320

aagcctttaa aac 1086

<210> 692
<211> 321
<212> PRT

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<213> *Corynebacterium glutamicum*

<400> 692

Met Ala Lys Arg Arg Gly Arg Gly Ala Ala Thr Phe Ala Ala Leu Gly
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Phe Gly Ala Ala Ala Gly Ile Ala Phe Gly Thr Tyr Val Leu Ala Pro
 20 25 30

Asn Leu Pro Glu Asn Ile Asp Pro Asn Ala Pro Thr Ser Ala Glu Leu
 35 40 45

Val Glu Ala Glu Thr Leu Ala Glu Val Asn Ala Val Gln Ala Asp Gln
 50 55 60

Ala Asp Ser Ile Ile Asp His Ile Val Glu Asp Val Val Ala Gly Thr
 65 70 75 80

Leu Thr Asp Arg Pro Val Leu Val Met Arg Thr Ala Asp Ala Glu Glu
 85 90 95

Ser Asp Val Ala Asp Val Ser Trp Leu Leu Gln Gln Ala Gly Ala Ile
 100 105 110

Asn Ala Gly Ser Ile Thr Leu Glu Glu Asn Phe Phe Ser Gln Asp Gly
 115 120 125

Ala Asp Gln Leu Lys Ser Ile Val Ala Asn Thr Leu Pro Ala Gly Ala
 130 135 140

Gln Leu Ser Glu Thr Gln Leu Asp Pro Gly Thr His Ala Gly Glu Ala
 145 150 155 160

Leu Gly Ala Ala Leu Leu Leu Asn Pro Glu Thr Gly Glu Pro Leu Ala
 165 170 175

Ser Thr Ala Glu Arg Gly Leu Leu Leu Asn Val Leu Arg Asp Asn Gly
 180 185 190

Tyr Ile Ser Tyr Glu Asp Gly Thr Ile Leu Pro Gly Gln Val Ile Val
 195 200 205

Met Ile Thr Gly Asp Ser Asp Gly Ser Gly Asp Gly Ala Phe Ala Ala
 210 215 220

Glu Thr Gln Ser Leu Phe Ala Arg Ala Leu Asp Ala Gln Gly Ser Gly
 225 230 235 240

Val Val Val Ala Gly Arg Ile His Thr Ala Ala Asp Thr Gly Val Ile
 245 250 255

Gly Arg Leu Arg Ala Asn Pro Asp Ala Ala Glu Asn Val Ser Thr Ile
 260 265 270

Asp Ser Val Asn Arg Thr Trp Gly Lys Met Ala Thr Val Leu Ser Val
 275 280 285

Arg Glu Glu Leu Ala Gly Arg Ser Gly Ala Phe Gly Ser Ala Ala Ser
 290 295 300

Ala Asp Ala Ala Ser Pro Ser Leu Asp Gly Thr Ala Ala Ala Pro Ala

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305                               310                               315                               320

Gln

<210> 693
<211> 507
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(484)
<223> RXN01618

<400> 693
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gtttaaggcc cattagaccc ctgatttaaa aggatctcac atg atc att atc gga 115
Met Ile Ile Ile Gly
1 5

gca gtt ttc gcc atc ctc gca gtt cta ctg cat gtt ttc atc ttc tac 163
Ala Val Phe Ala Ile Leu Ala Val Leu Leu His Val Phe Ile Phe Tyr
10 15 20

atg gaa tca ttc gca tgg act agt gag aaa gca cgt gga gtt ttc gcc 211
Met Glu Ser Phe Ala Trp Thr Ser Glu Lys Ala Arg Gly Val Phe Gly
25 30 35

acc acc gaa atc gac gcc gaa aac acc aag gag atg gcc tac aac caa 259
Thr Thr Glu Ile Asp Ala Glu Asn Thr Lys Glu Met Ala Tyr Asn Gln
40 45 50

ggc ttc tac aac ttc ttc ctg gca gtc atc gcc ggc gtg ggt gtt gcg 307
Gly Phe Tyr Asn Phe Phe Leu Ala Val Ile Ala Gly Val Gly Val Ala
55 60 65

ttc ctc ttc gct ggt tca act ggc atc ggc gca gcc ctc gca ctc gct 355
Phe Leu Phe Ala Gly Ser Thr Gly Ile Gly Ala Ala Leu Ala Leu Ala
70 75 80 85

ggc acc ggt tcc atg ctg gca gcc gct gca gtg ttg gct ttg agc tca 403
Gly Thr Gly Ser Met Leu Ala Ala Ala Ala Val Leu Ala Leu Ser Ser
90 95 100

ccc gac aag cgt ggt gca gcc ttc aag caa ggc acg ttc cgc ctg ctc 451
Pro Asp Lys Arg Gly Ala Ala Phe Lys Gln Gly Thr Phe Pro Leu Leu
105 110 115

gca gtg gtg ttc ctt gtg att gga ttg ctg gtt taagcagttt tttaaaggaa 504
Ala Val Val Phe Leu Val Ile Gly Leu Leu Val
120 125

ctt 507

<210> 694
<211> 128
<212> PRT

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<213> *Corynebacterium glutamicum*

<400> 694

Met Ile Ile Ile Gly Ala Val Phe Ala Ile Leu Ala Val Leu Leu His
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Val Phe Ile Phe Tyr Met Glu Ser Phe Ala Trp Thr Ser Glu Lys Ala
 20 25 30

Arg Gly Val Phe Gly Thr Thr Glu Ile Asp Ala Glu Asn Thr Lys Glu
 35 40 45

Met Ala Tyr Asn Gln Gly Phe Tyr Asn Phe Phe Leu Ala Val Ile Ala
 50 55 60

Gly Val Gly Val Ala Phe Leu Phe Ala Gly Ser Thr Gly Ile Gly Ala
 65 70 75 80

Ala Leu Ala Leu Ala Gly Thr Gly Ser Met Leu Ala Ala Ala Val
 85 90 95

Leu Ala Leu Ser Ser Pro Asp Lys Arg Gly Ala Ala Phe Lys Gln Gly
 100 105 110

Thr Phe Pro Leu Leu Ala Val Val Phe Leu Val Ile Gly Leu Leu Val
 115 120 125

<210> 695

<211> 507

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(484)

<223> FRXA01618

<400> 695

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gtttaaggcc cattagaccc ctgatttaaa aggatctcac atg atc att atc gga 115
 Met Ile Ile Ile Gly
 1 5

gca gtt ttc gcc atc ctc gca gtt cta ctg cat gtt ttc atc ttc tac 163
 Ala Val Phe Ala Ile Leu Ala Val Leu Leu His Val Phe Ile Phe Tyr
 10 15 20

atg gaa tca ttc gca tgg act agt gag aaa gca cgt gga gtt ttc ggc 211
 Met Glu Ser Phe Ala Trp Thr Ser Glu Lys Ala Arg Gly Val Phe Gly
 25 30 35

acc acc gaa atc gac gcc gaa aac acc aag gag atg gcc tac aac caa 259
 Thr Thr Glu Ile Asp Ala Glu Asn Thr Lys Glu Met Ala Tyr Asn Gln
 40 45 50

ggc ttc tac aac ttc ttc ctg gca gtc atc gcc gcc gtg ggt gtt ggc 307


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Gly Phe Tyr Asn Phe Phe Leu Ala Val Ile Ala Gly Val Gly Val Ala
 55                                60                                65

ttc ctc ttc gct ggt tca act ggc atc ggc gca gcc ctc gca ctc gct 355
Phe Leu Phe Ala Gly Ser Thr Gly Ile Gly Ala Ala Leu Ala Leu Ala
 70                                75                                80                                85

ggc acc ggt tcc atg ctg gca gcc gct gca gtg ttg gct ttg agc tca 403
Gly Thr Gly Ser Met Leu Ala Ala Ala Val Leu Ala Leu Ser Ser
 90                                95                                100

ccc gac aag cgt ggt gca gcc ttc aag caa ggc acg ttc ccg ctg ctc 451
Pro Asp Lys Arg Gly Ala Ala Phe Lys Gln Gly Thr Phe Pro Leu Leu
105                                110                                115

gca gtg gtg ttc ctt gtg att gga ttg ctg gtt taagcagttt tttaaaggaa 504
Ala Val Val Phe Leu Val Ile Gly Leu Leu Val
120                                125

ctt 507

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<210> 696
<211> 128
<212> PRT
<213> Corynebacterium glutamicum

<400> 696
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Val Phe Ile Phe Tyr Met Glu Ser Phe Ala Trp Thr Ser Glu Lys Ala
 20                                25                                30

Arg Gly Val Phe Gly Thr Thr Glu Ile Asp Ala Glu Asn Thr Lys Glu
 35                                40                                45

Met Ala Tyr Asn Gln Gly Phe Tyr Asn Phe Phe Leu Ala Val Ile Ala
 50                                55                                60

Gly Val Gly Val Ala Phe Leu Phe Ala Gly Ser Thr Gly Ile Gly Ala
 65                                70                                75                                80

Ala Leu Ala Leu Ala Gly Thr Gly Ser Met Leu Ala Ala Ala Ala Val
 85                                90                                95

Leu Ala Leu Ser Ser Pro Asp Lys Arg Gly Ala Ala Phe Lys Gln Gly
100                                105                                110

Thr Phe Pro Leu Leu Ala Val Val Phe Leu Val Ile Gly Leu Leu Val
115                                120                                125

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<210> 697
<211> 675
<212> DNA
<213> Corynebacterium glutamicum

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<220>

<221> CDS

<222> (101)..(652)

<223> RXN01634

<400> 697

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aacggcgacc acaacggcgc ttgccctcgg tggcacgcac atg gca gtt ggt caa 115
                                     Met Ala Val Gly Gln
                                     1 5

gaa act gat ctg ctc aac gct atg gaa aca ctc gct ggg gtt ccc tca 163
Glu Thr Asp Leu Leu Asn Ala Met Glu Thr Leu Ala Gly Val Pro Ser
          10          15          20

gac ttg gtg gtc act gaa atc ctc ccc gat acc acc agc tat gac aat 211
Asp Leu Val Val Thr Glu Ile Leu Pro Asp Thr Thr Ser Tyr Asp Asn
          25          30          35

ttt gaa ttc ttt gaa gtt cac aac acc ggc agt gca ccc gtg acc att 259
Phe Glu Phe Phe Glu Val His Asn Thr Gly Ser Ala Pro Val Thr Ile
          40          45          50

ggg gaa ggg gag tac acc ttc gcc tat tcc ttt gac gat tcc gcc gat 307
Gly Glu Gly Glu Tyr Thr Phe Ala Tyr Ser Phe Asp Ser Ala Asp
          55          60          65

acg tcc cgc gac aag gca ctg gat ctt ggc ggg gaa gtc acg gta gat 355
Thr Ser Ser Arg Asp Lys Ala Leu Asp Leu Gly Gly Glu Val Thr Val Asp
          70          75          80          85

gca ggc gaa acc att gtg gtg tgg att gag tac tcc agt tca act gtt 403
Ala Gly Glu Thr Ile Val Val Trp Ile Glu Tyr Ser Ser Ser Thr Val
          90          95          100

gat acc gct gcg ttt agt gag caa gac ttc cgt gat ttc tac gcc atg 451
Asp Thr Ala Ala Phe Ser Glu Gln Asp Phe Arg Asp Phe Tyr Gly Met
          105          110          115

gat tcc tca gcc cgc atc ttc cga gca act ggc cag gcg ggt ctc gct 499
Asp Ser Ser Ala Arg Ile Phe Arg Ala Thr Gly Gln Ala Gly Leu Ala
          120          125          130

aac ggt ggt gat cgt ggc atc cga gtt ctg tac aat ggt gaa gtt tct 547
Asn Gly Gly Asp Arg Gly Ile Arg Val Leu Tyr Asn Gly Glu Val Ser
          135          140          145

ggt tgg tcc cac tac cca tca gat agc gca gcg gtt caa aag gga att 595
Gly Trp Ser His Tyr Pro Ser Asp Ser Ala Ala Val Gln Lys Gly Ile
          150          155          160          165

gac ttc gcg ctg cca aaa gta ggg gag cag gcc agc att gca agt gcg 643
Asp Phe Ala Leu Pro Lys Val Gly Glu Gln Ala Ser Ile Ala Ser Ala
          170          175          180

cac caa aac tgatccaact ccaggatcaa tta 675
His Gln Asn

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<210> 698
 <211> 184
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 698
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 20 25 30
 Thr Ser Tyr Asp Asn Phe Glu Phe Phe Glu Val His Asn Thr Gly Ser
 35 40 45
 Ala Pro Val Thr Ile Gly Glu Gly Glu Tyr Thr Phe Ala Tyr Ser Phe
 50 55 60
 Asp Asp Ser Ala Asp Thr Ser Arg Asp Lys Ala Leu Asp Leu Gly Gly
 65 70 75 80
 Glu Val Thr Val Asp Ala Gly Glu Thr Ile Val Val Trp Ile Glu Tyr
 85 90 95
 Ser Ser Ser Thr Val Asp Thr Ala Ala Phe Ser Glu Gln Asp Phe Arg
 100 105 110
 Asp Phe Tyr Gly Met Asp Ser Ser Ala Arg Ile Phe Arg Ala Thr Gly
 115 120 125
 Gln Ala Gly Leu Ala Asn Gly Gly Asp Arg Gly Ile Arg Val Leu Tyr
 130 135 140
 Asn Gly Glu Val Ser Gly Trp Ser His Tyr Pro Ser Asp Ser Ala Ala
 145 150 155 160
 Val Gln Lys Gly Ile Asp Phe Ala Leu Pro Lys Val Gly Glu Gln Ala
 165 170 175
 Ser Ile Ala Ser Ala His Gln Asn
 180

<210> 699
 <211> 675
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(652)
 <223> FRXA01634

<400> 699
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 aacggcgacc acaacggcgc ttgccctcgg tggcacgcac atg gca gtt ggt caa 115
 Met Ala Val Gly Gln
 1 5
 gaa act gat ctg ctc aac gct atg gaa aca ctc gct ggg gtt ccc tca 163

Glu Thr Asp Leu Leu Asn Ala Met Glu Thr Leu Ala Gly Val Pro Ser
 10 15 20
 gac ttg gtc gtc act gaa atc ctc ccc gat acc acc agc tat gac aat 211
 Asp Leu Val Val Thr Glu Ile Leu Pro Asp Thr Thr Ser Tyr Asp Asn
 25 30 35
 ttt gaa ttc ttt gaa gtt cac aac acc ggc agt gca ccc gtg acc att 259
 Phe Glu Phe Phe Glu Val His Asn Thr Gly Ser Ala Pro Val Thr Ile
 40 45 50
 ggg gaa ggg gag tac acc ttc gcc tat tcc ttt gac gat tcc gcc gat 307
 Gly Glu Gly Glu Tyr Thr Phe Ala Tyr Ser Phe Asp Asp Ser Ala Asp
 55 60 65
 acg tcc cgc gac aag gca ctg gat ctt ggc ggg gaa gtc acg gta gat 355
 Thr Ser Arg Asp Lys Ala Leu Asp Leu Gly Gly Glu Val Thr Val Asp
 70 75 80 85
 gca ggc gaa acc att gtg gtg tgg att gag tac tcc agt tca act gtt 403
 Ala Gly Glu Thr Ile Val Val Trp Ile Glu Tyr Ser Ser Ser Thr Val
 90 95 100
 gat acc gct gcg ttt agt gag caa gac ttc cgt gat ttc tac ggc atg 451
 Asp Thr Ala Ala Phe Ser Glu Gln Asp Phe Arg Asp Phe Tyr Gly Met
 105 110 115
 gat tcc tca gcc cgc atc ttc cga gca act ggc cag gcg ggt ctc gct 499
 Asp Ser Ser Ala Arg Ile Phe Arg Ala Thr Gly Gln Ala Gly Leu Ala
 120 125 130
 aac ggt ggt gat cgt ggc atc cga gtt ctg tac aat ggt gaa gtt tct 547
 Asn Gly Gly Asp Arg Gly Ile Arg Val Leu Tyr Asn Gly Glu Val Ser
 135 140 145
 ggt tgg tcc cac tac cca tca gat agc gca gcg gtt caa aag gga att 595
 Gly Trp Ser His Tyr Pro Ser Asp Ser Ala Ala Val Gln Lys Gly Ile
 150 155 160 165
 gac ttc gcg ctg cca aaa gta ggg gag cag gcc agc att gca agt gcg 643
 Asp Phe Ala Leu Pro Lys Val Gly Glu Gln Ala Ser Ile Ala Ser Ala
 170 175 180
 cac caa aac tgatccaact ccaggatcaa tta 675
 His Gln Asn

<210> 700

<211> 184

<212> PRT

<213> Corynebacterium glutamicum

<400> 700

Met Ala Val Gly Gln Glu Thr Asp Leu Leu Asn Ala Met Glu Thr Leu
 1 5 10 15

Ala Gly Val Pro Ser Asp Leu Val Val Thr Glu Ile Leu Pro Asp Thr
 20 25 30

Thr Ser Tyr Asp Asn Phe Glu Phe Phe Glu Val His Asn Thr Gly Ser

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35              40              45
Ala Pro Val Thr Ile Gly Glu Gly Glu Tyr Thr Phe Ala Tyr Ser Phe
50              55              60

Asp Asp Ser Ala Asp Thr Ser Arg Asp Lys Ala Leu Asp Leu Gly Gly
65              70              75              80

Glu Val Thr Val Asp Ala Gly Glu Thr Ile Val Val Trp Ile Glu Tyr
85              90              95

Ser Ser Ser Thr Val Asp Thr Ala Ala Phe Ser Glu Gln Asp Phe Arg
100             105             110

Asp Phe Tyr Gly Met Asp Ser Ser Ala Arg Ile Phe Arg Ala Thr Gly
115             120             125

Gln Ala Gly Leu Ala Asn Gly Gly Asp Arg Gly Ile Arg Val Leu Tyr
130             135             140

Asn Gly Glu Val Ser Gly Trp Ser His Tyr Pro Ser Asp Ser Ala Ala
145             150             155             160

Val Gln Lys Gly Ile Asp Phe Ala Leu Pro Lys Val Gly Glu Gln Ala
165             170             175

Ser Ile Ala Ser Ala His Gln Asn
180

<210> 701
<211> 864
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(841)
<223> RXN01635

<400> 701
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aaaactgatc caactccagg atcaattact tctgatcaag ttg att cct ggc gga 115
Leu Ile Pro Gly Gly
1 5

ttg gac act cca gaa gag cct gaa gcc cct gaa gac tct ctt ttt gaa 163
Leu Asp Thr Pro Glu Glu Pro Glu Ala Pro Glu Asp Ser Leu Phe Glu
10 15 20

ggg cgc act ccc cct agg gat gca agc acc cgc ttg atc ctc act gaa 211
Gly Arg Thr Pro Pro Arg Asp Ala Ser Thr Arg Leu Ile Leu Thr Glu
25 30 35

cta atg gtc aac tcc acc aac atg ggc agt tct gat ggt ttt gag tat 259
Leu Met Val Asn Ser Thr Asn Met Gly Ser Ser Asp Gly Phe Glu Tyr
40 45 50

gtg gaa atc acc aac act act gcc gaa ccc atc gat ttt tcc gat tac 307
Val Glu Ile Thr Asn Thr Thr Ala Glu Pro Ile Asp Phe Ser Asp Tyr

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55	60	65	
acc ttg aac tac ctg tac ccg cag gat gag ttc acc aac acc aac gaa			355
Thr Leu Asn Tyr Leu Tyr	Pro Gln Asp Glu Phe	Thr Asn Thr Asn Glu	
70	75	80	85
gcc gtc tgg gct gcg gaa cct ggt gat gtc att att cag cct gga aaa			403
Ala Val Trp Ala Ala Glu	Pro Gly Asp Val Ile	Gln Pro Gly Lys	
	90	95	100
tct ctg gtg ttt tgg atc aaa aat ggc ccc aat gat gag gca acc gca			451
Ser Leu Val Phe Trp Ile	Lys Asn Gly Pro Asn Asp	Glu Ala Thr Ala	
	105	110	115
gca gat ttc aat gca gaa tat ggc acc aac ctg gag gct gga aaa gac			499
Ala Asp Phe Asn Ala Glu Tyr	Gly Thr Asn Leu Glu	Ala Gly Lys Asp	
	120	125	130
ctt gtt gaa atc tcc tca ggt ggg atg gcc aat ggt act gcc aga gga			547
Leu Val Glu Ile Ser Ser	Gly Gly Met Ala Asn Gly Thr	Ala Arg Gly	
	135	140	145
atg cag att cag acc aac act ggc cac ata gtc aac cgt ggt ttc tac			595
Met Gln Ile Gln Thr Asn Thr	Gly His Ile Val Asn Arg	Gly Phe Tyr	
	150	155	160
aac atg gct ggc gct tct gat gtg aaa gcc aac gag ggt ctt cat ttc			643
Asn Met Ala Gly Ala Ser	Asp Val Lys Ala Asn Glu	Gly Leu His Phe	
	170	175	180
gca gtg gat gag tct gat ctt ctg aag caa acg ctt gtc ggc agc ggt			691
Ala Val Asp Glu Ser Asp	Leu Leu Lys Gln Thr	Leu Val Gly Ser Gly	
	185	190	195
gcg cca acc ccg ggc act gtg tac act tcg cag att cct aat coa ctg			739
Ala Pro Thr Pro Gly Thr Val Tyr Thr	Ser Gln Ile Pro Asn	Pro Leu	
	200	205	210
tct gcc gtt atc gct gat tct tct gta cca ctc atc aca gat aat acc			787
Ser Ala Val Ile Ala Asp	Ser Ser Val Pro Leu Ile	Thr Asp Asn Thr	
	215	220	225
gca acc agt atc aac cct gcg gag ccg ttt acc ttc gcc ttc aaa tat			835
Ala Thr Ser Ile Asn Pro	Ala Glu Pro Phe Thr	Phe Ala Phe Lys Tyr	
	230	235	240
cac cga tgatgtccag gtgcgcacgg caa			864
His Arg			

<210> 702

<211> 247

<212> PRT

<213> Corynebacterium glutamicum

<400> 702

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 Leu Ile Leu Thr Glu Leu Met Val Asn Ser Thr Asn Met Gly Ser Ser
 35 40 45
 Asp Gly Phe Glu Tyr Val Glu Ile Thr Asn Thr Thr Ala Glu Pro Ile
 50 55 60
 Asp Phe Ser Asp Tyr Thr Leu Asn Tyr Leu Tyr Pro Gln Asp Glu Phe
 65 70 75 80
 Thr Asn Thr Asn Glu Ala Val Trp Ala Ala Glu Pro Gly Asp Val Ile
 85 90 95
 Ile Gln Pro Gly Lys Ser Leu Val Phe Trp Ile Lys Asn Gly Pro Asn
 100 105 110
 Asp Glu Ala Thr Ala Ala Asp Phe Asn Ala Glu Tyr Gly Thr Asn Leu
 115 120 125
 Glu Ala Gly Lys Asp Leu Val Glu Ile Ser Ser Gly Gly Met Ala Asn
 130 135 140
 Gly Thr Ala Arg Gly Met Gln Ile Gln Thr Asn Thr Gly His Ile Val
 145 150 155 160
 Asn Arg Gly Phe Tyr Asn Met Ala Gly Ala Ser Asp Val Lys Ala Asn
 165 170 175
 Glu Gly Leu His Phe Ala Val Asp Glu Ser Asp Leu Leu Lys Gln Thr
 180 185 190
 Leu Val Gly Ser Gly Ala Pro Thr Pro Gly Thr Val Tyr Thr Ser Gln
 195 200 205
 Ile Pro Asn Pro Leu Ser Ala Val Ile Ala Asp Ser Ser Val Pro Leu
 210 215 220
 Ile Thr Asp Asn Thr Ala Thr Ser Ile Asn Pro Ala Glu Pro Phe Thr
 225 230 235 240
 Phe Ala Phe Lys Tyr His Arg
 245

<210> 703

<211> 864

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(841)

<223> FRXA01635

<400> 703

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 aaaactgac caactccagg atcaattact tctgatcaag ttg att cct ggc gga 115
 Leu Ile Pro Gly Gly
 1 5

tgt	gac	act	cca	gaa	gag	oct	gaa	gcc	cct	gaa	gac	tct	ctt	ttt	gaa	163
Leu	Asp	Thr	Pro	Glu 10	Glu	Pro	Glu	Ala	Pro 15	Glu	Asp	Ser	Leu	Phe 20	Glu	
ggg	cgc	act	ccc	cct	agg	gat	gca	agc	acc	cgc	ttg	atc	ctc	act	gaa	211
Gly	Arg	Thr	Pro 25	Pro	Arg	Asp	Ala	Ser 30	Thr	Arg	Leu	Ile	Leu 35	Thr	Glu	
cta	atg	gtc	aac	tcc	acc	aac	atg	ggc	agt	tct	gat	ggg	ttt	gag	tat	259
Leu	Met	Val 40	Asn	Ser	Thr	Asn	Met 45	Gly	Ser	Ser	Asp	Gly 50	Phe	Glu	Tyr	
gtg	gaa	atc	acc	aac	act	act	gcc	gaa	ccc	atc	gat	ttt	tcc	gat	tac	307
Val	Glu 55	Ile	Thr	Asn	Thr	Thr 60	Ala	Glu	Pro	Ile	Asp 65	Phe	Ser	Asp	Tyr	
acc	ttg	aac	tac	ctg	tac	ccg	cag	gat	gag	ttc	acc	aac	acc	aac	gaa	355
Thr	Leu	Asn	Tyr	Leu	Tyr 75	Pro	Gln	Asp	Glu	Phe 80	Thr	Asn	Thr	Asn	Glu 85	
gcc	gtc	tgg	gct	gcg	gaa	cct	ggg	gat	gtc	att	att	cag	cct	gga	aaa	403
Ala	Val	Trp	Ala	Ala 90	Glu	Pro	Gly	Asp	Val 95	Ile	Ile	Gln	Leu	Gly 100	Lys	
tct	ctc	gtg	ttt	tgg	atc	aaa	aat	ggc	ccc	aat	gat	gag	gca	acc	gca	451
Ser	Leu	Val 105	Phe	Trp	Ile	Lys	Asn	Gly 110	Pro	Asn	Asp	Glu	Ala 115	Thr	Ala	
gca	gat	ttc	aat	gca	gaa	tat	ggc	acc	aac	ctg	gag	gct	gga	aaa	gac	499
Ala	Asp	Phe 120	Asn	Ala	Glu	Tyr	Gly 125	Thr	Asn	Leu	Glu	Ala 130	Gly	Lys	Asp	
ctt	gtt	gaa	atc	tcc	tca	ggg	ggg	atg	gcc	aat	ggg	act	gcc	aga	gga	547
Leu	Val	Glu 135	Ile	Ser	Ser	Gly 140	Gly	Met	Ala	Asn	Gly 145	Thr	Ala	Arg	Gly	
atg	cag	att	cag	acc	aac	act	ggc	cac	ata	gtc	aac	cggt	ggg	ttc	tac	595
Met	Gln	Ile 150	Gln	Thr	Asn 155	Thr	Gly	His	Ile 160	Val	Asn	Arg	Gly	Phe	Tyr 165	
aac	atg	gct	ggc	gct	tct	gat	gtg	aaa	gcc	aac	gag	ggg	ctt	cat	ttc	643
Asn	Met	Ala 170	Gly	Ala	Ser	Asp	Val	Lys 175	Ala	Asn	Glu	Gly	Leu 180	His	Phe	
gca	gtg	gat	gag	tct	gat	ctt	ctg	aag	caa	acg	ctt	gtc	ggc	agc	ggg	691
Ala	Val	Asp 185	Glu	Ser	Asp	Leu	Leu	Lys 190	Gln	Thr	Leu	Val 195	Gly	Ser	Gly	
gcg	cca	acc	ccg	ggc	act	gtg	tac	act	tcg	cag	att	cct	aat	cca	ctg	739
Ala	Pro	Thr 200	Pro	Gly	Thr	Val	Tyr 205	Thr	Ser	Gln	Ile	Pro 210	Asn	Pro	Leu	
tct	gcc	gtt	atc	gct	gat	tct	tct	gta	cca	ctc	atc	aca	gat	aat	acc	787
Ser	Ala 215	Val	Ile	Ala	Asp	Ser 220	Ser	Val	Pro	Leu	Ile 225	Thr	Asp	Asn	Thr	
gca	acc	agt	atc	aac	cct	gcg	gag	ccg	ttt	acc	ttc	gcc	ttc	aaa	tat	835
Ala	Thr	Ser 230	Ile	Asn	Pro 235	Pro	Glu	Pro	Phe	Thr 240	Phe	Ala	Phe	Lys	Tyr 245	

cac cga tgatgtccag gtgcgcacgg caa
His Arg

864

<210> 704
<211> 247
<212> PRT
<213> Corynebacterium glutamicum

<400> 704
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Leu Ile Leu Thr Glu Leu Met Val Asn Ser Thr Asn Met Gly Ser Ser
35 40 45
Asp Gly Phe Glu Tyr Val Glu Ile Thr Asn Thr Thr Ala Glu Pro Ile
50 55 60
Asp Phe Ser Asp Tyr Thr Leu Asn Tyr Leu Tyr Pro Gln Asp Glu Phe
65 70 75 80
Thr Asn Thr Asn Glu Ala Val Trp Ala Ala Glu Pro Gly Asp Val Ile
85 90 95
Ile Gln Pro Gly Lys Ser Leu Val Phe Thr Ile Lys Asn Gly Pro Asn
100 105 110
Asp Glu Ala Thr Ala Ala Asp Phe Asn Ala Glu Tyr Gly Thr Asn Leu
115 120 125
Glu Ala Gly Lys Asp Leu Val Glu Ile Ser Ser Gly Gly Met Ala Asn
130 135 140
Gly Thr Ala Arg Gly Met Gln Ile Gln Thr Asn Thr Gly His Ile Val
145 150 155 160
Asn Arg Gly Phe Tyr Asn Met Ala Gly Ala Ser Asp Val Lys Ala Asn
165 170 175
Glu Gly Leu His Phe Ala Val Asp Glu Ser Asp Leu Leu Lys Gln Thr
180 185 190
Leu Val Gly Ser Gly Ala Pro Thr Pro Gly Thr Val Tyr Thr Ser Gln
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Ile Pro Asn Pro Leu Ser Ala Val Ile Ala Asp Ser Ser Val Pro Leu
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Ile Thr Asp Asn Thr Ala Thr Ser Ile Asn Pro Ala Glu Pro Phe Thr
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Phe Ala Phe Lys Tyr His Arg
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 <223> RXN01647

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                                         Met Gly Asp Val Arg
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atg att cat gat cca ctt ggt agg cgc cgg cgg gcg ttg gtg ttt ggg   163
Met Ile His Asp Pro Leu Gly Arg Arg Arg Arg Ala Leu Val Phe Gly
                                         10                               20

gtg gtg gcg tgc gtg atg ttg gcg gtg gga tca ttg gcg ttg gct att   211
Val Val Ala Cys Val Met Leu Ala Val Gly Ser Leu Ala Leu Ala Ile
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ttt cga ccc gcg aag gat ccg gcc gat gcg ccg ttg atc cgc tct gaa   259
Phe Arg Pro Ala Lys Asp Pro Ala Asp Ala Pro Leu Ile Arg Ser Glu
                                         40                               45                               50

tcc gcc gcg ctc ttt gtg cag ctg gat ggg tcg gtg cat ccg gtg gct   307
Ser Gly Ala Leu Phe Val Gln Leu Asp Gly Ser Val His Pro Val Ala
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aat gtg gcc tcg gct ccg ttg att gtg ggg gag ccg gtg gat ccg gtg   355
Asn Val Ala Ser Ala Arg Leu Ile Val Gly Glu Pro Val Asp Pro Val
                                         70                               75                               80                               85

aac gcc agc gat gcg atc atc gcg gcc atg ccg cgc gga gtg ccg gtg   403
Asn Ala Ser Asp Ala Ile Ile Ala Gly Met Pro Arg Gly Val Pro Val
                                         90                               95                               100

ggg gtt cct gat gcg ccg ggg ctt ttc agc agc acc gaa gaa ccc gag   451
Gly Val Pro Asp Ala Pro Gly Leu Phe Ser Ser Thr Glu Glu Pro Glu
                                         105                               110                               115

caa gat tgg ttt gtg tgc cag gat gtc ggc act ggg gat cta cac att   499
Gln Asp Trp Phe Val Cys Gln Asp Val Gly Thr Gly Asp Leu His Ile
                                         120                               125                               130

acg gtt cct agg gcc gga cta ggg ccc acc ctg att gcg gaa gga aat   547
Thr Val Pro Arg Gly Gly Leu Gly Pro Thr Leu Ile Ala Glu Gly Asn
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ggg tgg ctg ggg gcg tcg aaa agc gaa acc ggc gag gtc acc tgg aac   595
Gly Trp Leu Gly Ala Ser Lys Ser Glu Thr Gly Glu Val Thr Trp Asn
                                         150                               155                               160                               165

ctg att acc gcg gac ggg cgc cgc gaa ctg ccg gcg tgg gcc agc gaa   643
Leu Ile Thr Ala Asp Gly Arg Arg Glu Leu Pro Ala Trp Gly Ser Glu
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cat ggg cgc att atg cgc cgc cac ctg ggg att tcc gag gac acc ccg   691

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CCDS:CCDS1000.1

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cgc gta tac ctg acc act gag ctg ctc aac gcg atc ccc gag cac gac	739
Arg Val Tyr Leu Thr Thr Glu Leu Leu Asn Ala Ile Pro Glu His Asp	
200 205 210	
gcg gtc cgc ttc cca gcc ccg ctg ccc gag ett gtc gac gcc tcc acc	787
Ala Val Arg Phe Pro Ala Pro Leu Pro Glu Leu Val Asp Ala Ser Thr	
215 220 225	
cgc aac tgg tta cgg ctc gac ggg gcg ctc gcc gaa atc acg ccg cta	835
Arg Asn Trp Leu Arg Leu Asp Gly Ala Leu Ala Glu Ile Thr Pro Leu	
230 235 240 245	
cag cgc ggg ttg ett atc gac gcc ggt tcc ggt gtt ttc ccc gac ccc	883
Gln Arg Gly Leu Leu Ile Asp Ala Gly Ser Gly Val Phe Pro Asp Pro	
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acc gcg ctt ctt ggt gtg cat gaa gaa aca gcc aac acc ttg acg ctg	931
Thr Ala Leu Leu Gly Val His Glu Glu Thr Ala Asn Thr Leu Thr Leu	
265 270 275	
ccc gag caa aca gtt tct tgg caa gat ctg gac ggt ggt ttt gcc tgc	979
Pro Glu Gln Thr Val Ser Trp Gln Asp Leu Asp Gly Gly Phe Ala Cys	
280 285 290	
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Ala Asp Gly Glu Gly Gln Ile Gly Phe Leu Glu Thr Leu Glu Ser Gly	
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Val Ala Leu Ser Gly Asp Ser Arg Ala Lys Ser Phe Ser Thr Asn Ala	
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Gly Gly Ala Val Gly Val Asp Ser Gly Phe Gly Tyr Tyr Val Val Ser	
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Asp Phe Gly Leu Met His Pro Val Ser Thr Gly Glu Ser Met Val Ala	
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Leu Gly Ile Thr Asp Val Gln Val Val Pro Trp Ser Val Leu Arg Leu	
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ttg ccg cag gga agt gaa tta gca aaa gag aca gcg ctc gcg ccc acc	1267
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Tyr	
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<211> 390

<212> PRT

<213> Corynebacterium glutamicum

<400> 706

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Leu Ala Leu Ala Ile Phe Arg Pro Ala Lys Asp Pro Ala Asp Ala Pro
 35 40 45

Leu Ile Arg Ser Glu Ser Gly Ala Leu Phe Val Gln Leu Asp Gly Ser
 50 55 60

Val His Pro Val Ala Asn Val Ala Ser Ala Arg Leu Ile Val Gly Glu
 65 70 75 80

Pro Val Asp Pro Val Asn Ala Ser Asp Ala Ile Ile Ala Gly Met Pro
 85 90 95

Arg Gly Val Pro Val Gly Val Pro Asp Ala Pro Gly Leu Phe Ser Ser
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Thr Glu Glu Pro Glu Gln Asp Trp Phe Val Cys Gln Asp Val Gly Thr
 115 120 125

Gly Asp Leu His Ile Thr Val Pro Arg Gly Gly Leu Gly Pro Thr Leu
 130 135 140

Ile Ala Glu Gly Asn Gly Trp Leu Gly Ala Ser Lys Ser Glu Thr Gly
 145 150 155 160

Glu Val Thr Trp Asn Leu Ile Thr Ala Asp Gly Arg Arg Glu Leu Pro
 165 170 175

Ala Trp Gly Ser Glu His Gly Arg Ile Met Arg Arg His Leu Gly Ile
 180 185 190

Ser Glu Asp Thr Pro Arg Val Tyr Leu Thr Thr Glu Leu Leu Asn Ala
 195 200 205

Ile Pro Glu His Asp Ala Val Arg Phe Pro Ala Pro Leu Pro Glu Leu
 210 215 220

Val Asp Ala Ser Thr Arg Asn Trp Leu Arg Leu Asp Gly Ala Leu Ala
 225 230 235 240

Glu Ile Thr Pro Leu Gln Arg Gly Leu Leu Ile Asp Ala Gly Ser Gly
 245 250 255

Val Phe Pro Asp Pro Thr Ala Leu Leu Gly Val His Glu Glu Thr Ala
 260 265 270

Asn Thr Leu Thr Leu Pro Glu Gln Thr Val Ser Trp Gln Asp Leu Asp
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Gly Gly Phe Ala Cys Ala Asp Gly Glu Gly Gln Ile Gly Phe Leu Glu
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Thr Leu Glu Ser Gly Val Ala Leu Ser Gly Asp Ser Arg Ala Lys Ser
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Ser	Ser	Thr	Glu	Glu	Pro	Glu	Gln	Asp	Trp	Phe	Val	Cys	Gln	Asp	Val		
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Gly	Thr	Gly	Asp	Leu	His	Ile	Thr	Val	Pro	Arg	Gly	Gly	Leu	Gly	Pro		
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Thr	Leu	Ile	Ala	Glu	Gly	Asn	Gly	Trp	Leu	Gly	Ala	Ser	Lys	Ser	Glu		
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Thr	Gly	Glu	Val	Thr	Trp	Asn	Leu	Ile	Thr	Ala	Asp	Gly	Arg	Arg	Glu		
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Leu	Pro	Ala	Trp	Gly	Ser	Glu	His	Gly	Arg	Ile	Met	Arg	Arg	His	Leu		
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Gly	Ile	Ser	Glu	Asp	Thr	Pro	Arg	Val	Tyr	Leu	Thr	Thr	Glu	Leu	Leu		
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Asn	Ala	Ile	Glu	Glu	His	Asp	Ala	Val	Arg	Phe	Pro	Ala	Pro	Leu	Pro		
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gag	ctt	gtc	gac	gcc	tcc	acc	cgc	aac	tgg	tta	cgg	ctc	gac	ggg	gcg	432	
Gly	Leu	Val	Asp	Ala	Ser	Thr	Arg	Asn	Trp	Leu	Arg	Leu	Asp	Gly	Ala		

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tcc ggt gtt ttc ccc gac ccc acc gcg ctt ctt ggt gtg cat gaa gaa Ser Gly Val Phe Pro Asp Pro Thr Ala Leu Leu Gly Val His Glu Glu 165 170 175			528
aca gcc aac acc ttg acg ctg ccc gag caa aca gtt tct tgg caa gat Thr Ala Asn Thr Leu Thr Leu Pro Glu Gln Thr Val Ser Trp Gln Asp 180 185 190			576
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ctg gaa act ctg gaa tgc ggg gtg gcg cta tct ggt gat tcc agg gcg Leu Glu Thr Leu Glu Ser Gly Val Ala Leu Ser Gly Asp Ser Arg Ala 210 215 220			672
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Thr Leu Ile Ala Glu Gly Asn Gly Trp Leu Gly Ala Ser Lys Ser Glu 50 55 60			

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 65 70 75 80
 Leu Pro Ala Trp Gly Ser Glu His Gly Arg Ile Met Arg Arg His Leu
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 Gly Ile Ser Glu Asp Thr Pro Arg Val Tyr Leu Thr Thr Glu Leu Leu
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 Asn Ala Ile Pro Glu His Asp Ala Val Arg Phe Pro Ala Pro Leu Pro
 115 120 125
 Glu Leu Val Asp Ala Ser Thr Arg Asn Trp Leu Arg Leu Asp Gly Ala
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 145 150 155 160
 Ser Gly Val Phe Pro Asp Pro Thr Ala Leu Leu Gly Val His Glu Glu
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 Thr Ala Asn Thr Leu Thr Leu Pro Glu Gln Thr Val Ser Trp Gln Asp
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 Leu Asp Gly Gly Phe Ala Cys Ala Asp Gly Glu Gly Gln Ile Gly Phe
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 Leu Glu Thr Leu Glu Ser Gly Val Ala Leu Ser Gly Asp Ser Arg Ala
 210 215 220
 Lys Ser Phe Ser Thr Asn Ala Gly Gly Ala Val Gly Val Asp Ser Gly
 225 230 235 240
 Phe Gly Tyr Tyr Val Val Ser Asp Phe Gly Leu Met His Pro Val Ser
 245 250 255
 Thr Gly Glu Ser Met Val Ala Leu Gly Ile Thr Asp Val Gln Val Val
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<211> 1856

<212> DNA

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<222> (1)..(1833)

<223> RXN01658

<400> 709

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Asn Phe Tyr Gly Phe Pro Asp Gln Leu Ala Met Asp Arg Phe Glu Val	
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Asn Ala Leu Gln Gln Asn Gln Gln Asp Trp Ile Asn Arg His Thr Val	
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tat acc cac ggc aac ggc ttc att gca gct caa gca aac cag gtg gat	240
Tyr Thr His Gly Asn Gly Phe Ile Ala Ala Gln Ala Asn Gln Val Asp	
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Glu Val Ala Arg Asp Val Gly Ser Thr Arg Gly Tyr Pro Val Tyr	
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acc gtc tct gat ttg cag tcg aat gct cgt gct gca gaa agc gaa gat	336
Thr Val Ser Asp Leu Gln Ser Asn Ala Arg Ala Ala Glu Ser Glu Asp	
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Ala Glu Glu Leu Gly Ile Lys Val Asp Glu Pro Arg Val Tyr Tyr Gly	
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Pro Leu Ile Ala Ser Ala Thr Asp Gly Ala Asp Tyr Ala Ile Val Gly	
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gac acc ggc gat ggc cca gtc gag tac gac act gac acc tcc agc tac	480
Asp Thr Gly Asp Gly Pro Val Glu Tyr Asp Thr Asp Thr Ser Ser Tyr	
145 150 155 160	
acc tac gaa ggt gct ggc ggc gtg gac att gga aac atg gtc aac cgt	528
Thr Tyr Glu Gly Ala Gly Gly Val Asp Ile Gly Asn Met Val Asn Arg	
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Ala Met Phe Ala Leu Arg Tyr Gln Glu Met Asn Met Leu Ser Asp	
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cgt gtt ggt tcc gaa tcc aag atc cta ttt gag cgc gat cct cgt tcc	624
Arg Val Gly Ser Glu Ser Lys Ile Leu Phe Glu Arg Asp Pro Arg Ser	
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Arg Val Glu Lys Val Ala Pro Trp Leu Thr Thr Asp Ser Lys Thr Tyr	
210 215 220	
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Pro Thr Val Ile Asp Gly Arg Ile Lys Trp Ile Val Asp Gly Tyr Thr	
225 230 235 240	
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Thr Leu Asp Ser Leu Pro Tyr Ser Arg Thr Ser Leu Thr Glu Ala	
245 250 255	
act cag gat gct gtc atg cct gac ggc acc cca cag cca ctg atc aca	816

Thr	Gln	Asp	Ala	Val	Met	Pro	Asp	Gly	Thr	Pro	Gln	Pro	Leu	Ile	Thr		
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Asp	Arg	Val	Gly	Tyr	Ile	Arg	Asn	Ser	Val	Lys	Ala	Val	Val	Asp	Ala		
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Tyr	Asp	Gly	Thr	Val	Glu	Leu	Tyr	Glu	Phe	Asp	Thr	Glu	Asp	Pro	Val		
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Leu	Lys	Ala	Trp	Arg	Gly	Val	Phe	Pro	Asp	Thr	Val	Lys	Asp	Gly	Ser		
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Glu	Ile	Ser	Asp	Glu	Leu	Arg	Ala	His	Leu	Arg	Tyr	Pro	Glu	Asp	Leu		
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Phe	Lys	Val	Gln	Arg	Asp	Met	Leu	Ala	Lys	Tyr	Asn	Val	Asp	Asp	Ser		
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Thr	Ala	Ala	Glu	Gly	Arg	Gln	Glu	Leu	Lys	Gln	Pro	Pro	Tyr	Tyr	Val		
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Pro	Phe	Arg	Gly	Leu	Gln	Arg	Glu	Tyr	Leu	Ser	Ala	His	Met	Ser	Ala		
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tcg	tct	gat	cca	gtt	acc	tac	ggg	gaa	atc	act	gtt	cgt	gtg	ctg	cct	1296	
Ser	Ser	Asp	Pro	Val	Thr	Tyr	Gly	Glu	Ile	Thr	Val	Arg	Val	Leu	Pro		
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Thr	Asp	Ser	Val	Thr	Gln	Gly	Pro	Lys	Gln	Ala	Gln	Asp	Ala	Met	Met		
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Ser	Ser	Asp	Gln	Val	Ala	Gln	Asp	Gln	Thr	Leu	Trp	Arg	Gly	Ser	Asn		
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gat	ctg	cac	aac	gga	aac	ctg	ttg	acc	ttg	cca	gtt	ggg	ggc	gga	gag	1440	
Asp	Leu	His	Asn	Gly	Asn	Leu	Leu	Thr	Leu	Pro	Val	Gly	Gly	Gly	Glu		
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Ile	Leu	Tyr	Val	Glu	Pro	Ile	Tyr	Ser	Gln	Arg	Lys	Asp	Gln	Ala	Ser		
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ggt tac gca cca acg atc gct gaa gcc cta tcg cag gtc gcc att gat			1584
Gly Tyr 515 Ala Pro Thr Ile Ala Glu Ala Leu Ser Gln Val Gly Ile Asp	520	525	
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Pro Lys Glu Ala Gln Asp Ile Glu Glu Val Asp Gly Thr Ala Thr Thr	535	540	
cca tcg act gat gag act gac act gac act gat cag cct gca acc gaa			1680
Pro Ser Thr Asp Glu Thr Asp Thr Asp Thr Asp Gln Pro Ala Thr Glu	550	555	560
acc cca act gca cca gtg agt gag gcg gaa gga atc gcg gcc atc aac			1728
Thr Pro Thr Ala Pro Val Ser Glu Ala Glu Gly Ile Ala Ala Ile Asn	565	570	575
gat gcg ttg agc aac ctt gaa gct gct cgc gat agc tct ttc gaa gag			1776
Asp Ala Leu Ser Asn Leu Glu Ala Ala Arg Asp Ser Ser Phe Glu Glu	580	585	590
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Tyr Gly Arg Ala Leu Asp Ala Leu Asp Arg Ala Val Asp Ser Tyr Gln	595	600	605
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50 55 60			
Tyr Thr His Gly Asn Gly Phe Ile Ala Ala Gln Ala Asn Gln Val Asp			
65 70 75 80			
Glu Val Ala Arg Asp Val Gly Ser Thr Arg Gly Gly Tyr Pro Val Tyr			
85 90 95			
Thr Val Ser Asp Leu Gln Ser Asn Ala Arg Ala Ala Glu Ser Glu Asp			
100 105 110			
Ala Glu Glu Leu Gly Ile Lys Val Asp Glu Pro Arg Val Tyr Tyr Gly			
115 120 125			

Pro Leu Ile Ala Ser Ala Thr Asp Gly Ala Asp Tyr Ala Ile Val Gly
 130 135 140
 Asp Thr Gly Asp Gly Pro Val Glu Tyr Asp Thr Asp Thr Ser Ser Tyr
 145 150 155 160
 Thr Tyr Glu Gly Ala Gly Gly Val Asp Ile Gly Asn Met Val Asn Arg
 165 170 175
 Ala Met Phe Ala Leu Arg Tyr Gln Glu Met Asn Met Leu Leu Ser Asp
 180 185 190
 Arg Val Gly Ser Glu Ser Lys Ile Leu Phe Glu Arg Asp Pro Arg Ser
 195 200 205
 Arg Val Glu Lys Val Ala Pro Trp Leu Thr Thr Asp Ser Lys Thr Tyr
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 Pro Thr Val Ile Asp Gly Arg Ile Lys Trp Ile Val Asp Gly Tyr Thr
 225 230 235 240
 Thr Leu Asp Ser Leu Pro Tyr Ser Thr Arg Thr Ser Leu Thr Glu Ala
 245 250 255
 Thr Gln Asp Ala Val Met Pro Asp Gly Thr Pro Gln Pro Leu Ile Thr
 260 265 270
 Asp Arg Val Gly Tyr Ile Arg Asn Ser Val Lys Ala Val Val Asp Ala
 275 280 285
 Tyr Asp Gly Thr Val Glu Leu Tyr Glu Phe Asp Thr Glu Asp Pro Val
 290 295 300
 Leu Lys Ala Trp Arg Gly Val Phe Pro Asp Thr Val Lys Asp Gly Ser
 305 310 315 320
 Glu Ile Ser Asp Glu Leu Arg Ala His Leu Arg Tyr Pro Glu Asp Leu
 325 330 335
 Phe Lys Val Gln Arg Asp Met Leu Ala Lys Tyr Asn Val Asp Asp Ser
 340 345 350
 Gly Thr Phe Phe Thr Asn Asp Ala Phe Trp Ser Val Pro Gly Asp Pro
 355 360 365
 Thr Ala Ala Glu Gly Arg Gln Glu Leu Lys Gln Pro Pro Tyr Tyr Val
 370 375 380
 Val Ala Ala Asp Pro Glu Thr Gly Glu Ser Ser Phe Gln Leu Ile Thr
 385 390 395 400
 Pro Phe Arg Gly Leu Gln Arg Glu Tyr Leu Ser Ala His Met Ser Ala
 405 410 415
 Ser Ser Asp Pro Val Thr Tyr Gly Glu Ile Thr Val Arg Val Leu Pro
 420 425 430
 Thr Asp Ser Val Thr Gln Gly Pro Lys Gln Ala Gln Asp Ala Met Met
 435 440 445
 Ser Ser Asp Gln Val Ala Gln Asp Gln Thr Leu Trp Arg Gly Ser Asn

450 455 460
 Asp Leu His Asn Gly Asn Leu Leu Thr Leu Pro Val Gly Gly Gly Glu
 465 470 475 480
 Ile Leu Tyr Val Glu Pro Ile Tyr Ser Gln Arg Lys Asp Gln Ala Ser
 485 490 495
 Ala Phe Pro Lys Leu Leu Arg Val Leu Val Phe Tyr Lys Gly Gln Val
 500 505 510
 Gly Tyr Ala Pro Thr Ile Ala Glu Ala Leu Ser Gln Val Gly Ile Asp
 515 520 525
 Pro Lys Glu Ala Gln Asp Ile Glu Glu Val Asp Gly Thr Ala Thr Thr
 530 535 540
 Pro Ser Thr Asp Glu Thr Asp Thr Asp Thr Asp Gln Pro Ala Thr Glu
 545 550 555 560
 Thr Pro Thr Ala Pro Val Ser Glu Ala Glu Gly Ile Ala Ala Ile Asn
 565 570 575
 Asp Ala Leu Ser Asn Leu Glu Ala Ala Arg Asp Ser Ser Phe Glu Glu
 580 585 590
 Tyr Gly Arg Ala Leu Asp Ala Leu Asp Arg Ala Val Asp Ser Tyr Gln
 595 600 605
 Ser Ala Gln
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<210> 711
 <211> 1485
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1485)
 <223> FRXA01658

<400> 711
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 Asp Pro Gln Ile Leu Ser Pro Thr Phe Thr Gln Gln Gln Leu Arg
 1 5 10 15

 aac ttc tac ggt ttc cca gac cag ctg gcg atg gac cgc ttt gaa gta 96
 Asn Phe Tyr Gly Phe Pro Asp Gln Leu Ala Met Asp Arg Phe Glu Val
 20 25 30

 gat ggc aaa ctc cgc gac ttt gtt gtg gca gca cgt gag ctc gat cca 144
 Asp Gly Lys Leu Arg Asp Phe Val Val Ala Ala Arg Glu Leu Asp Pro
 35 40 45

 aac gcc ctg cag caa aac cag cag gac tgg att aac cgt cac act gtt 192
 Asn Ala Leu Gln Gln Asn Gln Gln Asp Trp Ile Asn Arg His Thr Val
 50 55 60

 tat acc cac ggc aac ggc ttc att gca gct caa gca aac cag gtg gat 240

Tyr	Thr	His	Gly	Asn	Gly	Phe	Ile	Ala	Ala	Gln	Ala	Asn	Gln	Val	Asp	
65					70					75					80	
gag	gtc	gcc	cgc	gac	gtc	gga	tcc	act	cgt	ggt	ggt	tac	cct	gtc	tac	288
Glu	Val	Ala	Arg	Asp	Val	Gly	Ser	Thr	Arg	Gly	Gly	Tyr	Pro	Val	Tyr	
			85						90					95		
acc	gtc	tct	gat	ttg	cag	tcg	aat	gct	cgt	gct	gca	gaa	agc	gaa	gat	336
Thr	Val	Ser	Asp	Leu	Gln	Ser	Asn	Ala	Arg	Ala	Ala	Glu	Ser	Glu	Asp	
			100					105					110			
gct	gag	gag	ctt	ggc	atc	aag	gtt	gat	gag	cct	cgt	gtg	tac	tac	gga	384
Ala	Glu	Glu	Leu	Gly	Ile	Lys	Val	Asp	Glu	Pro	Arg	Val	Tyr	Tyr	Gly	
			115				120					125				
cca	ctg	att	gct	tct	gcg	act	gat	ggt	gct	gac	tac	gca	att	gtc	ggt	432
Pro	Leu	Ile	Ala	Ser	Ala	Thr	Asp	Gly	Ala	Asp	Tyr	Ala	Ile	Val	Gly	
			130				135				140					
gac	acc	ggc	gat	ggc	cca	gtc	gag	tac	gac	act	gac	acc	tcc	agc	tac	480
Asp	Thr	Gly	Asp	Gly	Pro	Val	Glu	Tyr	Asp	Thr	Asp	Thr	Ser	Ser	Tyr	
			145			150					155				160	
acc	tac	gaa	ggt	gct	ggc	ggc	gtg	gac	att	gga	aac	atg	gtc	aac	cgt	528
Thr	Tyr	Glu	Gly	Ala	Gly	Gly	Val	Asp	Ile	Gly	Asn	Met	Val	Asn	Arg	
				165				170					175			
gcg	atg	ttt	gca	ttg	cgc	tac	cag	gaa	atg	aac	atg	ctc	ctg	tct	gat	576
Ala	Met	Phe	Ala	Leu	Arg	Tyr	Gln	Glu	Met	Asn	Met	Leu	Leu	Ser	Asp	
			180					185					190			
cgt	gtt	ggt	tcc	gaa	tcc	aag	atc	cta	ttt	gag	cgc	gat	cct	cgt	tcc	624
Arg	Val	Gly	Ser	Glu	Ser	Lys	Ile	Leu	Phe	Glu	Arg	Asp	Pro	Arg	Ser	
			195				200					205				
cgt	gtg	gaa	aag	gtt	gca	cct	tgg	ttg	acc	act	gac	tcc	aag	acc	tac	672
Arg	Val	Glu	Lys	Val	Ala	Pro	Trp	Leu	Thr	Thr	Asp	Ser	Lys	Thr	Tyr	
			210			215					220					
cca	act	gtg	att	gat	ggt	cgc	atc	aag	tgg	atc	gtc	gat	ggc	tac	acc	720
Pro	Thr	Val	Ile	Asp	Gly	Arg	Ile	Lys	Trp	Ile	Val	Asp	Gly	Tyr	Thr	
			225			230				235					240	
acc	ttg	gat	agt	ctt	ccg	tac	tcc	acg	cgc	acc	tca	ctg	acg	gaa	gcg	768
Thr	Leu	Asp	Ser	Leu	Pro	Tyr	Ser	Thr	Arg	Thr	Ser	Leu	Thr	Glu	Ala	
				245					250					255		
act	cag	gat	gct	gtc	atg	cct	gac	ggc	acc	cca	cag	cca	ctg	atc	aca	816
Thr	Gln	Asp	Ala	Val	Met	Pro	Asp	Gly	Thr	Pro	Gln	Pro	Leu	Ile	Thr	
			260					265					270			
gat	agg	gtc	ggt	tac	atc	cgc	aac	tcc	gtg	aag	gct	gtt	gtt	gat	gcg	864
Asp	Arg	Val	Gly	Tyr	Ile	Arg	Asn	Ser	Val	Lys	Ala	Val	Val	Asp	Ala	
			275				280					285				
tac	gac	gga	act	gtt	gaa	ctc	tac	gaa	ttc	gac	acc	gaa	gat	cct	gtt	912
Tyr	Asp	Gly	Thr	Val	Glu	Tyr	Glu	Phe	Asp	Thr	Glu	Asp	Pro	Val		
			290			295				300						
ctg	aag	gca	tgg	cgt	ggc	gtg	ttc	cca	gac	acc	gtg	aag	gac	ggg	tcg	960
Leu	Lys	Ala	Trp	Arg	Gly	Val	Phe	Pro	Asp	Thr	Val	Lys	Asp	Gly	Ser	

305	310	315	320	
gag att tcc gat	gag ctt cgc gca cac ctg	cgt tac cca gaa gat ttg	1008	
Glu Ile Ser Asp	Glu Leu Arg Ala His Leu Arg	Pro Glu Asp Leu		
	325	330	335	
ttc aag gtc cag	cgt gac atg ctg gcc aag tac aac gtt	gat gat tct	1056	
Phe Lys Val Gln	Arg Asp Met Leu Ala Lys Tyr Asn Val	Asp Asp Ser		
	340	345	350	
gga aca ttc ttc	acc aac gat gcg ttc tgg tct gtc	cca ggt gac cca	1104	
Gly Thr Phe Phe	Thr Asn Asp Ala Phe Trp Ser Val	Pro Gly Asp Pro		
	355	360	365	
act gca gcg gag	ggc cgc cag gaa ctt aag cag cct	cct tac tac gtg	1152	
Thr Ala Ala Glu	Gly Arg Gln Glu Leu Lys Gln Pro	Pro Tyr Tyr Val		
	370	375	380	
gtg gca gca gac	cca gag acc ggt gag tcc agc ttc	cag ctg atc acc	1200	
Val Ala Ala Asp	Pro Glu Thr Gly Glu Ser Ser Phe	Gln Leu Ile Thr		
	385	390	395	400
cag ttc cgt gga	ctt cag cgc gag tac ctc tct gca	cac atg tct gcg	1248	
Pro Phe Arg Gly	Leu Gln Arg Glu Tyr Leu Ser Ala	His Met Ser Ala		
	405	410	415	
tcg tct gat cca	gtt acc tac ggt gaa atc act gtt	cgt gtg ctg cct	1296	
Ser Ser Asp Pro	Val Thr Tyr Gly Glu Ile Thr Val	Arg Val Leu Pro		
	420	425	430	
acc gat tct gtg	acc cag ggt cca aag cag gcc	cag gat gcg atg atg	1344	
Thr Asp Ser Val	Thr Gln Gly Pro Lys Gln Ala Gln	Asp Ala Met Met		
	435	440	445	
tca tct gac cag	gtt gct cag gac caa aca ctg	tggt gga tcg aac	1392	
Ser Ser Asp Gln	Val Ala Gln Asp Gln Thr Leu Trp	Arg Gly Ser Asn		
	450	455	460	
gat ctg cac aac	gga aac ctg ttg acc ttg cca	gtt ggt ggc gga gag	1440	
Asp Leu His Asn	Gly Asn Leu Leu Thr Leu Pro	Val Gly Gly Gly Glu		
	465	470	475	480
atc ctc tac gtt	gag ccg att tac tcg cag cgc	aag gat cag gca	1485	
Ile Leu Tyr Val	Glu Pro Ile Tyr Ser Gln Arg	Lys Asp Gln Ala		
	485	490	495	

<210> 712

<211> 495

<212> PRT

<213> Corynebacterium glutamicum

<400> 712

Asp	Pro	Gln	Ile	Leu	Ser	Pro	Thr	Phe	Thr	Gln	Gln	Gln	Gln	Leu	Arg
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Asn	Phe	Tyr	Gly	Phe	Pro	Asp	Gln	Leu	Ala	Met	Asp	Arg	Phe	Glu	Val
			20				25						30		

Asp	Gly	Lys	Leu	Arg	Asp	Phe	Val	Val	Ala	Ala	Arg	Glu	Leu	Asp	Pro
		35					40					45			

Asn Ala Leu Gln Gln Asn Gln Gln Asp Trp Ile Asn Arg His Thr Val
 50 55 60
 Tyr Thr His Gly Asn Gly Phe Ile Ala Ala Gln Ala Asn Gln Val Asp
 65 70 75 80
 Glu Val Ala Arg Asp Val Gly Ser Thr Arg Gly Gly Tyr Pro Val Tyr
 85 90 95
 Thr Val Ser Asp Leu Gln Ser Asn Ala Arg Ala Ala Glu Ser Glu Asp
 100 105 110
 Ala Glu Glu Leu Gly Ile Lys Val Asp Glu Pro Arg Val Tyr Tyr Gly
 115 120 125
 Pro Leu Ile Ala Ser Ala Thr Asp Gly Ala Asp Tyr Ala Ile Val Gly
 130 135 140
 Asp Thr Gly Asp Gly Pro Val Glu Tyr Asp Thr Asp Thr Ser Ser Tyr
 145 150 155 160
 Thr Tyr Glu Gly Ala Gly Gly Val Asp Ile Gly Asn Met Val Asn Arg
 165 170 175
 Ala Met Phe Ala Leu Arg Tyr Gln Glu Met Asn Met Leu Leu Ser Asp
 180 185 190
 Arg Val Gly Ser Glu Ser Lys Ile Leu Phe Glu Arg Asp Pro Arg Ser
 195 200 205
 Arg Val Glu Lys Val Ala Pro Trp Leu Thr Thr Asp Ser Lys Thr Tyr
 210 215 220
 Pro Thr Val Ile Asp Gly Arg Ile Lys Trp Ile Val Asp Gly Tyr Thr
 225 230 235 240
 Thr Leu Asp Ser Leu Pro Tyr Ser Thr Arg Thr Ser Leu Thr Glu Ala
 245 250 255
 Thr Gln Asp Ala Val Met Pro Asp Gly Thr Pro Gln Pro Leu Ile Thr
 260 265 270
 Asp Arg Val Gly Tyr Ile Arg Asn Ser Val Lys Ala Val Val Asp Ala
 275 280 285
 Tyr Asp Gly Thr Val Glu Leu Tyr Glu Phe Asp Thr Glu Asp Pro Val
 290 295 300
 Leu Lys Ala Trp Arg Gly Val Phe Pro Asp Thr Val Lys Asp Gly Ser
 305 310 315 320
 Glu Ile Ser Asp Glu Leu Arg Ala His Leu Arg Tyr Pro Glu Asp Leu
 325 330 335
 Phe Lys Val Gln Arg Asp Met Leu Ala Lys Tyr Asn Val Asp Asp Ser
 340 345 350
 Gly Thr Phe Phe Thr Asn Asp Ala Phe Trp Ser Val Pro Gly Asp Pro
 355 360 365

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<220>
<221> CDS
<222> (101)..(646)
<223> RXN01659
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 Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro Asn Ala Ser Glu Glu
 90 95 100

gat ttg tct cag ccg ttg gtg atc cgc ccc gag gag ccg ttg cag atg 451
 Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu Glu Pro Leu Gln Met
 105 110 115

ccg gtt cgc ggt gtg cag gaa agc cgc gga gtg gtc gag cca cgg tca 499
 Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val Val Glu Pro Arg Ser
 120 125 130

ttg ggt cgc gat gat gtg gag tgc att gcg gag ggc gat cca gag cgt 547
 Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu Gly Asp Pro Glu Arg
 135 140 145

ccg agc gat ctt tat gcc acg cgt gtg ctg cgt gat etc aat ggt cag 595
 Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg Asp Leu Asn Gly Gln
 150 155 160 165

tcc agt att ttc caa gat tcc acc gac gcg gat gag cca cca aaa aag 643
 Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp Glu Pro Pro Lys Lys
 170 175 180

tgg tagaaaaactg gtgtttttcg gcc 669
 Trp

<210> 714
 <211> 182
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 714
 Val Ala Gly Val Ala Gln Arg Phe Val Asp Glu Arg Ile His Val Gly
 1 5 10 15

Leu Asp Ser Met Pro Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp
 20 25 30

Trp Val Leu Ala Glu Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu
 35 40 45

Glu Ile Leu Arg Pro Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu
 50 55 60

Pro Pro Arg Ser Thr Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu
 65 70 75 80

Pro Ser Arg Leu Lys Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro
 85 90 95

Asn Ala Ser Glu Glu Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu
 100 105 110

Glu Pro Leu Gln Met Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val
 115 120 125

Val Glu Pro Arg Ser Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu

130

135

140

Gly Asp Pro Glu Arg Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg
 145 150 155 160

Asp Leu Asn Gly Gln Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp
 165 170 175

Glu Pro Pro Lys Lys Trp
 180

<210> 715

<211> 509

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(486)

<223> FRXA01659

<400> 715

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 Pro Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp Trp Val Leu Ala
 1 5 10 15

gaa acc atc aag ggt tcc acg cct tcc gat tgg gaa gag att ttg cgg 96
 Glu Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu Glu Ile Leu Arg
 20 25 30

ccg ttg gcg ctg ctc acg gac gcg tct ttc acg ttg cca cct cgt tcc 144
 Pro Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu Pro Pro Arg Ser
 35 40 45

acg cgt gcg caa acc ttg gat ttg aag cat ttg gaa cca agc cgt ctg 192
 Thr Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu Pro Ser Arg Leu
 50 55 60

aag ccg gag cag cca gaa aag cca gcg ttt act ccc aat gct tcg gaa 240
 Lys Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro Asn Ala Ser Glu
 65 70 75 80

gaa gat ttg tct cag ccg ttg gtg atc cgc ccc gag gag ccg ttg cag 288
 Glu Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu Glu Pro Leu Gln
 85 90 95

atg ccg gtt cgc ggt gtg cag gaa agc cgc gga gtg gtc gag cca cgg 336
 Met Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val Val Glu Pro Arg
 100 105 110

tca ttg ggt gcg gat gat gtg gag tcg att gcg gag gcc gat cca gag 384
 Ser Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu Gly Asp Pro Glu
 115 120 125

cgt ccg agc gat ctt tat gcc acg cgt gtg ctg cgt gat ctc aat ggt 432
 Arg Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg Asp Leu Asn Gly
 130 135 140

cag tcc agt att ttc caa gat tcc acc gac gcg gat gag cca cca aaa 480
 Gln Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp Glu Pro Pro Lys

145 150 155 160

aag tgg tagaaaaactg gtgttttttcg gcc 509

Lys Trp

<210> 716
 <211> 162
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 716
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 1 5 10 15

Glu Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu Glu Ile Leu Arg
 20 25 30

Pro Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu Pro Pro Arg Ser
 35 40 45

Thr Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu Pro Ser Arg Leu
 50 55 60

Lys Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro Asn Ala Ser Glu
 65 70 75 80

Glu Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu Glu Pro Leu Gln
 85 90 95

Met Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val Val Glu Pro Arg
 100 105 110

Ser Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu Gly Asp Pro Glu
 115 120 125

Arg Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg Asp Leu Asn Gly
 130 135 140

Gln Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp Glu Pro Pro Lys
 145 150 155 160

Lys Trp

<210> 717
 <211> 981
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(958)
 <223> RXN01663

<400> 717
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	Met	Glu	Ile	Ser	Val	
	1				5	
ttg atc atc gcc gca ctg atc ttg gtg gca ggc atc gta ctg tgg cgc	163					
Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly Ile Val Leu Trp Arg		10	15	20		
gcg gac tcg tct aaa cag gca gct aaa aag gct gaa tca cct gtg ggc	211					
Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala Glu Ser Pro Val Gly		25	30	35		
tca gtc gca cct gcg ccc gtg ctg gtt gaa gaa gag ccg gac cct gag	259					
Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu Glu Pro Asp Pro Glu		40	45	50		
ttt gag cca gaa ctg gac cct gaa cca gaa gcg caa cca gaa cca gag	307					
Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala Gln Pro Glu Pro Glu		55	60	65		
ctg gaa gtt gcg cct aga ttt gcg cca gaa cca gtt caa gat ctt gag	355					
Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro Val Gln Asp Leu Glu		70	75	80	85	
cgg gat cag gct gag gac att tat ttt gat gat tcc cct gaa ctc gat	403					
Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp Ser Pro Glu Leu Asp		90	95	100		
gct gat gtt gaa aat gcc ttg gct gag ctt act gag gta gaa gac tac	451					
Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr Glu Val Glu Asp Tyr		105	110	115		
cgg gaa gag cca gtg cag tct gag caa cct caa gcc cct gcc acg gcg	499					
Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln Ala Pro Ala Thr Ala		120	125	130		
gag gta gct gcg gac gag gag caa cgg gcc gtc gat aag cat tcg ttt	547					
Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val Asp Lys His Ser Phe		135	140	145		
ttg agc tct ttg cct ggt tcg cag cgc cgg gag cgc cga aac tgg gcg	595					
Leu Ser Ser Leu Pro Gly Ser Gln Arg Arg Glu Arg Arg Asn Trp Ala		150	155	160	165	
gcg aag cac cac ttc gat ttc atc aag gaa gat gcc ttt ttg acc gat	643					
Ala Lys His His Phe Asp Phe Ile Lys Glu Asp Ala Phe Leu Thr Asp		170	175	180		
gaa tgg tca agg ggt gcg gca tcg act ggt gcc gtt gca cgt gat gtg	691					
Glu Trp Ser Arg Gly Ala Ala Ser Thr Gly Ala Val Ala Arg Asp Val		185	190	195		
gtc agt ggc atg gct gaa gga tat gaa acg cat ctg gtg gat ttg gcg	739					
Val Ser Gly Met Ala Glu Gly Tyr Glu Thr His Leu Val Asp Leu Ala		200	205	210		
ggc gtg ccc gtg atg gcg atg cgc cgt gga att acc tct gac gtg gtc	787					
Gly Val Pro Val Met Ala Met Arg Arg Gly Ile Thr Ser Asp Val Val		215	220	225		
att gat gcg cgc cgc ggt gag cag cct gcc gat cca gag cgt gaa gaa	835					
Ile Asp Ala Arg Arg Gly Glu Gln Pro Ala Asp Pro Glu Arg Glu Glu						

230	235	240	245	
tct gat gat tta gtc gag att gat acc gtc tct gga ttc cgc ctg ctc				883
Ser Asp Asp Leu Val Glu Ile Asp Thr Val Ser Gly Phe Arg Leu Leu	250	255	260	
agt acg tgg cgg ggg ttg cgc agc gtt ttg tgg acg agc gca ttc acg				931
Ser Thr Trp Arg Gly Leu Arg Ser Val Leu Ser Thr Ser Ala Phe Thr	265	270	275	
tcg gtt tgg att cca tgc cag aag ctg tgactgctgt gtggatggaa				978
Ser Val Trp Ile Pro Cys Gln Lys Leu	280	285		
tct				981

<210> 718

<211> 286

<212> PRT

<213> Corynebacterium glutamicum

<400> 718

Met Glu Ile Ser Val Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly			
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Ile Val Leu Trp Arg Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala			
20	25	30	

Glu Ser Pro Val Gly Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu			
35	40	45	

Glu Pro Asp Pro Glu Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala			
50	55	60	

Gln Pro Glu Pro Glu Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro			
65	70	75	80

Val Gln Asp Leu Glu Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp			
85	90	95	

Ser Pro Glu Leu Asp Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr			
100	105	110	

Glu Val Glu Asp Tyr Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln			
115	120	125	

Ala Pro Ala Thr Ala Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val			
130	135	140	

Asp Lys His Ser Phe Leu Ser Ser Leu Pro Gly Ser Gln Arg Arg Glu			
145	150	155	160

Arg Arg Asn Trp Ala Ala Lys His His Phe Asp Phe Ile Lys Glu Asp			
165	170	175	

Ala Phe Leu Thr Asp Glu Trp Ser Arg Gly Ala Ala Ser Thr Gly Ala			
180	185	190	

Val Ala Arg Asp Val Val Ser Gly Met Ala Glu Gly Tyr Glu Thr His			
195	200	205	

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Leu Val Asp Leu Ala Gly Val Pro Val Met Ala Met Arg Arg Gly Ile
  210                      215                      220

Thr Ser Asp Val Val Ile Asp Ala Arg Arg Gly Glu Gln Pro Ala Asp
  225                      230                      235                      240

Pro Glu Arg Glu Glu Ser Asp Asp Leu Val Glu Ile Asp Thr Val Ser
                      245                      250                      255

Gly Phe Arg Leu Leu Ser Thr Trp Arg Gly Leu Arg Ser Val Leu Ser
                      260                      265                      270

Thr Ser Ala Phe Thr Ser Val Trp Ile Pro Cys Gln Lys Leu
  275                      280                      285

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<210> 719

<211> 535

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(535)

<223> FRXA01663

<400> 719

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cgtggcttga gtaacgcactg ccagtaaggt gtgtgatgtg atg gaa ata agt gtc 115
                      Met Glu Ile Ser Val
                      1                      5

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ttg atc atc gcc gca ctg atc ttg gtg gca gcc atc gta ctg tgg cgc 163
Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly Ile Val Leu Trp Arg
                      10                      15                      20

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gcg gac tcg tct aaa cag gca gct aaa aag gct gaa tca cct gtg ggc 211
Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala Glu Ser Pro Val Gly
                      25                      30                      35

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tca gtc gca cct gcg ccc gtg ctg gtt gaa gaa gag ccg gac cct gag 259
Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu Glu Pro Asp Pro Glu
                      40                      45                      50

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ttt gag cca gaa ctg gac cct gaa cca gaa gcg caa cca gaa cca gag 307
Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala Gln Pro Glu Pro Glu
                      55                      60                      65

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ctg gaa gtt gcg cct aga ttt gcg cca gaa cca gtt caa gat ctt gag 355
Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro Val Gln Asp Leu Glu
                      70                      75                      80                      85

```

```

ccg gat cag gct gag gac att tat ttt gat gat tcc cct gaa ctc gat 403
Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp Ser Pro Glu Leu Asp
                      90                      95                      100

```

```

gct gat gtt gaa aat gcc ttg gct gag ctt act gag gta gaa gac tac 451
Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr Glu Val Glu Asp Tyr
                      105                      110                      115

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ccg gaa gag cca gtg cag tct gag caa cct caa gcc cct gcc acg gcg 499
 Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln Ala Pro Ala Thr Ala
 120 125 130

gag gta gct gcg gac gag gag caa cgg ggc gtc gat 535
 Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val Asp
 135 140 145

<210> 720

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 720

Met Glu Ile Ser Val Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly
 1 5 10 15

Ile Val Leu Trp Arg Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala
 20 25 30

Glu Ser Pro Val Gly Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu
 35 40 45

Glu Pro Asp Pro Glu Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala
 50 55 60

Gln Pro Glu Pro Glu Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro
 65 70 75 80

Val Gln Asp Leu Glu Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp
 85 90 95

Ser Pro Glu Leu Asp Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr
 100 105 110

Glu Val Glu Asp Tyr Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln
 115 120 125

Ala Pro Ala Thr Ala Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val
 130 135 140

Asp

145

<210> 721

<211> 1038

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1015)

<223> RXN01669

<400> 721

cacccacagt caccaagaac atagccactc cacacacaac cactccacac acaaccacga 60

gggtcagcag caccatcacc ccaccggatt caaaggattt ttg tac gag att ttc 115

	Leu	Tyr	Glu	Ile	Phe	
	1				5	
gtt cca cac tcc cat gac acc gcc gac tcg att gat gat gct atg gag						163
Val Pro His Ser His Asp Thr Ala Asp Ser Ile Asp Asp Ala Met Glu						
	10			15	20	
gcg aac tca gag ggt att cga gcg ctg aag ttt agc ctt gta ttg atg						211
Ala Asn Ser Glu Gly Ile Arg Ala Leu Lys Phe Ser Leu Val Leu Met						
	25		30		35	
ctg ctc acg acg gtt ttg cag gct atc att gtg tct ttt tct gga tct						259
Leu Leu Thr Thr Val Leu Gln Ala Ile Ile Val Ser Phe Ser Gly Ser						
	40		45		50	
gtt gca ctg ttg gcg gat acg gtt cac aac ctt tcc gac gca ttg act						307
Val Ala Leu Leu Ala Asp Thr Val His Asn Leu Ser Asp Ala Leu Thr						
	55		60		65	
gcg att cct ctt tgg att gct ttc ata ctt tcc cgg cgc gca gcg act						355
Ala Ile Pro Leu Trp Ile Ala Phe Ile Leu Ser Arg Arg Ala Ala Thr						
	70		75		80	85
caa aaa tat acg tat gga ttc aat cgt gca gag gat tta gcg ggg ttg						403
Gln Lys Tyr Thr Tyr Gly Phe Asn Arg Ala Glu Asp Leu Ala Gly Leu						
			90		95	100
ttt att gtc gcg atg att gct ctt tcg gcg att gtt gct gca tgg cag						451
Phe Ile Val Ala Met Ile Ala Leu Ser Ala Ile Val Ala Ala Trp Gln						
	105		110		115	
gcg atc gac cgg atg att aat cct cgc ccg atg gag aat att gaa tgg						499
Ala Ile Asp Arg Met Ile Asn Pro Arg Pro Met Glu Asn Ile Glu Trp						
	120		125		130	
gtg att gcg gca ggt gtt att ggt ttc tta gga aat gag gct gtg gca						547
Val Ile Ala Ala Gly Val Ile Gly Phe Leu Gly Asn Glu Ala Val Ala						
	135		140		145	
atg tat cgc att cgg gtt ggt aag agg att ggc tcg gct gct ttg gtt						595
Met Tyr Arg Ile Arg Val Gly Lys Arg Ile Gly Ser Ala Ala Leu Val						
	150		155		160	165
gca gat gcc gtt cat gct cgc acg gat ggt ttt act tca ctt gca gtt						643
Ala Asp Gly Val His Ala Arg Thr Asp Gly Phe Thr Ser Leu Ala Val						
	170		175		180	
gtc gca ggt ggt gtt gga gtt ttt ctg gga ttc ccc ctg gct gac cca						691
Val Ala Gly Gly Val Gly Val Phe Leu Gly Phe Pro Leu Ala Asp Pro						
	185		190		195	
att atc gga ttg atc att tct gcg atg att gcc acc ctt ctt gtt ggt						739
Ile Ile Gly Leu Ile Ile Ser Ala Met Ile Ala Thr Leu Leu Val Gly						
	200		205		210	
acg atc cgt tcg gtt gcc aga cgc ctc atg gat gga att gag ccg gag						787
Thr Ile Arg Ser Val Gly Arg Arg Leu Met Asp Gly Ile Glu Pro Glu						
	215		220		225	
ttg gta gag aag gct acg cac gcg atc tgg cat gtg aag gaa att gag						835
Leu Val Glu Lys Ala Thr His Ala Ile Trp His Val Lys Glu Ile Glu						

230	235	240	245	
tcg att gat cga	ctg agg ttg agg	tggtt gga cac	cgt ctt cac ggc	883
Ser Ile Asp Arg	Leu Arg Leu Arg	Trp Val Gly His	Arg Leu His Gly	
	250	255	260	
gat gcc acg gtc	agc act tct aca	tca tcg cta tcg	gaa gcc acc gca	931
Asp Ala Thr Val	Ser Thr Ser Thr	Ser Ser Leu Ser	Glu Ala Thr Ala	
	265	270	275	
atc gcc ctt gag	gct gag ctt tcc	gtc aaa caa cat	ctt ccc aat gtg	979
Ile Ala Leu Glu	Ala Glu Leu Ser	Val Lys Gln His	Leu Pro Asn Val	
	280	285	290	
gat gaa atg act	gtg acc atc acc	cct tcc aaa cct	tgagtcccg	1025
Asp Glu Met Thr	Val Thr Ile Thr	Pro Ser Lys Pro		
	295	300	305	
gatacaattg ttg				1038

<210> 722

<211> 305

<212> PRT

<213> Corynebacterium glutamicum

<400> 722

Leu Tyr Glu Ile Phe Val Pro His Ser His Asp Thr Ala Asp Ser Ile
1 5 10 15

Asp Asp Ala Met Glu Ala Asn Ser Glu Gly Ile Arg Ala Leu Lys Phe
20 25 30

Ser Leu Val Leu Met Leu Leu Thr Thr Val Leu Gln Ala Ile Ile Val
35 40 45

Ser Phe Ser Gly Ser Val Ala Leu Leu Ala Asp Thr Val His Asn Leu
50 55 60

Ser Asp Ala Leu Thr Ala Ile Pro Leu Trp Ile Ala Phe Ile Leu Ser
65 70 75 80

Arg Arg Ala Ala Thr Gln Lys Tyr Thr Tyr Gly Phe Asn Arg Ala Glu
85 90 95

Asp Leu Ala Gly Leu Phe Ile Val Ala Met Ile Ala Leu Ser Ala Ile
100 105 110

Val Ala Ala Trp Gln Ala Ile Asp Arg Met Ile Asn Pro Arg Pro Met
115 120 125

Glu Asn Ile Glu Trp Val Ile Ala Ala Gly Val Ile Gly Phe Leu Gly
130 135 140

Asn Glu Ala Val Ala Met Tyr Arg Ile Arg Val Gly Lys Arg Ile Gly
145 150 155 160

Ser Ala Ala Leu Val Ala Asp Gly Val His Ala Arg Thr Asp Gly Phe
165 170 175

Thr Ser Leu Ala Val Val Ala Gly Gly Val Gly Val Phe Leu Gly Phe

180 185 190
 Pro Leu Ala Asp Pro Ile Ile Gly Leu Ile Ile Ser Ala Met Ile Ala
 195 200 205
 Thr Leu Leu Val Gly Thr Ile Arg Ser Val Gly Arg Arg Leu Met Asp
 210 215 220
 Gly Ile Glu Pro Glu Leu Val Glu Lys Ala Thr His Ala Ile Trp His
 225 230 235 240
 Val Lys Glu Ile Glu Ser Ile Asp Arg Leu Arg Leu Arg Trp Val Gly
 245 250 255
 His Arg Leu His Gly Asp Ala Thr Val Ser Thr Ser Thr Ser Ser Leu
 260 265 270
 Ser Glu Ala Thr Ala Ile Ala Leu Glu Ala Glu Leu Ser Val Lys Gln
 275 280 285
 His Leu Pro Asn Val Asp Glu Met Thr Val Thr Ile Thr Pro Ser Lys
 290 295 300

Pro
305

<210> 723

<211> 755

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(732)

<223> FRXA01669

<400> 723

cac aac ctt tcc gac gca ttg act gcg att cct ctt tgg att gct ttc 48

His Asn Leu Ser Asp Ala Leu Thr Ala Ile Pro Leu Trp Ile Ala Phe

1

5

10

15

ata ctt tcc cgg cgc gca gcg act caa aaa tat acg tat gga ttc aat 96

Ile Leu Ser Arg Arg Ala Ala Thr Gln Lys Tyr Thr Tyr Gly Phe Asn

20

25

30

cgt gca gag gat tta gcg ggg ttg ttt att gtc gcg atg att gct ctt 144

Arg Ala Glu Asp Leu Ala Gly Leu Phe Ile Val Ala Met Ile Ala Leu

35

40

45

tgc gcg att gtt gct gca tgg cag gcg atc gac cgg atg att aat cct 192

Ser Ala Ile Val Ala Ala Trp Gln Ala Ile Asp Arg Met Ile Asn Pro

50

55

60

cgc cgc atg gag aat att gaa tgg gtg att gcg gca ggt gtt att ggt 240

Arg Pro Met Glu Asn Ile Glu Trp Val Ile Ala Ala Gly Val Ile Gly

65

70

75

80

ttc tta gga aat gag gct gtg gca atg tat cgc att cgg gtt ggt aag 288

Phe Leu Gly Asn Glu Ala Val Ala Met Tyr Arg Ile Arg Val Gly Lys

85

90

95

agg att ggc tgc gct gct ttg gtt gca gat ggc gtt cat gct cgc acg 336
 Arg Ile Gly Ser Ala Ala Leu Val Ala Asp Gly Val His Ala Arg Thr
 100 105 110

gat ggt ttt act tca ctt gca gtt gtc gca ggt ggt gtt gga gtt ttt 384
 Asp Gly Phe Thr Ser Leu Ala Val Val Ala Gly Gly Val Gly Val Phe
 115 120 125

ctg gga ttc ccc ctg gct gac cca att atc gga ttg atc att tct gcg 432
 Leu Gly Phe Pro Leu Ala Asp Pro Ile Ile Gly Leu Ile Ile Ser Ala
 130 135 140

atg att gcc acc ctt ctt gtt ggt acg atc cgt tgc gtt ggc aga cgc 480
 Met Ile Ala Thr Leu Leu Val Gly Thr Ile Arg Ser Val Gly Arg Arg
 145 150 155 160

ctc atg gat gga att gag ccg gag ttg gta gag aag gct acg cac gcg 528
 Leu Met Asp Gly Ile Glu Pro Glu Leu Val Glu Lys Ala Thr His Ala
 165 170 175

atc tgg cat gtg aag gaa att gag tgc att gat cga ctg agg ttg agg 576
 Ile Trp His Val Lys Glu Ile Glu Ser Ile Asp Arg Leu Arg Leu Arg
 180 185 190

tgg gtt gga cac cgt ctt cac ggc gat gcc acg gtc agc act tct aca 624
 Trp Val Gly His Arg Leu His Gly Asp Ala Thr Val Ser Thr Ser Thr
 195 200 205

tca tgc cta tgc gaa gcc acc gca atc gcc ctt gag gct gag ctt tcc 672
 Ser Ser Leu Ser Glu Ala Thr Ala Ile Ala Leu Glu Ala Glu Leu Ser
 210 215 220

gtc aaa caa cat ctt ccc aat gtg gat gaa atg act gtg acc atc acc 720
 Val Lys Gln His Leu Pro Asn Val Asp Glu Met Thr Val Thr Ile Thr
 225 230 235 240

cct tcc aaa cct tgagtcgcgt gatacaattg ttg 755
 Pro Ser Lys Pro

<210> 724

<211> 244

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 724

His Asn Leu Ser Asp Ala Leu Thr Ala Ile Pro Leu Trp Ile Ala Phe
 1 5 10 15

Ile Leu Ser Arg Arg Ala Ala Thr Gln Lys Tyr Thr Tyr Gly Phe Asn
 20 25 30

Arg Ala Glu Asp Leu Ala Gly Leu Phe Ile Val Ala Met Ile Ala Leu
 35 40 45

Ser Ala Ile Val Ala Ala Trp Gln Ala Ile Asp Arg Met Ile Asn Pro
 50 55 60

Arg Pro Met Glu Asn Ile Glu Trp Val Ile Ala Ala Gly Val Ile Gly

65	70	75	80
Phe Leu Gly Asn Glu Ala Val Ala Met Tyr Arg Ile Arg Val Gly Lys	85	90	95
Arg Ile Gly Ser Ala Ala Leu Val Ala Asp Gly Val His Ala Arg Thr	100	105	110
Asp Gly Phe Thr Ser Leu Ala Val Val Ala Gly Gly Val Gly Val Phe	115	120	125
Leu Gly Phe Pro Leu Ala Asp Pro Ile Ile Gly Leu Ile Ile Ser Ala	130	135	140
Met Ile Ala Thr Leu Leu Val Gly Thr Ile Arg Ser Val Gly Arg Arg	145	150	155
Leu Met Asp Gly Ile Glu Pro Glu Leu Val Glu Lys Ala Thr His Ala	165	170	175
Ile Trp His Val Lys Glu Ile Glu Ser Ile Asp Arg Leu Arg Leu Arg	180	185	190
Trp Val Gly His Arg Leu His Gly Asp Ala Thr Val Ser Thr Ser Thr	195	200	205
Ser Ser Leu Ser Glu Ala Thr Ala Ile Ala Leu Glu Ala Glu Leu Ser	210	215	220
Val Lys Gln His Leu Pro Asn Val Asp Glu Met Thr Val Thr Ile Thr	225	230	235
Pro Ser Lys Pro			

<210> 725

<211> 465

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(442)

<223> RXN01672

<400> 725

agtagcaaaag ggtgcagtcg aaggaccagc atccaagact gctgccgaag aaaccgactc 60

cggtgacaac	ggatccgacg	aaaacggcga	ggaataattt	atg gca tcc cga gaa	115
				Met Ala Ser Arg Glu	
				1	5

gta tcc atc acc cga atc tca cca cta gca acc ttc cga gtt gca ctg	163
Val Ser Ile Thr Arg Ile Ser Pro Leu Ala Thr Phe Arg Val Ala Leu	
10	15
20	

gca atg tcc atc atc gga ctc gtg gcg tgg atc atc tgc gta acc gtc	211
Ala Met Ser Ile Ile Gly Leu Val Ala Trp Ile Ile Cys Val Thr Val	
25	30
	35

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ctc tat ttc gga ctt aac gtg gct ggc gtc tgg cag aac ttc aac gat 259
Leu Tyr Phe Gly Leu Asn Val Ala Gly Val Trp Gln Asn Phe Asn Asp
      40                      45                      50

gtc atc ggc ggt gtt ggt gca gaa caa acc atc acc ttc ggg ctc gtc 307
Val Ile Gly Gly Val Gly Ala Glu Gln Thr Ile Thr Phe Gly Leu Val
      55                      60                      65

ctg agc att tcc gca ctt ctg gga gct atc gga ggc att acc gtc gct 355
Leu Ser Ile Ser Ala Leu Leu Gly Ala Ile Gly Ala Ile Thr Val Ala
      70                      75                      80                      85

gtg ctt gca cca ttg tgt gca atc atc tac aac tcg att gtt gac ctc 403
Val Leu Ala Pro Leu Cys Ala Ile Ile Tyr Asn Ser Ile Val Asp Leu
      90                      95                      100

ttc ggt gga ctg cag att caa ctg caa gaa gaa gta gac taacctctga 452
Phe Gly Gly Leu Gln Ile Gln Leu Gln Glu Glu Val Asp
      105                      110

aacacaaacc cct 465

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<210> 726

<211> 114

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 726

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Met Ala Ser Arg Glu Val Ser Ile Thr Arg Ile Ser Pro Leu Ala Thr
  1             5             10             15

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```

Phe Arg Val Ala Leu Ala Met Ser Ile Ile Gly Leu Val Ala Trp Ile
      20             25             30

```

```

Ile Cys Val Thr Val Leu Tyr Phe Gly Leu Asn Val Ala Gly Val Trp
      35             40             45

```

```

Gln Asn Phe Asn Asp Val Ile Gly Gly Val Gly Ala Glu Gln Thr Ile
      50             55             60

```

```

Thr Phe Gly Leu Val Leu Ser Ile Ser Ala Leu Leu Gly Ala Ile Gly
      65             70             75             80

```

```

Ala Ile Thr Val Ala Val Leu Ala Pro Leu Cys Ala Ile Ile Tyr Asn
      85             90             95

```

```

Ser Ile Val Asp Leu Phe Gly Gly Leu Gln Ile Gln Leu Gln Glu Glu
      100            105            110

```

Val Asp

<210> 727

<211> 332

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1) . . (309)

<223> FRXA01672

<400> 727

tca cca cta gca acc ttc cga gtt gca ctg gca atg tcc atc atc gga 48
Ser Pro Leu Ala Thr Phe Arg Val Ala Leu Ala Met Ser Ile Ile Gly
1 5 10 15

ctc gtg gcg tgg atc atc tgc gta acc gtc ctc tat ttc gga ctt aac 96
Leu Val Ala Trp Ile Ile Cys Val Thr Val Leu Tyr Phe Gly Leu Asn
20 25 30

gtg gct ggc gtc tgg cag aac ttc aac gat gtc atc ggc ggt gtt ggt 144
Val Ala Gly Val Trp Gln Asn Phe Asn Asp Val Ile Gly Gly Val Gly
35 40 45

gca gaa caa acc atc acc ttc ggg ctc gtc ctg agc att tcc gca ctt 192
Ala Glu Gln Thr Ile Thr Phe Gly Leu Val Leu Ser Ile Ser Ala Leu
50 55 60

ctg gga gct atc gga gcg att acc gtc gct gtg ctt gca cca ttg tgt 240
Leu Gly Ala Ile Gly Ala Ile Thr Val Ala Val Leu Ala Pro Leu Cys
65 70 75 80

gca atc atc tac aac tgc att gtt gac ctc ttc ggt gga ctg cag att 288
Ala Ile Ile Tyr Asn Ser Ile Val Asp Leu Phe Gly Gly Leu Gln Ile
85 90 95

caa ctg caa gaa gaa gta gac taacctctga aacacaaacc cct 332
Gln Leu Gln Glu Glu Val Asp
100

<210> 728

<211> 103

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 728

Ser Pro Leu Ala Thr Phe Arg Val Ala Leu Ala Met Ser Ile Ile Gly
1 5 10 15

Leu Val Ala Trp Ile Ile Cys Val Thr Val Leu Tyr Phe Gly Leu Asn
20 25 30

Val Ala Gly Val Trp Gln Asn Phe Asn Asp Val Ile Gly Gly Val Gly
35 40 45

Ala Glu Gln Thr Ile Thr Phe Gly Leu Val Leu Ser Ile Ser Ala Leu
50 55 60

Leu Gly Ala Ile Gly Ala Ile Thr Val Ala Val Leu Ala Pro Leu Cys
65 70 75 80

Ala Ile Ile Tyr Asn Ser Ile Val Asp Leu Phe Gly Gly Leu Gln Ile
85 90 95

Gln Leu Gln Glu Glu Val Asp
100

<210> 729
 <211> 1023
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1000)
 <223> RXN01694

<400> 729
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ttcgaaaaagc catgtccacc acgtgttota tctctggcgggc atg caa aaa atc acc 115
 Met Gln Lys Ile Thr 5

cca aac atc tgg tgc caa ggc acc gca gac gaa gca gcc gaa ttc tac 163
 Pro Asn Ile Trp Cys Gln Gly Thr Ala Asp Glu Ala Ala Glu Phe Tyr 10 15 20

gtc aat gcg ttt tct gag ttt ccg ggt ggc gca gaa gta ctc acc aca 211
 Val Asn Ala Phe Ser Glu Phe Pro Gly Gly Ala Glu Val Leu Thr Thr 25 30 35

gtt aag tat ccc gaa gct ggc ttg ctg gac ttc cag gag cct ttc gca 259
 Val Lys Tyr Pro Glu Ala Gly Leu Leu Asp Phe Gln Glu Pro Phe Ala 40 45 50

gga aaa acc ttg acg gtg gaa ctc gct atc tca ggc ttt aag atc atc 307
 Gly Lys Thr Leu Thr Val Glu Leu Ala Ile Ser Gly Phe Lys Ile Ile 55 60 65

ttg atc aat gct ggt gaa gag ttc act ccc aac cca tgc atc agc ttc 355
 Leu Ile Asn Ala Gly Glu Glu Phe Thr Pro Asn Pro Ser Ile Ser Phe 70 75 80 85

atg gtg aat ttt gat gcg gtg cgt gat gaa aat gcc aaa gag cac ctt 403
 Met Val Asn Phe Asp Ala Val Arg Asp Glu Asn Ala Lys Glu His Leu 90 95 100

gat gcg gtg tgg gaa aaa ctc cat gaa ggc ggc agc aca ctg atg cca 451
 Asp Ala Val Trp Glu Lys Leu His Glu Gly Gly Ser Thr Leu Met Pro 105 110 115

gtc gat act tac cca ttt tcg gaa tac tac ggg tgg gta caa gac aaa 499
 Val Asp Thr Tyr Pro Phe Ser Glu Tyr Tyr Gly Trp Val Gln Asp Lys 120 125 130

tat ggt gtg agc tgg caa ttg atg ctc agc cgc cca gaa gaa aag cca 547
 Tyr Gly Val Ser Trp Gln Leu Met Leu Ser Arg Pro Glu Glu Lys Pro 135 140 145

ggt ccc gca gta atc cca acg ctc tta ttt ggt ggg gca gct caa aat 595
 Gly Pro Ala Val Ile Pro Thr Leu Leu Phe Gly Gly Ala Ala Gln Asn 150 155 160 165

cag gca ggc cca gct caa gaa aac tac gtt gag gtg ttc ccg aac tcc 643
 Gln Ala Gly Pro Ala Gln Glu Asn Tyr Val Glu Val Phe Pro Asn Ser 170 175 180

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caa ctt ggt gat cgt gca cct tat gga cag caa aca ggt cct gcc act 691
Gln Leu Gly Asp Arg Ala Pro Tyr Gly Gln Gln Thr Gly Pro Ala Thr
      185                      190                      195

cct gag gcc ctc atg ttt tcc cag ttc caa ctc gac ggt cag tgg att 739
Pro Glu Ala Leu Met Phe Ser Gln Phe Gln Leu Asp Gly Gln Trp Ile
      200                      205                      210

ttc gcg atg gat tcc gga gtt gag caa gat ttc acc ttc agt gag ggt 787
Phe Ala Met Asp Ser Gly Val Glu Gln Asp Phe Thr Phe Ser Glu Gly
      215                      220                      225

gtc tca ttg atg tat gaa gct cat ggt caa gaa gaa ctc gat gcc atc 835
Val Ser Leu Met Tyr Glu Ala His Gly Gln Glu Glu Leu Asp Ala Ile
      230                      235                      240                      245

tgg aat gca ctc tcg gca gtt cca gaa gct gag gct tgt ggt tgg ttg 883
Trp Asn Ala Leu Ser Ala Val Pro Glu Ala Glu Ala Cys Gly Trp Leu
      250                      255                      260

aag gac aag ttc ggc gtg agc tgg cag att gtt ccc gac aac atg gag 931
Lys Asp Lys Phe Gly Val Ser Trp Gln Ile Val Pro Asp Asn Met Glu
      265                      270                      275

gag ctc atg gct aaa ccc ggc gcg tat gaa aag ctt ctt gcg atg aag 979
Glu Leu Met Ala Lys Pro Gly Ala Tyr Glu Lys Leu Leu Ala Met Lys
      280                      285                      290

aag atc aat atc gcg gag ttc tagcagttct aagcgctcca cgc 1023
Lys Ile Asn Ile Ala Glu Phe
      295                      300

<210> 730
<211> 300
<212> PRT
<213> Corynebacterium glutamicum

<400> 730
Met Gln Lys Ile Thr Pro Asn Ile Trp Cys Gln Gly Thr Ala Asp Glu
  1                      5                      10                      15

Ala Ala Glu Phe Tyr Val Asn Ala Phe Ser Glu Phe Pro Gly Gly Ala
      20                      25                      30

Glu Val Leu Thr Thr Val Lys Tyr Pro Glu Ala Gly Leu Leu Asp Phe
      35                      40                      45

Gln Glu Pro Phe Ala Gly Lys Thr Leu Thr Val Glu Leu Ala Ile Ser
      50                      55                      60

Gly Phe Lys Ile Ile Leu Ile Asn Ala Gly Glu Glu Phe Thr Pro Asn
      65                      70                      75                      80

Pro Ser Ile Ser Phe Met Val Asn Phe Asp Ala Val Arg Asp Glu Asn
      85                      90                      95

Ala Lys Glu His Leu Asp Ala Val Trp Glu Lys Leu His Glu Gly Gly
      100                      105                      110

Ser Thr Leu Met Pro Val Asp Thr Tyr Pro Phe Ser Glu Tyr Tyr Gly

```


115										120										125									
Trp	Val	Gln	Asp	Lys	Tyr	Gly	Val	Ser	Trp	Gln	Leu	Met	Leu	Ser	Arg														
	130						135					140																	
Pro	Glu	Glu	Lys	Pro	Gly	Pro	Ala	Val	Ile	Pro	Thr	Leu	Leu	Phe	Gly														
	145				150					155					160														
Gly	Ala	Ala	Gln	Asn	Gln	Ala	Gly	Pro	Ala	Gln	Glu	Asn	Tyr	Val	Glu														
				165					170					175															
Val	Phe	Pro	Asn	Ser	Gln	Leu	Gly	Asp	Arg	Ala	Pro	Tyr	Gly	Gln	Gln														
		180						185					190																
Thr	Gly	Pro	Ala	Thr	Pro	Glu	Ala	Leu	Met	Phe	Ser	Gln	Phe	Gln	Leu														
		195					200						205																
Asp	Gly	Gln	Trp	Ile	Phe	Ala	Met	Asp	Ser	Gly	Val	Glu	Gln	Asp	Phe														
	210					215					220																		
Thr	Phe	Ser	Glu	Gly	Val	Ser	Leu	Met	Tyr	Glu	Ala	His	Gly	Gln	Glu														
	225				230					235					240														
Glu	Leu	Asp	Ala	Ile	Trp	Asn	Ala	Leu	Ser	Ala	Val	Pro	Glu	Ala	Glu														
				245				250						255															
Ala	Cys	Gly	Trp	Leu	Lys	Asp	Lys	Phe	Gly	Val	Ser	Trp	Gln	Ile	Val														
			260					265					270																
Pro	Asp	Asn	Met	Glu	Glu	Leu	Met	Ala	Lys	Pro	Gly	Ala	Tyr	Glu	Lys														
		275					280					285																	
Leu	Leu	Ala	Met	Lys	Lys	Ile	Asn	Ile	Ala	Glu	Phe																		
	290					295					300																		

<210> 731
 <211> 1023
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1000)
 <223> FRXA01694

<400> 731
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 ttctgaaaagc catgtocacc acgtgttcta tcttggcggc atg caa aaa atc acc 115
 Met Gln Lys Ile Thr
 1 5
 cca aac atc tgg tgc caa ggc acc gca gac gaa gca gcc gaa ttc tac 163
 Pro Asn Ile Trp Cys Gln Gly Thr Ala Asp Glu Ala Ala Glu Phe Tyr
 10 15 20
 gtc aat gcg ttt tct gag ttt ccg ggt ggc gca gaa gta ctc acc aca 211
 Val Asn Ala Phe Ser Glu Phe Pro Gly Gly Ala Glu Val Leu Thr Thr
 25 30 35

gtt aag tat ccc gaa gct ggc ttg ctg gac ttc cag gag cct ttc gca 259
 Val Lys Tyr Pro Glu Ala Gly Leu Asp Phe Gln Glu Pro Phe Ala
 40 45 50

gga aaa acc ttg acg gtg gaa ctc gct atc tca ggc ttt aag atc atc 307
 Gly Lys Thr Leu Thr Val Glu Leu Ala Ile Ser Gly Phe Lys Ile Ile
 55 60 65

ttg atc aat gct ggt gaa gag ttc act ccc aac cca tgg atc agc ttc 355
 Leu Ile Asn Ala Gly Glu Glu Phe Thr Pro Asn Pro Ser Ile Ser Phe
 70 75 80 85

atg gtg aat ttt gat gcg gtg cgt gat gaa aat gcc aaa gag cac ctt 403
 Met Val Asn Phe Asp Ala Val Arg Asp Glu Asn Ala Lys Glu His Leu
 90 95 100

gat gcg gtg tgg gaa aaa ctc cat gaa ggc ggc agc aca ctg atg cca 451
 Asp Ala Val Trp Glu Lys Leu His Glu Gly Gly Ser Thr Leu Met Pro
 105 110 115

gtc gat act tac cca ttt tcg gaa tac tac ggg tgg gta caa gac aaa 499
 Val Asp Thr Tyr Pro Phe Ser Glu Tyr Tyr Gly Trp Val Gln Asp Lys
 120 125 130

tat ggt gtg agc tgg caa ttg atg ctc agc cgc cca gaa gaa aag cca 547
 Tyr Gly Val Ser Trp Gln Leu Met Leu Ser Arg Pro Glu Glu Lys Pro
 135 140 145

ggt ccc gca gta atc cca acg ctc tta ttt ggt ggg gca gct caa aat 595
 Gly Pro Ala Val Ile Pro Thr Leu Leu Phe Gly Gly Ala Ala Gln Asn
 150 155 160 165

cag gca ggc cca gct caa gaa aac tac gtt gag gtg ttc cag aac tcc 643
 Gln Ala Gly Pro Ala Gln Glu Asn Tyr Val Glu Val Phe Pro Asn Ser
 170 175 180

caa ctt ggt gat cgt gca cct tat gga cag caa aca ggt cct gcc act 691
 Gln Leu Gly Asp Arg Ala Pro Tyr Gly Gln Gln Thr Gly Pro Ala Thr
 185 190 195

cct gag gcc ctc atg ttt tcc cag ttc caa ctc gac ggt cag tgg att 739
 Pro Glu Ala Leu Met Phe Ser Gln Phe Gln Leu Asp Gly Gln Trp Ile
 200 205 210

ttc gcg atg gat tcc gga gtt gag caa gat ttc acc ttc agt gag ggt 787
 Phe Ala Met Asp Ser Gly Val Glu Gln Asp Phe Thr Phe Ser Glu Gly
 215 220 225

gtc tca ttg atg tat gaa gct cat ggt caa gaa gaa ctc gat gcc atc 835
 Val Ser Leu Met Tyr Glu Ala His Gly Gln Glu Glu Leu Asp Ala Ile
 230 235 240 245

tgg aat gca ctc tcg gca gtt cca gaa gct gag gct tgt ggt tgg ttg 883
 Trp Asn Ala Leu Ser Ala Val Pro Glu Ala Glu Ala Cys Gly Trp Leu
 250 255 260

aag gac aag ttc ggc gtg agc tgg cag att gtt ccc gac aac atg gag 931
 Lys Asp Lys Phe Gly Val Ser Trp Gln Ile Val Pro Asp Asn Met Glu
 265 270 275

gag ctc atg gct aaa ccc ggc gcg tat gaa aag ctt ctt gcg atg aag 979

Glu Leu Met Ala Lys Pro Gly Ala Tyr Glu Lys Leu Leu Ala Met Lys
 280 285 290

aag atc aat atc gcg gag ttc tagcagttct aagcgctcca cgc 1023
 Lys Ile Asn Ile Ala Glu Phe
 295 300

<210> 732

<211> 300

<212> PRT

<213> Corynebacterium glutamicum

<400> 732

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 20 25 30

Glu Val Leu Thr Thr Val Lys Tyr Pro Glu Ala Gly Leu Leu Asp Phe
 35 40 45

Gln Glu Pro Phe Ala Gly Lys Thr Leu Thr Val Glu Leu Ala Ile Ser
 50 55 60

Gly Phe Lys Ile Ile Leu Ile Asn Ala Gly Glu Glu Phe Thr Pro Asn
 65 70 75 80

Pro Ser Ile Ser Phe Met Val Asn Phe Asp Ala Val Arg Asp Glu Asn
 85 90 95

Ala Lys Glu His Leu Asp Ala Val Trp Glu Lys Leu His Glu Gly Gly
 100 105 110

Ser Thr Leu Met Pro Val Asp Thr Tyr Pro Phe Ser Glu Tyr Tyr Gly
 115 120 125

Trp Val Gln Asp Lys Tyr Gly Val Ser Trp Gln Leu Met Leu Ser Arg
 130 135 140

Pro Glu Glu Lys Pro Gly Pro Ala Val Ile Pro Thr Leu Leu Phe Gly
 145 150 155 160

Gly Ala Ala Gln Asn Gln Ala Gly Pro Ala Gln Glu Asn Tyr Val Glu
 165 170 175

Val Phe Pro Asn Ser Gln Leu Gly Asp Arg Ala Pro Tyr Gly Gln Gln
 180 185 190

Thr Gly Pro Ala Thr Pro Glu Ala Leu Met Phe Ser Gln Phe Gln Leu
 195 200 205

Asp Gly Gln Trp Ile Phe Ala Met Asp Ser Gly Val Glu Gln Asp Phe
 210 215 220

Thr Phe Ser Glu Gly Val Ser Leu Met Tyr Glu Ala His Gly Gln Glu
 225 230 235 240

Glu Leu Asp Ala Ile Trp Asn Ala Leu Ser Ala Val Pro Glu Ala Glu
 245 250 255

Ala Cys Gly Trp Leu Lys Asp Lys Phe Gly Val Ser Trp Gln Ile Val
260 265 270

Pro Asp Asn Met Glu Glu Leu Met Ala Lys Pro Gly Ala Tyr Glu Lys
275 280 285

Leu Leu Ala Met Lys Lys Ile Asn Ile Ala Glu Phe
290 295 300

<210> 733

<211> 1302

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1279)

<223> RXN01696

<400> 733

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acagaccttt gtgcggcttc cttttctagg agcatgtaac ttg tct acc cca atc 115
Leu Ser Thr Pro Ile
1 5

ggc ctt ggc ctt cct ccg acc cca cct cca gtg ttg gcg cca cgt cgt 163
Gly Leu Gly Leu Pro Pro Thr Pro Pro Val Leu Ala Pro Arg Arg
10 15 20

aaa aca cgc caa ctc atg gtc ggc aaa gtg ggc gtt ggt tgc gat cac 211
Lys Thr Arg Gln Leu Met Val Gly Lys Val Gly Val Gly Ser Asp His
25 30 35

ccg att tcc gtc cag tgc atg acc acc acc aaa acc cac gac atc aac 259
Pro Ile Ser Val Gln Ser Met Thr Thr Thr Lys Thr His Asp Ile Asn
40 45 50

ggc acc ctg caa cag atc gca cag ttg aca gcc acc ggt tgt gac atc 307
Gly Thr Leu Gln Gln Ile Ala Gln Leu Thr Ala Thr Gly Cys Asp Ile
55 60 65

gtc cgc gtt gcc tgc cca aag act gtt gat gcg gaa gca ctg ccg atc 355
Val Arg Val Ala Cys Pro Lys Thr Val Asp Ala Glu Ala Leu Pro Ile
70 75 80 85

atc gca aag aag tct ccg atc cca gtg atc gca gat atc cac ttc cag 403
Ile Ala Lys Lys Ser Pro Ile Pro Val Ile Ala Asp Ile His Phe Gln
90 95 100

ccc aag tac atc ttc gcg gca atc gat gca ggt tgc gcc gcc gtt cgt 451
Pro Lys Tyr Ile Phe Ala Ala Ile Asp Ala Gly Cys Ala Ala Val Arg
105 110 115

gtg aac cca ggc aac atc aag gaa ttc gat ggt cgc gtt aaa gaa gta 499
Val Asn Pro Gly Asn Ile Lys Glu Phe Asp Gly Arg Val Lys Glu Val
120 125 130

gca aaa gct gca ggc gat gcc gga att cca att cgt att ggt gtc aac 547

Ala Lys Ala Ala Gly Asp Ala Gly Ile Pro Ile Arg Ile Gly Val Asn	
135 140 145	
ggc gga tcc ctg gat aag cgc atc ctg gac aaa tac cac ggc aaa gcc	595
Gly Gly Ser Leu Asp Lys Arg Ile Leu Asp Lys Tyr His Gly Lys Ala	
150 155 160 165	
acc cca gaa gct ctc gtg gaa tcc gca atg tgg gaa gcc ggc ctg ttt	643
Thr Pro Glu Ala Leu Val Glu Ser Ala Met Trp Glu Ala Gly Leu Phe	
170 175 180	
gaa gag cac ggc ttc ggc gac atc gca atc tct gtg aag cac tcc gac	691
Glu Glu His Gly Phe Gly Asp Ile Ala Ile Ser Val Lys His Ser Asp	
185 190 195	
cca gta ctc atg gtg gag gcc tac cgc cag ctc gct gaa caa agc gac	739
Pro Val Leu Met Val Glu Ala Tyr Arg Gln Leu Ala Gln Ser Asp	
200 205 210	
tac cca ctg cac ctc ggt gtt act gaa gct ggt ccc aag ttc atg gga	787
Tyr Pro Leu His Leu Gly Val Thr Glu Ala Gly Pro Lys Phe Met Gly	
215 220 225	
aca atc aag tct tcc gta gca ttc ggc gct ctg ctg tcc cag ggc atc	835
Thr Ile Lys Ser Ser Val Ala Phe Gly Ala Leu Leu Ser Gln Gly Ile	
230 235 240 245	
ggc gac act atc cgt gtg tct ctt tct gct gac cca gtg gaa gaa atc	883
Gly Asp Thr Ile Arg Val Ser Leu Ser Ala Asp Pro Val Glu Glu Ile	
250 255 260	
aag gtt ggc gac cag att ctg cag tcc ctc aac ctg cgc cca cgc aag	931
Lys Val Gly Asp Gln Ile Leu Gln Ser Leu Asn Leu Arg Pro Arg Lys	
265 270 275	
ctg gaa atc gtg tcc tgc cca tca tgt ggc cgc gca cag gtc gat gtg	979
Leu Glu Ile Val Ser Cys Pro Ser Cys Gly Arg Ala Gln Val Asp Val	
280 285 290	
tac tca ctt gct gaa gaa gtc acc gaa gca ctc gac ggc atg gaa gtt	1027
Tyr Ser Leu Ala Glu Glu Val Thr Glu Ala Leu Asp Gly Met Glu Val	
295 300 305	
cca ctg cgc gtc gct gtc atg ggt tgc gtt gtt aac ggc cca ggt gag	1075
Pro Leu Arg Val Ala Val Met Gly Cys Val Val Asn Gly Pro Gly Glu	
310 315 320 325	
gct cgc gac gct gac ctc ggt gtt gca tcc ggt aac ggc aag ggc cag	1123
Ala Arg Asp Ala Asp Leu Gly Val Ala Ser Gly Asn Gly Lys Gly Gln	
330 335 340	
atc ttt gtc aag ggc gaa gtc atc aag act gtc cca gaa tcc cag atc	1171
Ile Phe Val Lys Gly Glu Val Ile Lys Thr Val Pro Glu Ser Gln Ile	
345 350 355	
gtg gaa acc ctc atc gaa gaa gca atg cgt atc gca gag gaa atg gac	1219
Val Glu Thr Leu Ile Glu Glu Ala Met Arg Ile Ala Glu Glu Met Asp	
360 365 370	
cca gaa gtc ctc gct gca gca agt gct tcc ggt atg aag gct gaa gtg	1267
Pro Glu Val Leu Ala Ala Ala Ser Ala Ser Gly Met Lys Ala Glu Val	

375

380

385

aag gta acc aag taagttttgg ttaattaagg cac
Lys Val Thr Lys
390

1302

<210> 734

<211> 393

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 734

Leu Ser Thr Pro Ile Gly Leu Gly Leu Pro Pro Thr Pro Pro Pro Val
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Leu Ala Pro Arg Arg Lys Thr Arg Gln Leu Met Val Gly Lys Val Gly
20 25 30

Val Gly Ser Asp His Pro Ile Ser Val Gln Ser Met Thr Thr Thr Lys
35 40 45

Thr His Asp Ile Asn Gly Thr Leu Gln Gln Ile Ala Gln Leu Thr Ala
50 55 60

Thr Gly Cys Asp Ile Val Arg Val Ala Cys Pro Lys Thr Val Asp Ala
65 70 75 80

Glu Ala Leu Pro Ile Ile Ala Lys Lys Ser Pro Ile Pro Val Ile Ala
85 90 95

Asp Ile His Phe Gln Pro Lys Tyr Ile Phe Ala Ala Ile Asp Ala Gly
100 105 110

Cys Ala Ala Val Arg Val Asn Pro Gly Asn Ile Lys Glu Phe Asp Gly
115 120 125

Arg Val Lys Glu Val Ala Lys Ala Ala Gly Asp Ala Gly Ile Pro Ile
130 135 140

Arg Ile Gly Val Asn Gly Gly Ser Leu Asp Lys Arg Ile Leu Asp Lys
145 150 155 160

Tyr His Gly Lys Ala Thr Pro Glu Ala Leu Val Glu Ser Ala Met Trp
165 170 175

Glu Ala Gly Leu Phe Glu Glu His Gly Phe Gly Asp Ile Ala Ile Ser
180 185 190

Val Lys His Ser Asp Pro Val Leu Met Val Glu Ala Tyr Arg Gln Leu
195 200 205

Ala Glu Gln Ser Asp Tyr Pro Leu His Leu Gly Val Thr Glu Ala Gly
210 215 220

Pro Lys Phe Met Gly Thr Ile Lys Ser Ser Val Ala Phe Gly Ala Leu
225 230 235 240

Leu Ser Gln Gly Ile Gly Asp Thr Ile Arg Val Ser Leu Ser Ala Asp
245 250 255

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Pro Val Glu Glu Ile Lys Val Gly Asp Gln Ile Leu Gln Ser Leu Asn
      260                      265                      270

Leu Arg Pro Arg Lys Leu Glu Ile Val Ser Cys Pro Ser Cys Gly Arg
      275                      280                      285

Ala Gln Val Asp Val Tyr Ser Leu Ala Glu Glu Val Thr Glu Ala Leu
      290                      295                      300

Asp Gly Met Glu Val Pro Leu Arg Val Ala Val Met Gly Cys Val Val
      305                      310                      315                      320

Asn Gly Pro Gly Glu Ala Arg Asp Ala Asp Leu Gly Val Ala Ser Gly
      325                      330                      335

Asn Gly Lys Gly Gln Ile Phe Val Lys Gly Glu Val Ile Lys Thr Val
      340                      345                      350

Pro Glu Ser Gln Ile Val Glu Thr Leu Ile Glu Glu Ala Met Arg Ile
      355                      360                      365

Ala Glu Glu Met Asp Pro Glu Val Leu Ala Ala Ala Ser Ala Ser Gly
      370                      375                      380

Met Lys Ala Glu Val Lys Val Thr Lys
      385                      390

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<210> 735
<211> 620
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (1)..(597)
<223> PRXA01696

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His Ser Asp Pro Val Leu Met Val Glu Ala Tyr Arg Gln Leu Ala Glu
1 5 10 15

caa agc gac tac cca ctg cac ctc ggt gtt act gaa gct ggt ccc aag 96
Gln Ser Asp Tyr Pro Leu His Leu Gly Val Thr Glu Ala Gly Pro Lys
20 25 30

ttc atg gga aca atc aag tct tcc gta gca ttc ggc gct ctg ctg tcc 144
Phe Met Gly Thr Ile Lys Ser Ser Val Ala Phe Gly Ala Leu Leu Ser
35 40 45

cag ggc atc ggc gac act atc cgt gtg tct ctt tct gct gac cca gtg 192
Gln Gly Ile Gly Asp Thr Ile Arg Val Ser Leu Ser Ala Asp Pro Val
50 55 60

gaa gaa atc aag gtt ggc gac cag att ctg cag tcc ctc aac ctg cgc 240
Glu Glu Ile Lys Val Gly Asp Gln Ile Leu Gln Ser Leu Asn Leu Arg
65 70 75 80

cca cgc aag ctg gaa atc gtg tcc tgc cca tca tgt ggc cgc gca cag 288
Pro Arg Lys Leu Glu Ile Val Ser Cys Pro Ser Cys Gly Arg Ala Gln

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	85	90	95	
gtc gat gtg tac tca ctt gct gaa gaa gtc acc gaa gca ctc gac ggc				336
Val Asp Val Tyr Ser Leu Ala Glu Glu Val Thr Glu Ala Leu Asp Gly				
	100	105	110	
atg gaa gtt cca ctg cgc gtc gct gtc atg ggt tgc gtt gtt aac ggc				384
Met Glu Val Pro Leu Arg Val Ala Val Met Gly Cys Val Val Asn Gly				
	115	120	125	
cca ggt gag gct cgc gac gct gac ctc ggt gtt gca tcc ggt aac ggc				432
Pro Gly Glu Ala Arg Asp Ala Asp Leu Gly Val Ala Ser Gly Asn Gly				
	130	135	140	
aag ggc cag atc ttt gtc aag ggc gaa gtc atc aag act gtc cca gaa				480
Lys Gly Gln Ile Phe Val Lys Gly Glu Val Ile Lys Thr Val Pro Glu				
	145	150	155	160
tcc cag atc gtg gaa acc ctc atc gaa gaa gca atg cgt atc gca gag				528
Ser Gln Ile Val Glu Thr Leu Ile Glu Glu Ala Met Arg Ile Ala Glu				
	165	170	175	
gaa atg gac cca gaa gtc ctc gct gca gca agt gct tcc ggt atg aag				576
Glu Met Asp Pro Glu Val Leu Ala Ala Ser Ala Ser Gly Met Lys				
	180	185	190	
gct gaa gtg aag gta acc aag taagttttgg ttaattaagg cac				620
Ala Glu Val Lys Val Thr Lys				
	195			
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<213> Corynebacterium glutamicum				
<400> 736				
His Ser Asp Pro Val Leu Met Val Glu Ala Tyr Arg Gln Leu Ala Glu				
	1	5	10	15
Gln Ser Asp Tyr Pro Leu His Leu Gly Val Thr Glu Ala Gly Pro Lys				
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Phe Met Gly Thr Ile Lys Ser Ser Val Ala Phe Gly Ala Leu Leu Ser				
	35	40	45	
Gln Gly Ile Gly Asp Thr Ile Arg Val Ser Leu Ser Ala Asp Pro Val				
	50	55	60	
Glu Glu Ile Lys Val Gly Asp Gln Ile Leu Gln Ser Leu Asn Leu Arg				
	65	70	75	80
Pro Arg Lys Leu Glu Ile Val Ser Cys Pro Ser Cys Gly Arg Ala Gln				
	85	90	95	
Val Asp Val Tyr Ser Leu Ala Glu Glu Val Thr Glu Ala Leu Asp Gly				
	100	105	110	
Met Glu Val Pro Leu Arg Val Ala Val Met Gly Cys Val Val Asn Gly				
	115	120	125	

Pro Gly Glu Ala Arg Asp Ala Asp Leu Gly Val Ala Ser Gly Asn Gly
 130 135 140

Lys Gly Gln Ile Phe Val Lys Gly Glu Val Ile Lys Thr Val Pro Glu
 145 150 155 160

Ser Gln Ile Val Glu Thr Leu Ile Glu Glu Ala Met Arg Ile Ala Glu
 165 170 175

Glu Met Asp Pro Glu Val Leu Ala Ala Ser Ala Ser Gly Met Lys
 180 185 190

Ala Glu Val Lys Val Thr Lys
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<210> 737
 <211> 1080
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1057)
 <223> RXN01697

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cccgattaaa aaatgccccc gcgcaacgaa actagtaatc atg ttt caa gga cta 115
 Met Phe Gln Gly Leu
 1 5

aaa gaa ctc acc gca gca aaa ggc cgc acg ctg ctg atc acc gtc acc 163
 Lys Glu Leu Thr Ala Ala Lys Gly Arg Thr Leu Leu Ile Thr Val Thr
 10 15 20

gtc ggg ctg atc gcc gtg ctg gtt act ttc ctc tct gcc ctc acc gcc 211
 Val Gly Leu Ile Ala Val Leu Val Thr Phe Leu Ser Ala Leu Thr Ala
 25 30 35

ggg ctt ggc cac caa tca gta tcc gca ctg aaa tac cta gcg ggt gat 259
 Gly Leu Gly His Gln Ser Val Ser Ala Leu Lys Tyr Leu Ala Gly Asp
 40 45 50

aat gaa ctt atc ctc gcc gat tcc gga tcc acc acg ctt tcc gcg tcc 307
 Asn Glu Leu Ile Leu Ala Asp Ser Gly Ser Thr Thr Leu Ser Ala Ser
 55 60 65

acg ctt tct gat caa gca gtt gcc caa ctc gaa gac gaa ggc gca cag 355
 Thr Leu Ser Asp Gln Ala Val Ala Gln Leu Glu Asp Glu Gly Ala Gln
 70 75 80 85

atg ctg tgg cag gtc cgc gac cga gta gca gac acc ccc acc atg ctc 403
 Met Leu Trp Gln Val Arg Asp Arg Val Ala Asp Thr Pro Thr Met Leu
 90 95 100

ctc aac tcc cct gac ctt gcg cct ggt gaa gta tcc ctt cct gcc gaa 451
 Leu Asn Ser Pro Asp Leu Ala Pro Gly Glu Val Ser Leu Pro Ala Glu
 105 110 115

ctc gct gat tgc gaa ctc gct act gcg cat gat gta gtg gat tct tcc 499
 Leu Ala Asp Ser Glu Leu Ala Thr Ala His Asp Val Val Asp Ser Ser
 120 125 130

aac gat ctg tac ctc gat cac ctg ccc gtg gta ttg atg aac acc tcc 547
 Asn Asp Leu Tyr Leu Asp His Leu Pro Val Val Leu Met Asn Thr Ser
 135 140 145

gat tta gcc tca ctc gcg caa gtc cga ggc gtg aca gga cca gca ggc 595
 Asp Leu Ala Ser Leu Ala Gln Val Arg Gly Val Thr Gly Pro Ala Gly
 150 155 160 165

gca ttc gcc tct gac gtt gcg ctc ccc tcc gac acc gtt gcg ctc tct 643
 Ala Phe Ala Ser Asp Val Ala Leu Pro Ser Asp Thr Val Ala Leu Ser
 170 175 180

gga tcc gaa cgg tgg aac gca tcc gcc tcc tac cag gcc gaa cag atg 691
 Gly Ser Glu Arg Trp Asn Ala Ser Ala Ser Tyr Gln Gly Glu Gln Met
 185 190 195

tca ctc aac ctc atg atc gtc atg ctg tat gtt atc tcc gca ctc gtg 739
 Ser Leu Asn Leu Met Ile Val Met Leu Tyr Val Ile Ser Ala Leu Val
 200 205 210

ctc gcc gca ttc ttc acc gtc tgg acc atc caa cgc ctc cgc gcc atc 787
 Leu Gly Ala Phe Phe Thr Val Trp Thr Ile Gln Arg Leu Arg Gly Ile
 215 220 225

gcc atc tct agt gct ttg gga gca gcc cgc cga gta ctt atc gcc gac 835
 Ala Ile Ser Ser Ala Leu Gly Ala Ala Arg Arg Val Leu Ile Ala Asp
 230 235 240 245

gct ctc gcc caa gcc atc atc gtc tta gga atc gcc atc acc gca gcc 883
 Ala Leu Gly Gln Ala Ile Ile Val Leu Gly Ile Gly Ile Thr Ala Gly
 250 255 260

aca ttg atc aca gtc atc tcc gca ttc gcc atg gga gac gca atg ccc 931
 Thr Leu Ile Thr Val Ile Ser Ala Phe Gly Met Gly Asp Ala Met Pro
 265 270 275

gtg gtc atc tcc tcc tcc acc acg ctc ttc ccc gca ctt atc ctc gcc 979
 Val Val Ile Ser Ser Ser Thr Thr Leu Phe Pro Ala Leu Ile Leu Ala
 280 285 290

gca gca gga ctc atc ggt gcc gcc att tca ctc gcc ccc atc ctt cgc 1027
 Ala Ala Gly Leu Ile Gly Ala Ala Ile Ser Leu Gly Pro Ile Leu Arg
 295 300 305

gtc gaa cca cgc tcc gca ctc atg aac gca taagaaaagg aacgtcacat 1077
 Val Glu Pro Arg Ser Ala Leu Met Asn Ala
 310 315

gac 1080

<210> 738

<211> 319

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 738

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Met Phe Gln Gly Leu Lys Glu Leu Thr Ala Ala Lys Gly Arg Thr Leu
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Leu Ile Thr Val Thr Val Gly Leu Ile Ala Val Leu Val Thr Phe Leu
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Ser Ala Leu Thr Ala Gly Leu Gly His Gln Ser Val Ser Ala Leu Lys
      35           40           45

Tyr Leu Ala Gly Asp Asn Glu Leu Ile Leu Ala Asp Ser Gly Ser Thr
  50           55           60

Thr Leu Ser Ala Ser Thr Leu Ser Asp Gln Ala Val Ala Gln Leu Glu
  65           70           75           80

Asp Glu Gly Ala Gln Met Leu Trp Gln Val Arg Asp Arg Val Ala Asp
      85           90           95

Thr Pro Thr Met Leu Leu Asn Ser Pro Asp Leu Ala Pro Gly Glu Val
  100           105           110

Ser Leu Pro Ala Glu Leu Ala Asp Ser Glu Leu Ala Thr Ala His Asp
      115           120           125

Val Val Asp Ser Ser Asn Asp Leu Tyr Leu Asp His Leu Pro Val Val
  130           135           140

Leu Met Asn Thr Ser Asp Leu Ala Ser Leu Ala Gln Val Arg Gly Val
  145           150           155           160

Thr Gly Pro Ala Gly Ala Phe Ala Ser Asp Val Ala Leu Pro Ser Asp
      165           170           175

Thr Val Ala Leu Ser Gly Ser Glu Arg Trp Asn Ala Ser Ala Ser Tyr
  180           185           190

Gln Gly Glu Gln Met Ser Leu Asn Leu Met Ile Val Met Leu Tyr Val
  195           200           205

Ile Ser Ala Leu Val Leu Gly Ala Phe Phe Thr Val Trp Thr Ile Gln
  210           215           220

Arg Leu Arg Gly Ile Ala Ile Ser Ser Ala Leu Gly Ala Ala Arg Arg
  225           230           235           240

Val Leu Ile Ala Asp Ala Leu Gly Gln Ala Ile Ile Val Leu Gly Ile
      245           250           255

Gly Ile Thr Ala Gly Thr Leu Ile Thr Val Ile Ser Ala Phe Gly Met
  260           265           270

Gly Asp Ala Met Pro Val Val Ile Ser Ser Ser Thr Thr Leu Phe Pro
  275           280           285

Ala Leu Ile Leu Ala Ala Ala Gly Leu Ile Gly Ala Ala Ile Ser Leu
  290           295           300

Gly Pro Ile Leu Arg Val Glu Pro Arg Ser Ala Leu Met Asn Ala
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<210> 739
 <211> 826
 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <221> CDS
 <222> (101)..(826)
 <223> FRXA01697

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 Met Phe Gln Gly Leu
 1 5
 aaa gaa ctc acc gca gca aaa ggc cgc acg ctg ctg atc acc gtc acc 163
 Lys Glu Leu Thr Ala Ala Lys Gly Arg Thr Leu Leu Ile Thr Val Thr
 10 15 20
 gtc ggg ctg atc gcc gtg ctg gtt act ttc ctc tct gcc ctc acc gcc 211
 Val Gly Leu Ile Ala Val Leu Val Thr Phe Leu Ser Ala Leu Thr Ala
 25 30 35
 ggg ctt ggc cac caa tca gta tcc gca ctg aaa tac cta gcg ggt gat 259
 Gly Leu Gly His Gln Ser Val Ser Ala Leu Lys Tyr Leu Ala Gly Asp
 40 45 50
 aat gaa ctt atc ctc gcc gat tcc gga tcc acc acg ctt tcc gcg tcc 307
 Asn Glu Leu Ile Leu Ala Asp Ser Gly Ser Thr Leu Ser Ala Ser
 55 60 65
 acg ctt tct gat caa gca gtt gcc caa ctc gaa gac gaa ggc gca cag 355
 Thr Leu Ser Asp Gln Ala Val Ala Gln Leu Glu Asp Glu Gly Ala Gln
 70 75 80 85
 atg ctg tgg cag gtc cgc gac cga gta gca gac acc ccc acc atg ctc 403
 Met Leu Trp Gln Val Arg Asp Arg Val Ala Asp Thr Pro Thr Met Leu
 90 95 100
 ctc aac tcc cct gac ctt gcg cct ggt gaa gta tcc ctt cct gcc gaa 451
 Leu Asn Ser Pro Asp Leu Ala Pro Gly Glu Val Ser Leu Pro Ala Glu
 105 110 115
 ctc gct gat tcg gaa ctc gct act gcg cat gat gta gtg gat tct tcc 499
 Leu Ala Asp Ser Glu Leu Ala Thr Ala His Asp Val Val Asp Ser Ser
 120 125 130
 aac gat ctg tac ctc gat cac ctg ccc gtg gta ttg atg aac acc tcc 547
 Asn Asp Leu Tyr Leu Asp His Leu Pro Val Val Leu Met Asn Thr Ser
 135 140 145
 gat tta gcc tca ctc gcg caa gtc cga ggc gtg aca gga cca gca ggc 595
 Asp Leu Ala Ser Leu Ala Gln Val Arg Gly Val Thr Gly Pro Ala Gly
 150 155 160 165
 gca ttc gcc tct gac gtt gcg ctc ccc tcc gac acc gtt gcg ctc tct 643
 Ala Phe Ala Ser Asp Val Ala Leu Pro Ser Asp Thr Val Ala Leu Ser
 170 175 180

gga tcc gaa cgg tgg aac gca tcc gcc tcc tac cag ggc gaa cag atg 691
 Gly Ser Glu Arg Trp Asn Ala Ser Ala Ser Tyr Gln Gly Glu Gln Met
 185 190 195

tca ctc aac ctc atg atc gtc atg ctg tat gtc atc tcc gca ctc gtg 739
 Ser Leu Asn Leu Met Ile Val Met Leu Tyr Val Ile Ser Ala Leu Val
 200 205 210

ctc ggc gca ttc ttc acc gtc tgg acc atc caa cgc ctc cgc ggc atc 787
 Leu Gly Ala Phe Phe Thr Val Trp Thr Ile Gln Arg Leu Arg Gly Ile
 215 220 225

gcc atc tct agt gct ttg gga gca gcc cgc cga gta ctt 826
 Ala Ile Ser Ser Ala Leu Gly Ala Ala Arg Arg Val Leu
 230 235 240

<210> 740

<211> 242

<212> PRT

<213> Corynebacterium glutamicum

<400> 740

Met Phe Gln Gly Leu Lys Glu Leu Thr Ala Ala Lys Gly Arg Thr Leu
 1 5 10 15

Leu Ile Thr Val Thr Val Gly Leu Ile Ala Val Leu Val Thr Phe Leu
 20 25 30

Ser Ala Leu Thr Ala Gly Leu Gly His Gln Ser Val Ser Ala Leu Lys
 35 40 45

Tyr Leu Ala Gly Asp Asn Glu Leu Ile Leu Ala Asp Ser Gly Ser Thr
 50 55 60

Thr Leu Ser Ala Ser Thr Leu Ser Asp Gln Ala Val Ala Gln Leu Glu
 65 70 75 80

Asp Glu Gly Ala Gln Met Leu Trp Gln Val Arg Asp Arg Val Ala Asp
 85 90 95

Thr Pro Thr Met Leu Leu Asn Ser Pro Asp Leu Ala Pro Gly Glu Val
 100 105 110

Ser Leu Pro Ala Glu Leu Ala Asp Ser Glu Leu Ala Thr Ala His Asp
 115 120 125

Val Val Asp Ser Ser Asn Asp Leu Tyr Leu Asp His Leu Pro Val Val
 130 135 140

Leu Met Asn Thr Ser Asp Leu Ala Ser Leu Ala Gln Val Arg Gly Val
 145 150 155 160

Thr Gly Pro Ala Gly Ala Phe Ala Ser Asp Val Ala Leu Pro Ser Asp
 165 170 175

Thr Val Ala Leu Ser Gly Ser Glu Arg Trp Asn Ala Ser Ala Ser Tyr
 180 185 190

Gln Gly Glu Gln Met Ser Leu Asn Leu Met Ile Val Met Leu Tyr Val
 195 200 205

Ile Ser Ala Leu Val Leu Gly Ala Phe Phe Thr Val Trp Thr Ile Gln
210 215 220

Arg Leu Arg Gly Ile Ala Ile Ser Ser Ala Leu Gly Ala Ala Arg Arg
225 230 235 240

Val Leu

<210> 741

<211> 472

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(472)

<223> RXN01701

<400> 741

gccgatcaaa ttcattgatt gttaatcgga agttttttga acaggtaaag ctatggggacc 60

tggtcagtgct ctgttgccgg atgtattaag gagaatgccc atg ctg agc cac gaa 115
Met Leu Ser His Glu
1 5

gaa att gtt gcg atc gca gaa gat ttg ctg tct aaa cgc tac ggc ggt 163
Glu Ile Val Ala Ile Ala Glu Asp Leu Ser Lys Arg Tyr Gly Gly
10 15 20

gta caa act ctt tct gac gtg gag cag ctc aac ggt tcc ggc acc tcc 211
Val Gln Thr Leu Ser Asp Val Glu Gln Leu Asn Gly Ser Gly Thr Ser
25 30 35

gcg gtg ctg cgt gcc agg gtg gct aac tcc cca ttc ctc caa cag cgc 259
Ala Val Leu Arg Ala Arg Val Ala Asn Ser Pro Phe Leu Gln Gln Arg
40 45 50

tcc gtg gtg ctg aag tac gtg ccc agc acc gga gac gtc ttt gat gat 307
Ser Val Val Leu Lys Tyr Val Pro Ser Thr Gly Asp Val Phe Asp Asp
55 60 65

tct gcg ctg gtg cgt gaa atc gtc tcc tac cag ttc acc acc tcc ttg 355
Ser Ala Leu Val Arg Glu Ile Val Ser Tyr Phe Thr Thr Ser Leu
70 75 80 85

tcg gaa gat gtc cgc cca ggg cca gtc att ttg gcc tat gac att gac 403
Ser Glu Asp Val Arg Pro Gly Pro Val Ile Leu Ala Tyr Asp Ile Asp
90 95 100

aag cgc atc ctg gtc att tca gat tcc ggc aac ggc gac acc ttt gcg 451
Lys Arg Ile Leu Val Ile Ser Asp Ser Gly Asn Gly Asp Thr Phe Ala
105 110 115

gat ctg atc gat cag cgt ccg 472
Asp Leu Ile Asp Gln Arg Pro
120

<210> 742
 <211> 124
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 742
 Met Leu Ser His Glu Glu Ile Val Ala Ile Ala Glu Asp Leu Leu Ser
 1 5 10 15
 Lys Arg Tyr Gly Gly Val Gln Thr Leu Ser Asp Val Glu Gln Leu Asn
 20 25 30
 Gly Ser Gly Thr Ser Ala Val Leu Arg Ala Arg Val Ala Asn Ser Pro
 35 40 45
 Phe Leu Gln Gln Arg Ser Val Val Leu Lys Tyr Val Pro Ser Thr Gly
 50 55 60
 Asp Val Phe Asp Asp Ser Ala Leu Val Arg Glu Ile Val Ser Tyr Gln
 65 70 75 80
 Phe Thr Thr Ser Leu Ser Glu Asp Val Arg Pro Gly Pro Val Ile Leu
 85 90 95
 Ala Tyr Asp Ile Asp Lys Arg Ile Leu Val Ile Ser Asp Ser Gly Asn
 100 105 110
 Gly Asp Thr Phe Ala Asp Leu Ile Asp Gln Arg Pro
 115 120

<210> 743
 <211> 433
 <212> DNA
 <213> *Corynebacterium glutamicum*
 <220>
 <221> CDS
 <222> (101)..(433)
 <223> FRXA01701

<400> 743
 gccgatcaaa ttcattgatt gttaaatcgga agttttttga acaggtaaag ctatggggacc 60
 tgttcagtgct ctgttgccgg atgtattaag gagaatgccc atg ctg agc cac gaa 115
 Met Leu Ser His Glu
 1 5
 gaa att gtt gcg atc gca gaa gat ttg ctg tct aaa cgc tac ggc ggt 163
 Glu Ile Val Ala Ile Ala Glu Asp Leu Leu Ser Lys Arg Tyr Gly Gly
 10 15 20
 gta caa act ctt tct gac gtg gag cag ctc aac ggt tcc ggc acc tcc 211
 Val Gln Thr Leu Ser Asp Val Glu Gln Leu Asn Gly Ser Gly Thr Ser
 25 30 35
 gcg gtg ctg cgt gcc agg gtg gct aac tcc cca ttc ctc caa cag cgc 259
 Ala Val Leu Arg Ala Arg Val Ala Asn Ser Pro Phe Leu Gln Gln Arg
 40 45 50
 tcc gtg gtg ctg aag tac gtg ccc agc acc gga gac gtc ttt gat gat 307

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Ser Val Val Leu Lys Tyr Val Pro Ser Thr Gly Asp Val Phe Asp Asp
  55                      60                      65
tct gcg ctg gtg cgt gaa atc gtc tcc tac cag ttc acc acc tcc ttg 355
Ser Ala Leu Val Arg Glu Ile Val Ser Tyr Gln Phe Thr Thr Ser Leu
  70                      75                      80                      85
tcg gaa gat gtc cgc cca ggg cca gtc att ttg gcc tat gac att gac 403
Ser Glu Asp Val Arg Pro Gly Pro Val Ile Leu Ala Tyr Asp Ile Asp
                      90                      95                      100

aag cgc atc ctg gtc att tca gat tcc ggc 433
Lys Arg Ile Leu Val Ile Ser Asp Ser Gly
      105                      110

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<210> 744
<211> 111
<212> PRT
<213> Corynebacterium glutamicum

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<400> 744
Met Leu Ser His Glu Glu Ile Val Ala Ile Ala Glu Asp Leu Leu Ser
  1                      5                      10                      15
Lys Arg Tyr Gly Gly Val Gln Thr Leu Ser Asp Val Glu Gln Leu Asn
                      20                      25                      30
Gly Ser Gly Thr Ser Ala Val Leu Arg Ala Arg Val Ala Asn Ser Pro
                      35                      40                      45
Phe Leu Gln Gln Arg Ser Val Val Leu Lys Tyr Val Pro Ser Thr Gly
  50                      55                      60
Asp Val Phe Asp Asp Ser Ala Leu Val Arg Glu Ile Val Ser Tyr Gln
  65                      70                      75                      80
Phe Thr Thr Ser Leu Ser Glu Asp Val Arg Pro Gly Pro Val Ile Leu
                      85                      90                      95
Ala Tyr Asp Ile Asp Lys Arg Ile Leu Val Ile Ser Asp Ser Gly
      100                      105                      110

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<210> 745
<211> 1236
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(1213)
<223> RXN01703

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<400> 745
gttagacaaa tgggtaaaca gagctgacct agcgggaatcc gccatcaacg aaaggcattc 60
cgcgagggtt tgggggtctgc ctogaacaaa tcttggggtt gtg gca tgg cca tcc 115
Val Ala Trp Pro Ser
      1                      5

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aac gcc aaa gaa aaa ctg ttt atc cac tgg cac tac tgg tgg caa gcg 163
 Asn Ala Lys Glu Lys Leu Phe Ile His Trp His Tyr Trp Trp Gln Ala
 10 15 20

cat tat cta gac tgc ctg gtg gat gct gct cgt cga cgc acc aca aag 211
 His Tyr Leu Asp Cys Leu Val Asp Ala Arg Arg Arg Thr Lys
 25 30 35

gcc cgt cgc gac cgc atc agg gac acc atc cgc ggc att tgc gtg cgc 259
 Ala Arg Arg Asp Arg Ile Arg Asp Thr Ile Arg Gly Ile Ser Val Arg
 40 45 50

aat gtg ggc aag ctg acc tgc aat cgt tat tac gac gac aaa gct tgg 307
 Asn Val Gly Lys Leu Thr Ser Asn Arg Tyr Tyr Asp Asp Lys Ala Trp
 55 60 65

ctg gcc ctt gct ctt ggg cgt gcc gga aaa gtg cga aag gtg cgc aca 355
 Leu Ala Leu Ala Leu Gly Arg Ala Gly Lys Val Arg Lys Val Arg Thr
 70 75 80 85

cca aaa tca ttg ccc tgc ttg gaa caa aac atc gtc gat ggc att gat 403
 Pro Lys Ser Leu Pro Ser Leu Glu Gln Asn Ile Val Asp Gly Ile Asp
 90 95 100

tcc ctt act ggt gtg ctg ccg tgg cgt tcc gcc gaa acc ttc tac aac 451
 Ser Leu Thr Gly Val Leu Pro Trp Arg Ser Gly Glu Thr Phe Tyr Asn
 105 110 115

gtt ccc tcc aac ggt cct gct gcg atc atg atg gcc cgc acc gac cgt 499
 Val Pro Ser Asn Gly Pro Ala Ala Ile Met Met Ala Arg Thr Asp Arg
 120 125 130

ttg gac gag gct atg aaa atc acc gat tgg att ttt gac aac ctg atc 547
 Leu Asp Glu Ala Met Lys Ile Thr Asp Trp Ile Phe Asp Asn Leu Ile
 135 140 145

gat ggc gac ggc ctt gtg atg gac gga ttg cgc atg cgc atg cac gga 595
 Asp Gly Asp Gly Leu Val Met Asp Gly Leu Arg Met Arg Met His Gly
 150 155 160 165

cct gag ctt gtc cgt tcc atc cac ccg tat tgc caa ggt gtc gcc att 643
 Pro Glu Leu Val Arg Ser Ile His Pro Tyr Cys Gln Gly Val Ala Ile
 170 175 180

ggt gcg tgt ttg gaa att gct ctc aaa ctg cgt gag cgc gca ggc ttg 691
 Gly Ala Cys Leu Glu Ile Ala Leu Lys Leu Arg Glu Arg Ala Gly Leu
 185 190 195

acc act act gtg gtg gat cac tgg tgc gat gcc gat aag gca gaa gac 739
 Thr Thr Thr Val Val Asp His Trp Ser Asp Ala Asp Thr Ala Glu Asp
 200 205 210

tcc ctc aaa tac ttt gca cac atc cac gct gtg gtt cag gct gtg tgc 787
 Ser Leu Lys Tyr Phe Ala His Ile His Ala Val Val Gln Ala Val Ser
 215 220 225

cgg aag atg acc aac ttc cac gcc gtt att gat tgg gac acc ggt gac 835
 Arg Lys Met Thr Asn Phe His Gly Val Ile Asp Trp Asp Thr Gly Asp
 230 235 240 245

ggc gac ggc ggt ttg ttc aag ggc att ttg gtc cgc tat tta gct gat 883

Gly Asp Gly Gly Leu Phe Lys Gly Ile Leu Val Arg Tyr Leu Ala Asp
 250 255 260
 gtg gcc atc cgc ctg cct gac gat tca cca acc aac cgg gaa acc aaa 931
 Val Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr Asn Arg Glu Thr Lys
 265 270
 aag att gca gca cgc ctg gta ctg gaa tgc gcg gaa agc gta tgg aac 979
 Lys Ile Ala Ala Arg Leu Val Leu Glu Ser Ala Glu Ser Val Trp Asn
 280 285 290
 cac cga ttg gaa gtt gat ggc ctt ccg gta ttc gcc aca gac tgg aca 1027
 His Arg Leu Glu Val Asp Gly Leu Pro Val Phe Ala Thr Asp Trp Thr
 295 300 305
 acg gat gca cgc ctg cca caa aac ttt ggt ttg agt tcc tct agt ttg 1075
 Thr Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu Ser Ser Ser Ser Leu
 310 315 320 325
 agc gat ctg gtg agt gtt gtg cgc gtg gat gaa cgt gat ctg tcc gtg 1123
 Ser Asp Leu Val Ser Val Val Arg Val Asp Glu Arg Asp Leu Ser Val
 330 335 340
 caa ttg tcc ggt tgg atg ctc atg gaa gca gca gcg aaa gtg gcc gaa 1171
 Gln Leu Ser Gly Trp Met Leu Met Glu Ala Ala Ala Lys Val Ala Glu
 345 350 355
 gaa ctg gaa aac aac ggc aat agt tac acc ggt cgc tcc cga 1213
 Glu Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly Arg Ser Arg
 360 365 370
 tagccccgat agtgtatgtg ctg 1236

 <210> 746
 <211> 371
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 746
 Val Ala Trp Pro Ser Asn Ala Lys Glu Lys Leu Phe Ile His Trp His
 1 5 10 15
 Tyr Trp Trp Gln Ala His Tyr Leu Asp Cys Leu Val Asp Ala Ala Arg
 20 25 30
 Arg Arg Thr Thr Lys Ala Arg Arg Asp Arg Ile Arg Asp Thr Ile Arg
 35 40 45
 Gly Ile Ser Val Arg Asn Val Gly Lys Leu Thr Ser Asn Arg Tyr Tyr
 50 55 60
 Asp Asp Lys Ala Trp Leu Ala Leu Ala Leu Gly Arg Ala Gly Lys Val
 65 70 75 80
 Arg Lys Val Arg Thr Pro Lys Ser Leu Pro Ser Leu Glu Gln Asn Ile
 85 90 95
 Val Asp Gly Ile Asp Ser Leu Thr Gly Val Leu Pro Trp Arg Ser Gly
 100 105 110

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Glu Thr Phe Tyr Asn Val Pro Ser Asn Gly Pro Ala Ala Ile Met Met
115                               120

Ala Arg Thr Asp Arg Leu Asp Glu Ala Met Lys Ile Thr Asp Trp Ile
130                               135                               140

Phe Asp Asn Leu Ile Asp Gly Asp Gly Leu Val Met Asp Gly Leu Arg
145                               150                               155                               160

Met Arg Met His Gly Pro Glu Leu Val Arg Ser Ile His Pro Tyr Cys
165                               170                               175

Gln Gly Val Ala Ile Gly Ala Cys Leu Glu Ile Ala Leu Lys Leu Arg
180                               185                               190

Glu Arg Ala Gly Leu Thr Thr Thr Val Val Asp His Trp Ser Asp Ala
195                               200                               205

Asp Lys Ala Glu Asp Ser Leu Lys Tyr Phe Ala His Ile His Ala Val
210                               215                               220

Val Gln Ala Val Ser Arg Lys Met Thr Asn Phe His Gly Val Ile Asp
225                               230                               235                               240

Trp Asp Thr Gly Asp Gly Asp Gly Gly Leu Phe Lys Gly Ile Leu Val
245                               250                               255

Arg Tyr Leu Ala Asp Val Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr
260                               265                               270

Asn Arg Glu Thr Lys Lys Ile Ala Ala Arg Leu Val Leu Glu Ser Ala
275                               280                               285

Glu Ser Val Trp Asn His Arg Leu Glu Val Asp Gly Leu Pro Val Phe
290                               295                               300

Ala Thr Asp Trp Thr Thr Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu
305                               310                               315                               320

Ser Ser Ser Ser Leu Ser Asp Leu Val Ser Val Val Arg Val Asp Glu
325                               330                               335

Arg Asp Leu Ser Val Gln Leu Ser Gly Trp Met Leu Met Glu Ala Ala
340                               345                               350

Ala Lys Val Ala Glu Glu Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly
355                               360                               365

Arg Ser Arg
370

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<210> 747

<211> 494

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(471)

<223> FRXA01703

<400> 747
 ctc aaa tac ttt gca cac atc cac gct gtg gtt cag gct gtg tcg cgg 48
 Leu Lys Tyr Phe Ala His Ile His Ala Val Val Ser Arg
 1 5 10 15

aag atg acc aac ttc cac ggc gtt att gat tgg gac acc ggt gac ggc 96
 Lys Met Thr Asn Phe His Gly Val Ile Asp Trp Asp Thr Gly Asp Gly
 20 25 30

gac ggc ggt ttg ttc aag ggc att ttg gtc cgc tat tta gct gat gtg 144
 Asp Gly Gly Leu Phe Lys Gly Ile Leu Val Arg Tyr Leu Ala Asp Val
 35 40 45

gcc atc cgc ctg cct gac gat tca cca acc aac cgg gaa acc aaa aag 192
 Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr Asn Arg Glu Thr Lys Lys
 50 55 60

att gca gca cgc ctg gta ctg gaa tcg gcg gaa agc gta tgg aac cac 240
 Ile Ala Ala Arg Leu Val Leu Glu Ser Ala Glu Ser Val Trp Asn His
 65 70 75 80

cga ttg gaa gtt gat ggc ctt ccg gta ttc gcc aca gac tgg aca acg 288
 Arg Leu Glu Val Asp Gly Leu Pro Val Phe Ala Thr Asp Trp Thr Thr
 85 90 95

gat gca cgc ctg cca caa aac ttt ggt ttg agt tcc tct agt ttg agc 336
 Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu Ser Ser Ser Ser Leu Ser
 100 105 110

gat ctg gtg agt gtt gtg cgc gtg gat gaa cgt gat ctg tcc gtg caa 384
 Asp Leu Val Ser Val Val Arg Val Asp Glu Arg Asp Leu Ser Val Gln
 115 120 125

ttg tcc ggt tgg atg ctc atg gaa gca gca gcg aaa gtg gcc gaa gaa 432
 Leu Ser Gly Trp Met Leu Met Glu Ala Ala Ala Lys Val Ala Glu Glu
 130 135 140

ctg gaa aac aac ggc aat agt tac acc ggt cgc tcc cga tagccccgat 481
 Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly Arg Ser Arg
 145 150 155

agtgatgtg ctg 494

<210> 748

<211> 157

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 748

Leu Lys Tyr Phe Ala His Ile His Ala Val Val Gln Ala Val Ser Arg
 1 5 10 15

Lys Met Thr Asn Phe His Gly Val Ile Asp Trp Asp Thr Gly Asp Gly
 20 25 30

Asp Gly Gly Leu Phe Lys Gly Ile Leu Val Arg Tyr Leu Ala Asp Val
 35 40 45

Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr Asn Arg Glu Thr Lys Lys

50		55		60
Ile Ala Ala Arg Leu	Val Leu Glu Ser Ala Glu Ser Val Trp Asn His			
65	70	75	80	
Arg Leu Glu Val Asp	Gly Leu Pro Val Phe Ala Thr Asp Trp Thr Thr			
85	90	95		
Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu Ser Ser Ser Ser Leu Ser				
100	105	110		
Asp Leu Val Ser Val Val Arg Val Asp Glu Arg Asp Leu Ser Val Gln				
115	120	125		
Leu Ser Gly Trp Met Leu Met Glu Ala Ala Ala Lys Val Ala Glu Glu				
130	135	140		
Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly Arg Ser Arg				
145	150	155		

<210> 749

<211> 555

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(532)

<223> RXN01709

<400> 749

gcaagtggaa ccacgatggg aacggtaact gctgccgctg cgggtattact cgtagtattca 60

gaaattaggt gtcgatgcag caatacggaa ctttgccaat	gtg ttt gaa caa gct	115
	Val Phe Glu Gln Ala	
	1	5

ctc ggg ctc acc acc ctt gca caa aca gct gga gcg ggc gca gcg ggg	163
Leu Gly Leu Thr Thr Leu Ala Gln Thr Thr Ala Gly Ala Ala Gly	
10	15

ggc ttg ggt ttc atg gca atg gcg ttg ttg tct gca ggg atg cgc tcc	211
Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser Ala Gly Met Arg Ser	
25	30

ggc gtg gac atg att ctt aat gaa acc ggg ggt gaa aag atg ctt gca	259
Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly Glu Lys Met Leu Ala	
40	45

cag gca gat tta gtc atc act gga gaa gga cgc att gat gca cag acc	307
Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg Ile Asp Ala Gln Thr	
55	60

ctc agc ggg aaa gct cct act gga atc gcc aaa cgg gca cgt gcg aaa	355
Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys Arg Ala Arg Ala Lys	
70	75

gga att cca gta ctg gcg gtt tgt ggg cag agc cta ttg ggt cca gca	403
Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser Leu Leu Gly Pro Ala	
90	95

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atc tca aat gag cta ttt gaa gac atc tac agc ttt acc gat ttc gaa 451
Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser Phe Thr Asp Phe Glu
      105                      110
tct gac atc aat gaa tgc att cga aac ccg ctc cca att ttg gaa ggt 499
Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu Pro Ile Leu Glu Gly
      120                      125
atc ggt ttt aac atc gcc aaa cat cat ctg agt tagcgatatt tcagcaaacc 552
Ile Gly Phe Asn Ile Ala Lys His His Leu Ser
      135                      140

gat 555

```

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<210> 750
<211> 144
<212> PRT
<213> Corynebacterium glutamicum

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<400> 750
Val Phe Glu Gln Ala Leu Gly Leu Thr Thr Leu Ala Gln Thr Ala Gly
  1             5             10             15
Ala Gly Ala Ala Gly Gly Leu Gly Phe Met Ala Met Ala Leu Leu Ser
      20             25
Ala Gly Met Arg Ser Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly
      35             40             45
Glu Lys Met Leu Ala Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg
      50             55             60
Ile Asp Ala Gln Thr Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys
      65             70             75             80
Arg Ala Arg Ala Lys Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser
      85             90             95
Leu Leu Gly Pro Ala Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser
      100            105            110
Phe Thr Asp Phe Glu Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu
      115            120            125
Pro Ile Leu Glu Gly Ile Gly Phe Asn Ile Ala Lys His His Leu Ser
      130            135            140

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<210> 751
<211> 368
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (16)..(345)

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<223> FRXA01709

<400> 751

ttgttgctctg cagggatg cgc tcc ggc gtg gac atg att ctt aat gaa acc 51
 Met Arg Ser Gly Val Asp Met Ile Leu Asn Glu Thr
 1 5 10

ggg ggt gaa aag atg ctt gca cag gca gat tta gtc atc act gga gaa 99
 Gly Gly Glu Lys Met Leu Ala Gln Ala Asp Leu Val Ile Thr Gly Glu
 15 20 25

gga cgc att gat gca cag acc ctc agc ggg aaa gct cct act gga atc 147
 Gly Arg Ile Asp Ala Gln Thr Leu Ser Gly Lys Ala Pro Thr Gly Ile
 30 35 40

gcc aaa cgg gca cgt gcg aaa gga att cca gta ctg cgc gtt tgt ggg 195
 Ala Lys Arg Ala Arg Lys Gly Ile Pro Val Leu Ala Val Cys Gly
 45 50 55 60

cag agc cta ttg ggt cca gca atc tca aat gag cta ttt gaa gac atc 243
 Gln Ser Leu Leu Gly Pro Ala Ile Ser Asn Glu Leu Phe Glu Asp Ile
 65 70 75

tac agc ttt acc gat ttc gaa tct gac atc aat gaa tgc att cga aac 291
 Tyr Ser Phe Thr Asp Phe Glu Ser Asp Ile Asn Glu Cys Ile Arg Asn
 80 85 90

cgg ctc cca att ttg gaa ggt atc ggt ttt aac atc gcc aaa cat cat 339
 Pro Leu Pro Ile Leu Glu Gly Ile Gly Phe Asn Ile Ala Lys His His
 95 100 105

ctg agt tagcgatatt tcagcaaacc gat 368
 Leu Ser
 110

<210> 752

<211> 110

<212> PRT

<213> Corynebacterium glutamicum

<400> 752

Met Arg Ser Gly Val Asp Met Ile Leu Asn Glu Thr Gly Gly Glu Lys
 1 5 10 15

Met Leu Ala Gln Ala Asp Leu Val Ile Thr Gly Glu Gly Arg Ile Asp
 20 25 30

Ala Gln Thr Leu Ser Gly Lys Ala Pro Thr Gly Ile Ala Lys Arg Ala
 35 40 45

Arg Ala Lys Gly Ile Pro Val Leu Ala Val Cys Gly Gln Ser Leu Leu
 50 55 60

Gly Pro Ala Ile Ser Asn Glu Leu Phe Glu Asp Ile Tyr Ser Phe Thr
 65 70 75 80

Asp Phe Glu Ser Asp Ile Asn Glu Cys Ile Arg Asn Pro Leu Pro Ile
 85 90 95

Leu Glu Gly Ile Gly Phe Asn Ile Ala Lys His His Leu Ser

110

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<220>
<221> CDS
<222> (101)..(1258)
<223> RXN01711
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4400> 753																	
tctcgtgagt	ttctccccgg	tagcaccttc	tatatcagcc	cccaacggcg	gtcggagcag	60											
gtgggatagac atcggaacg cggttgcatg gccgttggcc								atg	ttg	ttg	atg	gca	115				
								Met	Leu	Leu	Met	Ala					
								1				5					
cat	cgc	ttc	ttc	gtg	ctt	gcg	att	aac	ggc	gca	gtc	acc	gac	gat	ttc	163	
His	Arg	Phe	Phe	Val	Leu	Ala	Ile	Asn	Gly	Ala	Val	Thr	Asp	Asp	Phe		
				10					15					20			
acg	acg	gtt	tat	agt	gct	tta	cga	cgt	ttc	gtt	gaa	ggt	att	ccg	gtc	211	
Thr	Thr	Val	Tyr	Ser	Ala	Leu	Arg	Arg	Phe	Val	Glu	Gly	Ile	Pro	Val		
				25					30					35			
tac	aac	gag	gtc	tac	cac	ttc	gtc	gat	ccg	cac	tac	ctc	tat	aac	ccg	259	
Tyr	Asn	Glu	Val	Tyr	His	Phe	Val	Asp	Pro	His	Tyr	Leu	Tyr	Asn	Pro		
				40					45					50			
ggc	gcc	acc	ctc	cta	ttg	gca	cca	ttg	gga	tat	atc	acc	cat	ttc	acg	307	
Gly	Ala	Thr	Leu	Leu	Leu	Ala	Pro	Leu	Gly	Tyr	Ile	Thr	His	Phe	Thr		
				55					60					65			
ttg	gct	cgg	tgg	atg	ttc	atc	gcg	gtg	aac	ctc	ctt	gcc	att	gtt	tta	355	
Leu	Ala	Arg	Trp	Met	Phe	Ile	Ala	Val	Asn	Leu	Leu	Ala	Ile	Val	Leu		
				70					75					80			
gcg	ttc	ggg	ctg	ctg	acc	aga	ctc	tcc	ggt	ggc	gcg	ctg	cgc	agc	atg	403	
Ala	Phe	Gly	Leu	Leu	Thr	Arg	Leu	Ser	Gly	Trp	Ala	Leu	Arg	Ser	Met		
				90					95					100			
gtg	tgg	ccg	att	gcg	atc	gcc	ttg	gcg	atg	ctg	aca	gaa	acc	gtg	caa	451	
Val	Trp	Pro	Ile	Ala	Ile	Ala	Leu	Ala	Met	Leu	Thr	Glu	Thr	Val	Gln		
				105					110					115			
aac	acc	ctc	att	ttc	tcc	aac	atc	aac	ggc	atc	ctg	ctg	ctc	atg	ttg	499	
Asn	Thr	Leu	Ile	Phe	Ser	Asn	Ile	Asn	Gly	Ile	Leu	Leu	Leu	Met	Leu		
				120					125					130			
gcg	att	ttc	ctg	tgg	tgc	gtg	gtg	cac	aaa	aaa	tcc	tgg	ttg	ggc	gga	547	
Ala	Ile	Phe	Leu	Trp	Cys	Val	Val	His	Lys	Lys	Ser	Trp	Leu	Gly	Gly		
				135					140					145			
cta	gtc	att	ggt	ttg	gcc	att	ttg	atc	aaa	ccc	atg	ttc	ctg	cca	ctt	595	
Leu	Val	Ile	Gly	Leu	Ala	Ile	Leu	Ile	Lys	Pro	Met	Phe	Leu	Pro	Leu		
				150					155					160			
ctc	ttc	cta	cct	ttg	gtg	aaa	aaq	caa	tgg	gga	tgc	ctc	atc	ctc	ggc	643	


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Leu Phe Leu Pro Leu Val Lys Lys Gln Trp Gly Ser Leu Ile Leu Gly
      170      175      180

att tta acc cca gtg att ttc aat gca gtg gcc tgg ttc tta gtt ccg 691
Ile Leu Thr Pro Val Ile Phe Asn Ala Val Ala Trp Phe Leu Val Pro
      185      190      195

gga gca tct gaa tac gtc acc cgc acg atg ccc tac ctt ggt gaa act 739
Gly Ala Ser Glu Tyr Val Thr Arg Thr Met Pro Tyr Leu Gly Glu Thr
      200      205      210

cga gat ttt gcc aac agc tca ctc cca ggc ttg gcc atc tat ttc gga 787
Arg Asp Phe Ala Asn Ser Ser Leu Pro Gly Leu Ala Ile Tyr Phe Gly
      215      220      225

atg ccc acc tgg atg gaa atc acc tgg ttc ctc atc ttc gcc gca atg 835
Met Pro Thr Trp Met Glu Ile Thr Trp Phe Leu Ile Phe Gly Ala Met
      230      235      240      245

gtc gcc ctc gca gtg ctg gca ctc ctg aga ttc cgt aac acc gag cca 883
Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe Arg Asn Thr Glu Pro
      250      255      260

tac ttc tgg gca gca acc acc acc ggt gta ctc ctg act gcc gta ttc 931
Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu Leu Thr Gly Val Phe
      265      270      275

ttc ctg tcc tca ctg gga cag atg tac tac tcc atg atg atc ttc cct 979
Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser Met Met Ile Phe Pro
      280      285      290

atg atc ttc acc ctg ctc gga agc cga tcc gta ttc cac aac tgg gtt 1027
Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val Phe His Asn Trp Val
      295      300      305

gcc tgg gtc gcc gcc tac ttc tta cta tcc cct gac act ttc acc tcc 1075
Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro Asp Thr Phe Thr Ser
      310      315      320      325

cag cga cta ccc gat gta gcc cgc tgg atg gaa ttt ttc agc gcg acc 1123
Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu Phe Phe Ser Ala Thr
      330      335      340

gtt ggt tgg gga cta ttg ata gtg gtt aca ttt gtc tcg gcg cta atc 1171
Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe Val Ser Ala Leu Ile
      345      350      355

tgg ttt att ggt gat atc cga gcc aag gga act ccg agc tca ccc att 1219
Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr Pro Ser Ser Pro Ile
      360      365      370

acc act gat cca acg cac gac cat ctt gag agg aca gca tgacagactt 1268
Thr Thr Asp Pro Thr His Asp His Leu Glu Arg Thr Ala
      375      380      385

caaactcatc agc 1281

<210> 754
<211> 386
<212> PRT

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<213> *Corynebacterium glutamicum*

<400> 754

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Met Leu Leu Met Ala His Arg Phe Phe Val Leu Ala Ile Asn Gly Ala
 1          5          10          15

Val Thr Asp Asp Phe Thr Thr Val Tyr Ser Ala Leu Arg Arg Phe Val
          20          25          30

Glu Gly Ile Pro Val Tyr Asn Glu Val Tyr His Phe Val Asp Pro His
          35          40          45

Tyr Leu Tyr Asn Pro Gly Ala Thr Leu Leu Leu Ala Pro Leu Gly Tyr
 50          55          60

Ile Thr His Phe Thr Leu Ala Arg Trp Met Phe Ile Ala Val Asn Leu
 65          70          75          80

Leu Ala Ile Val Leu Ala Phe Gly Leu Leu Thr Arg Leu Ser Gly Trp
          85          90          95

Ala Leu Arg Ser Met Val Trp Pro Ile Ala Ile Ala Leu Ala Met Leu
          100          105          110

Thr Glu Thr Val Gln Asn Thr Leu Ile Phe Ser Asn Ile Asn Gly Ile
          115          120          125

Leu Leu Leu Met Leu Ala Ile Phe Leu Trp Cys Val Val His Lys Lys
          130          135          140

Ser Trp Leu Gly Gly Leu Val Ile Gly Leu Ala Ile Leu Ile Lys Pro
          145          150          155          160

Met Phe Leu Pro Leu Leu Phe Leu Pro Leu Val Lys Lys Gln Trp Gly
          165          170          175

Ser Leu Ile Leu Gly Ile Leu Thr Pro Val Ile Phe Asn Ala Val Ala
          180          185          190

Trp Phe Leu Val Pro Gly Ala Ser Glu Tyr Val Thr Arg Thr Met Pro
          195          200          205

Tyr Leu Gly Glu Thr Arg Asp Phe Ala Asn Ser Ser Leu Pro Gly Leu
          210          215          220

Ala Ile Tyr Phe Gly Met Pro Thr Trp Met Glu Ile Thr Trp Phe Leu
          225          230          235          240

Ile Phe Gly Ala Met Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe
          245          250          255

Arg Asn Thr Glu Pro Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu
          260          265          270

Leu Thr Gly Val Phe Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser
          275          280          285

Met Met Ile Phe Pro Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val
          290          295          300

Phe His Asn Trp Val Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro

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<210> 755
<211> 1281
<212> DNA
<213> Corynebacterium glutamicum
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<220>																				
<221> CDS																				
<222> (101)..(1258)																				
<223> FRXA01711																				
<400> 755																				
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gtgggatagc	atcggcgaacg	cggttgcatg	gcggttggcc	atg	ttg	ttg	atg	gcg	115											
				Met	Leu	Leu	Met	Ala	5											
cat	cgc	ttc	ttc	gtg	ctt	gcg	att	aac	ggc	gca	gtc	acc	gac	gat	ttc	163				
His	Arg	Phe	Phe	Val	Leu	Ala	Ile	Asn	Gly	Ala	Val	Thr	Asp	Asp	Phe	20				
				10					15											
acg	acg	ggt	tat	agt	gct	tta	cga	cgt	ttc	ggt	gaa	ggt	att	ccg	gtc	211				
Thr	Thr	Val	Tyr	Ser	Ala	Leu	Arg	Arg	Phe	Val	Glu	Gly	Ile	Pro	Val	35				
			25					30												
tac	aac	gag	gtc	tac	cac	ttc	gtc	gat	ccg	cac	tac	ctc	tat	aac	ccg	259				
Tyr	Asn	Glu	Val	Tyr	His	Phe	Val	Asp	Pro	His	Tyr	Leu	Tyr	Asn	Pro	50				
			40					45												
ggc	gcc	acc	ctc	cta	ttg	gca	cca	ttg	gga	tat	atc	acc	cat	ttc	acg	307				
Gly	Ala	Thr	Leu	Leu	Leu	Ala	Pro	Leu	Gly	Tyr	Ile	Thr	His	Phe	Thr	65				
			55				60													
ttg	gct	cgg	tgg	atg	ttc	atc	gcg	gtg	aac	ctc	ctt	gcc	att	ggt	tta	355				
Leu	Ala	Arg	Trp	Met	Phe	Ile	Ala	Val	Asn	Leu	Leu	Ala	Ile	Val	Leu	85				
			70			75			80											
gcg	ttc	ggg	ctg	ctg	acc	aga	ctc	tcc	ggt	tgg	gcg	ctg	cgc	agc	atg	403				
Ala	Phe	Gly	Leu	Leu	Thr	Arg	Leu	Ser	Gly	Trp	Ala	Leu	Arg	Ser	Met	95				
			90						95					100						
gtg	trg	cgc	att	gcg	atc	gcc	ttg	gcg	atg	ctg	aca	gaa	acc	gtg	caa	451				
Val	Trp	Pro	Ile	Ala	Ile	Ala	Leu	Ala	Met	Leu	Thr	Glu	Thr	Val	Gln					

	105	110	115	
	aac acc ctc att ttc tcc aac atc aac ggc atc ctg ctg ctc atg ttg			499
	Asn Thr Leu Ile Phe Ser Asn Ile Asn Gly Ile Leu Leu Met Leu			
	120	125	130	
	gcg att ttc ctg tgg tgc gtg gtg cac aaa aaa tcc tgg ttg ggc gga			547
	Ala Ile Phe Leu Trp Cys Val Val His Lys Lys Ser Trp Leu Gly Gly			
	135	140	145	
	cta gtc att ggt ttg gcc att ttg atc aaa ccc atg ttc ctg cca ctt			595
	Leu Val Ile Gly Leu Ala Ile Leu Ile Lys Pro Met Phe Leu Pro Leu			
	150	155	160	165
	ctc ttc cta cct ttg gtg aaa aag caa tgg gga tgc ctc atc ctc ggc			643
	Leu Phe Leu Pro Leu Val Lys Lys Gln Trp Gly Ser Leu Ile Leu Gly			
	170	175	180	
	att tta acc cca gtg att ttc aat gca gtg gcc tgg ttc tta gtt ccg			691
	Ile Leu Thr Pro Val Ile Phe Asn Ala Val Ala Trp Phe Leu Val Pro			
	185	190	195	
	gga gca tct gaa tac gtc acc cgc acg atg ccc tac ctt ggt gaa act			739
	Gly Ala Ser Glu Tyr Val Thr Arg Thr Met Pro Tyr Leu Gly Glu Thr			
	200	205	210	
	cga gat ttt gcc aac agc tca ctc cca ggc ttg gcc atc tat ttc gga			787
	Arg Asp Phe Ala Asn Ser Ser Leu Pro Gly Leu Ala Ile Tyr Phe Gly			
	215	220	225	
	atg ccc acc tgg atg gaa atc acc tgg ttc ctc atc ttc ggc gca atg			835
	Met Pro Thr Trp Met Glu Ile Thr Trp Phe Leu Ile Phe Gly Ala Met			
	230	235	240	245
	gtc ggc ctc gca gtg ctg gca ctc ctg aga ttc cgt aac acc gag cca			883
	Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe Arg Asn Thr Glu Pro			
	250	255	260	
	tac ttc tgg gca gca acc acc acc ggt gta ctc ctg act ggc gta ttc			931
	Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu Leu Thr Gly Val Phe			
	265	270	275	
	ttc ctg tcc tca ctg gga cag atg tac tac tcc atg atg atc ttc cct			979
	Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser Met Met Ile Phe Pro			
	280	285	290	
	atg atc ttc acc ctg ctc gga agc cga tcc gta ttc cac aac tgg gtt			1027
	Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val Phe His Asn Trp Val			
	295	300	305	
	gcc tgg gtc gcc gcc tac ttc tta cta tcc cct gac act ttc acc tcc			1075
	Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro Asp Thr Phe Thr Ser			
	310	315	320	325
	cag cga cta ccc gat gta gcc cgc tgg atg gaa ttt ttc agc gcg acc			1123
	Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu Phe Phe Ser Ala Thr			
	330	335	340	
	gtt ggt tgg gga cta ttg ata gtg gtt aca ttt gtc tgc gcg cta atc			1171
	Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe Val Ser Ala Leu Ile			
	345	350	355	

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tgg ttt att ggt gat atc cga gcc aag gga act ccg agc tca ccc att 1219
Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr Pro Ser Ser Pro Ile
      360              365              370

acc act gat cca acg cac gac cat ctt gag agg aca gca tgacagactt 1268
Thr Thr Asp Pro Thr His Asp His Leu Glu Arg Thr Ala
      375              380              385

caaactcatc agc 1281

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<210> 756

<211> 386

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 756

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Met Leu Leu Met Ala His Arg Phe Phe Val Leu Ala Ile Asn Gly Ala
  1              5              10              15

Val Thr Asp Asp Phe Thr Thr Val Tyr Ser Ala Leu Arg Arg Phe Val
              20              25              30

Glu Gly Ile Pro Val Tyr Asn Glu Val Tyr His Phe Val Asp Pro His
      35              40              45

Tyr Leu Tyr Asn Pro Gly Ala Thr Leu Leu Leu Ala Pro Leu Gly Tyr
      50              55              60

Ile Thr His Phe Thr Leu Ala Arg Trp Met Phe Ile Ala Val Asn Leu
      65              70              75              80

Leu Ala Ile Val Leu Ala Phe Gly Leu Leu Thr Arg Leu Ser Gly Trp
      85              90              95

Ala Leu Arg Ser Met Val Trp Pro Ile Ala Ile Ala Leu Ala Met Leu
      100             105             110

Thr Glu Thr Val Gln Asn Thr Leu Ile Phe Ser Asn Ile Asn Gly Ile
      115             120             125

Leu Leu Leu Met Leu Ala Ile Phe Leu Trp Cys Val Val His Lys Lys
      130             135             140

Ser Trp Leu Gly Gly Leu Val Ile Gly Leu Ala Ile Leu Ile Lys Pro
      145             150             155             160

Met Phe Leu Pro Leu Leu Phe Leu Pro Leu Val Lys Lys Gln Trp Gly
      165             170             175

Ser Leu Ile Leu Gly Ile Leu Thr Pro Val Ile Phe Asn Ala Val Ala
      180             185             190

Trp Phe Leu Val Pro Gly Ala Ser Glu Tyr Val Thr Arg Thr Met Pro
      195             200             205

Tyr Leu Gly Glu Thr Arg Asp Phe Ala Asn Ser Ser Leu Pro Gly Leu
      210             215             220

Ala Ile Tyr Phe Gly Met Pro Thr Trp Met Glu Ile Thr Trp Phe Leu

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225                230                235                240
Ile Phe Gly Ala Met Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe
      245                250                255

Arg Asn Thr Glu Pro Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu
      260                265                270

Leu Thr Gly Val Phe Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser
      275                280                285

Met Met Ile Phe Pro Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val
      290                295                300

Phe His Asn Trp Val Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro
305                310                315                320

Asp Thr Phe Thr Ser Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu
      325                330                335

Phe Phe Ser Ala Thr Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe
      340                345                350

Val Ser Ala Leu Ile Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr
      355                360                365

Pro Ser Ser Pro Ile Thr Thr Asp Pro Thr His Asp His Leu Glu Arg
      370                375                380

Thr Ala
385

<210> 757
<211> 1123
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1123)
<223> RXN01721

<400> 757
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caaacatgat gcgtacctgc caccgcgaga cggcaatcgc gtg ctt gtg gac aga 115
Val Leu Val Asp Arg
1 5

ttc gga cgc atc gcg cgt gac ctg cgg gtg tca ctg acc gac cga tgc 163
Phe Gly Arg Ile Ala Arg Asp Leu Arg Val Ser Leu Thr Asp Arg Cys
10 15 20

aac ctc cgc tgc acc tat tgc atg ccc gcg gag ggt tta gag tgg ctg 211
Asn Leu Arg Cys Thr Tyr Cys Met Pro Ala Glu Gly Leu Glu Trp Leu
25 30 35

ccc acc gag cag acg ctt aac gac gcc gag gtg ctg cga ctc atc cgc 259
Pro Thr Glu Gln Thr Leu Asn Asp Ala Glu Val Leu Arg Leu Ile Arg
40 45 50

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att gcg gtg gtt aag ctg ggc att cgt caa att cga ttc acc ggc ggc 307
 Ile Ala Val Val Lys Leu Gly Ile Arg Gln Ile Arg Phe Thr Gly Gly
 55 60 65

gag cct tta ctg cgg aaa aat ttg gaa gac atc atc gcc ggc acc gca 355
 Glu Pro Leu Leu Arg Lys Asn Leu Glu Asp Ile Ile Ala Gly Thr Ala
 70 75 80 85

gcc ctg cgc acc gac gaa ggc gaa aaa gtt cac atc gct ctc acc acc 403
 Ala Leu Arg Thr Asp Glu Gly Glu Lys Val His Ile Ala Leu Thr Thr
 90 95 100

aac ggc ctt ggc cta gac aaa cgc atc gca gga ctg aaa gaa gct ggt 451
 Asn Gly Leu Gly Leu Asp Lys Arg Ile Ala Gly Leu Lys Glu Ala Gly
 105 110 115

ctt gac cgg gtc aat att tca ctc gac acc atc gac gcc gaa cgc tac 499
 Leu Asp Arg Val Asn Ile Ser Leu Asp Thr Ile Asp Ala Glu Arg Tyr
 120 125 130

gtc tgc cta acc aag cgt gat cga ttg tcc ggt gtg ttg gcg tcc atc 547
 Val Ser Leu Thr Lys Arg Asp Arg Leu Ser Gly Val Leu Ala Ser Ile
 135 140 145

gat gcc gct gtt gcc gct ggc ctt cac cca gtg aag atc aac gcc gtg 595
 Asp Ala Ala Val Ala Ala Gly Leu His Pro Val Lys Ile Asn Ala Val
 150 155 160 165

gtc atg cct ggg gtc aat gaa gta gat atc gtc ccc ctt gcg gaa tac 643
 Val Met Pro Gly Val Asn Glu Val Asp Ile Val Pro Phe Ala Glu Tyr
 170 175 180

tgc att tcc aaa ggc tcc caa ctg cga ttc atc gaa caa atg cca ctt 691
 Cys Ile Ser Lys Gly Ser Gln Leu Arg Phe Ile Glu Gln Met Pro Leu
 185 190 195

ggc ccg cgc gag cag tgg aaa cgc ggc gat atg gtc aca gcc gaa gaa 739
 Gly Pro Arg Glu Gln Trp Lys Arg Gly Asp Met Val Thr Ala Glu Glu
 200 205 210

atc ctg gcg cgc ctg gaa gaa aaa ttc acc tta tcc ccc gcc aag gaa 787
 Ile Leu Ala Arg Leu Glu Glu Lys Phe Thr Leu Ser Pro Ala Lys Glu
 215 220 225

ccc cga gga gct gca cct gct gcg ctg tgg aat gtg gta gat aaa tcc 835
 Pro Arg Gly Ala Ala Pro Ala Ala Leu Trp Asn Val Val Asp Lys Ser
 230 235 240 245

aac cct gat atc act gga caa atc ggc atc atc gcc tgc gtg acg cac 883
 Asn Pro Asp Ile Thr Gly Gln Ile Gly Ile Ile Ala Ser Val Thr His
 250 255 260

cca ttt tgc gga gat tgc gat cgc tcc cgc ctc acc acc gac ggc acc 931
 Pro Phe Cys Gly Asp Cys Asp Arg Ser Arg Leu Thr Thr Asp Gly Thr
 265 270 275

atc cga aac tgc ctt ttc tcc cgc act gaa act ccc cta cgt gac gcg 979
 Ile Arg Asn Cys Leu Phe Ser Arg Thr Glu Thr Pro Leu Arg Asp Ala
 280 285 290

ctt cgc gac ggc gcc tcc gac gat gag ctc gcg caa ctg tgg gca ggc 1027
 Leu Arg Asp Gly Ala Ser Asp Asp Glu Leu Ala Gln Leu Trp Ala Gly
 295 300 305

gcc atg tgg gag aag aaa ccc ggc cat ggc atc gac gat gaa ggc ttc 1075
 Ala Met Trp Glu Lys Lys Pro Gly His Gly Ile Asp Asp Glu Gly Phe
 310 315 320 325

ctc caa cca gat cgc ccc atg tct gcc atc ggg gct agc cca tac cag 1123
 Leu Gln Pro Asp Arg Pro Met Ser Ala Ile Gly Ala Ser Pro Tyr Gln
 330 335 340

<210> 758

<211> 341

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 758

Val Leu Val Asp Arg Phe Gly Arg Ile Ala Arg Asp Leu Arg Val Ser
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Leu Thr Asp Arg Cys Asn Leu Arg Cys Thr Tyr Cys Met Pro Ala Glu
 20 25 30

Gly Leu Glu Trp Leu Pro Thr Glu Gln Thr Leu Asn Asp Ala Glu Val
 35 40 45

Leu Arg Leu Ile Arg Ile Ala Val Val Lys Leu Gly Ile Arg Gln Ile
 50 55 60

Arg Phe Thr Gly Gly Glu Pro Leu Leu Arg Lys Asn Leu Glu Asp Ile
 65 70 75 80

Ile Ala Gly Thr Ala Ala Leu Arg Thr Asp Glu Gly Glu Lys Val His
 85 90 95

Ile Ala Leu Thr Thr Asn Gly Leu Gly Leu Asp Lys Arg Ile Ala Gly
 100 105 110

Leu Lys Glu Ala Gly Leu Asp Arg Val Asn Ile Ser Leu Asp Thr Ile
 115 120 125

Asp Ala Glu Arg Tyr Val Ser Leu Thr Lys Arg Asp Arg Leu Ser Gly
 130 135 140

Val Leu Ala Ser Ile Asp Ala Ala Val Ala Ala Gly Leu His Pro Val
 145 150 155 160

Lys Ile Asn Ala Val Val Met Pro Gly Val Asn Glu Val Asp Ile Val
 165 170 175

Pro Leu Ala Glu Tyr Cys Ile Ser Lys Gly Ser Gln Leu Arg Phe Ile
 180 185 190

Glu Gln Met Pro Leu Gly Pro Arg Glu Gln Trp Lys Arg Gly Asp Met
 195 200 205

Val Thr Ala Glu Glu Ile Leu Ala Arg Leu Glu Glu Lys Phe Thr Leu
 210 215 220

Ser Pro Ala Lys Glu Pro Arg Gly Ala Ala Pro Ala Ala Leu Trp Asn
 225 230 235 240

Val Val Asp Lys Ser Asn Pro Asp Ile Thr Gly Gln Ile Gly Ile Ile
 245 250 255

Ala Ser Val Thr His Pro Phe Cys Gly Asp Cys Asp Arg Ser Arg Leu
 260 265 270

Thr Thr Asp Gly Thr Ile Arg Asn Cys Leu Phe Ser Arg Thr Glu Thr
 275 280 285

Pro Leu Arg Asp Ala Leu Arg Asp Gly Ala Ser Asp Asp Glu Leu Ala
 290 295 300

Gln Leu Trp Ala Gly Ala Met Trp Glu Lys Lys Pro Gly His Gly Ile
 305 310 315 320

Asp Asp Glu Gly Phe Leu Gln Pro Asp Arg Pro Met Ser Ala Ile Gly
 325 330 335

Ala Ser Pro Tyr Gln
 340

<210> 759

<211> 657

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(634)

<223> RXN01734

<400> 759

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acacgggcac cgggcggatt tcaactcctgg atgtgcaacc atg aca gat cca att 115
 Met Thr Asp Pro Ile
 1 5

gag cag gca ttt gaa cgc atc cgc gcc gaa gcc atg cgc aga aat gga 163
 Glu Gln Ala Phe Glu Arg Ile Arg Ala Glu Ala Met Arg Arg Asn Gly
 10 15 20

tcc gtt ccc gac ctc aat aaa aac gat gct ttt cga cgc cca cct ggc 211
 Ser Val Pro Asp Leu Asn Lys Asn Asp Ala Phe Arg Arg Pro Pro Ala
 25 30 35

cgg aaa ggg ggc gtc gaa aag cgc aaa aaa ggc cgt gca agc ggc cta 259
 Pro Lys Gly Gly Val Glu Lys Arg Lys Lys Gly Arg Ala Ser Gly Leu
 40 45 50

gac ggc cgc cag aaa cga tat gtg cgc ggc gcg gag tcg ctg gga tcg 307
 Asp Gly Arg Gln Lys Arg Tyr Val Arg Gly Ala Glu Ser Leu Gly Ser
 55 60 65

gtg ctg aac aag gaa att cag cgt cgt ggc tgg ggc aaa gac att gcc 355
 Val Leu Asn Lys Glu Ile Gln Arg Arg Gly Trp Gly Lys Asp Ile Ala
 70 75 80 85

ggc ggt tgg gtg acg tcc aac tgg gaa gag ctt gtt ggc gcg aag att 403
 Gly Gly Trp Val Thr Ser Asn Trp Glu Glu Leu Val Gly Ala Lys Ile
 90 95 100

gcg cag cat acg cgc gtg gaa atg atc aaa gat aag aag ctt ttt atc 451
 Ala Gln His Thr Arg Val Glu Met Ile Lys Asp Lys Lys Leu Phe Ile
 105 110 115

act tgt gat tcc aca gcg tgg gcc acc aat ctg cgc atg atg cag cgg 499
 Thr Cys Asp Ser Thr Ala Trp Ala Thr Asn Leu Arg Met Met Gln Arg
 120 125 130

caa atc ctg cag gta atc gct gaa aaa gtg ggt cca aat att att aca 547
 Gln Ile Leu Gln Val Ile Ala Glu Lys Val Gly Pro Asn Ile Ile Thr
 135 140 145

gag ctg cgt att ttt ggg cct cag gcc cca agc tgg cgc aag ggg ccg 595
 Glu Leu Arg Ile Phe Gly Pro Gln Ala Pro Ser Trp Arg Lys Gly Pro
 150 155 160 165

ttg cac gta aaa gga cgc ggt ccg aga gac aca tac gga tagtttggtg 644
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<210> 760
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 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45

Arg Ala Ser Gly Leu Asp Gly Arg Gln Lys Arg Tyr Val Arg Gly Ala
 50 55 60

Glu Ser Leu Gly Ser Val Leu Asn Lys Glu Ile Gln Arg Arg Gly Trp
 65 70 75 80

Gly Lys Asp Ile Ala Gly Gly Trp Val Thr Ser Asn Trp Glu Glu Leu
 85 90 95

Val Gly Ala Lys Ile Ala Gln His Thr Arg Val Glu Met Ile Lys Asp
 100 105 110

Lys Lys Leu Phe Ile Thr Cys Asp Ser Thr Ala Trp Ala Thr Asn Leu
 115 120 125

Arg Met Met Gln Arg Gln Ile Leu Gln Val Ile Ala Glu Lys Val Gly
 130 135 140

Pro Asn Ile Ile Thr Glu Leu Arg Ile Phe Gly Pro Gln Ala Pro Ser
145 150 155 160

Trp Arg Lys Gly Pro Leu His Val Lys Gly Arg Gly Pro Arg Asp Thr
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Tyr Gly

<210> 761

<211> 657

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(634)

<223> FRXA01734

<400> 761

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Met Thr Asp Pro Ile
1 5

gag cag gca ttt gaa cgc atc cgc gcc gaa gcc atg cgc aga aat gga 163
Glu Gln Ala Phe Glu Arg Ile Arg Ala Glu Ala Met Arg Arg Asn Gly
10 15 20

tcc gtt ccc gac ctc aat aaa aac gat gct ttt cga cgc cca cct gcg 211
Ser Val Pro Asp Leu Asn Lys Asn Asp Ala Phe Arg Arg Pro Pro Ala
25 30 35

ccg aaa ggg ggc gtc gaa aag cgc aaa aaa ggc cgt gca agc ggc cta 259
Pro Lys Gly Gly Val Glu Lys Arg Lys Lys Gly Arg Ala Ser Gly Leu
40 45 50

gac ggc cgc cag aaa cga tat gtg cgc gcc gcg gag tcg ctg gga tcg 307
Asp Gly Arg Gln Lys Arg Tyr Val Arg Gly Ala Glu Ser Leu Gly Ser
55 60 65

gtg ctg aac aag gaa att cag cgt cgt gcc tgg gcc aaa gac att gcc 355
Val Leu Asn Lys Glu Ile Gln Arg Arg Gly Trp Gly Lys Asp Ile Ala
70 75 80 85

ggc ggt tgg gtg acg tcc aac tgg gaa gag ctt gtt gcc gcg aag att 403
Gly Gly Trp Val Thr Ser Asn Trp Glu Glu Leu Val Gly Ala Lys Ile
90 95 100

gcg cag cat acg cgc gtg gaa atg atc aaa gat aag aag ctt ttt atc 451
Ala Gln His Thr Arg Val Glu Met Ile Lys Asp Lys Lys Leu Phe Ile
105 110 115

act tgt gat tcc aca gcg tgg gcc acc aat ctg cgc atg atg cag cgg 499
Thr Cys Asp Ser Thr Ala Trp Ala Thr Asn Leu Arg Met Met Gln Arg
120 125 130

caa atc ctg cag gta atc gct gaa aaa gtg ggt cca aat att att aca 547
Gln Ile Leu Gln Val Ile Ala Glu Lys Val Gly Pro Asn Ile Ile Thr

135 140 145
 gag ctg cgt att ttt ggg cct cag gcc cca agc tgg cgc aag ggg ccg 595
 Glu Leu Arg Ile Phe Gly Pro Gln Ala Pro Ser Trp Arg Lys Gly Pro
 150 155 160
 ttg cac gta aaa gga cgc ggt ccg aga gac aca tac gga tagtttggtg 644
 Leu His Val Lys Gly Arg Gly Pro Arg Asp Thr Tyr Gly
 170 175
 ataaaaaccg tcg 657

 <210> 762
 <211> 178
 <212> PRT
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 20 25 30
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 35 40 45
 Arg Ala Ser Gly Leu Asp Gly Arg Gln Lys Arg Tyr Val Arg Gly Ala
 50 55 60
 Glu Ser Leu Gly Ser Val Leu Asn Lys Glu Ile Gln Arg Arg Gly Trp
 65 70 75 80
 Gly Lys Asp Ile Ala Gly Gly Trp Val Thr Ser Asn Trp Glu Glu Leu
 85 90 95
 Val Gly Ala Lys Ile Ala Gln His Thr Arg Val Glu Met Ile Lys Asp
 100 105 110
 Lys Lys Leu Phe Ile Thr Cys Asp Ser Thr Ala Trp Ala Thr Asn Leu
 115 120 125
 Arg Met Met Gln Arg Gln Ile Leu Gln Val Ile Ala Glu Lys Val Gly
 130 135 140
 Pro Asn Ile Ile Thr Glu Leu Arg Ile Phe Gly Pro Gln Ala Pro Ser
 145 150 155 160
 Trp Arg Lys Gly Pro Leu His Val Lys Gly Arg Gly Pro Arg Asp Thr
 165 170 175
 Tyr Gly

<210> 763
 <211> 627
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(604)

<223> RXN01742

<400> 763

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ttcatctggc cttatttcat cacagttaca atcatctgtc atg cag gaa aag cca 115
Met Gln Glu Lys Pro
1 5

gag atg cca gcg att gag gtc atc cgt tca gcg aaa cgc acc aaa act 163
Glu Met Pro Ala Ile Glu Val Ile Arg Ser Ala Lys Arg Thr Lys Thr
10 15 20

gtt caa gct cga att gtg gac ggg caa atc cag gtg cgc atc cct gcg 211
Val Gln Ala Arg Ile Val Asp Gly Gln Ile Gln Val Arg Ile Pro Ala
25 30 35

agg atg tct aaa gcg gag gaa gaa aaa gcg gtg ggg gag atc gtc gca 259
Arg Met Ser Lys Ala Glu Glu Glu Lys Ala Val Gly Glu Ile Val Ala
40 45 50

aag cta aag cga cgc acc caa tcg gcc gtc tca agc gac gct gac ctg 307
Lys Leu Lys Lys Arg Arg Thr Gln Ser Ala Val Ser Ser Asp Ala Asp Leu
55 60 65

att gag cgc gcc cat aag ttg aac aag act gtg ttg gag ggg cgg gcg 355
Ile Glu Arg Ala His Lys Leu Asn Lys Thr Val Leu Glu Gly Arg Ala
70 75 80 85

cgg gtg gaa agt att cgg tgg gtg agt aat cag aag ggg cgg tgg ggg 403
Arg Val Glu Ser Ile Arg Trp Val Ser Asn Gln Lys Gly Arg Trp Gly
90 95 100

tcg tgc acg gtg gcg act gcg gag att cgg att tcg gat cgt tta aag 451
Ser Cys Thr Val Ala Glu Thr Ala Glu Ile Arg Ile Ser Asp Arg Leu Lys
105 110 115

cac gtg ccg gat tat gtg ttg gat gcg gtg ttg gtg cat gag ctg acg 499
His Val Pro Asp Tyr Val Leu Asp Ala Val Leu Val His Glu Leu Thr
120 125 130

cat acg ttt att gcg ggg cat tcg gcg gag ttt tgg gag tgg gca gac 547
His Thr Phe Ile Ala Gly His Ser Ala Glu Phe Trp Glu Trp Ala Asp
135 140 145

aaa acg ccc ctg gca gag agg gcc aag gcc tat ttg gag gcg tat cag 595
Lys Thr Pro Leu Ala Glu Arg Ala Lys Gly Tyr Leu Glu Ala Tyr Gln
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Arg Trp Gly

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<210> 764

<211> 168

<212> PRT

<213> Corynebacterium glutamicum

<400> 764

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 20 25 30

Val Arg Ile Pro Ala Arg Met Ser Lys Ala Glu Glu Glu Lys Ala Val
 35 40 45

Gly Glu Ile Val Ala Lys Leu Lys Arg Arg Thr Gln Ser Ala Val Ser
 50 55 60

Ser Asp Ala Asp Leu Ile Glu Arg Ala His Lys Leu Asn Lys Thr Val
 65 70 75 80

Leu Glu Gly Arg Ala Arg Val Glu Ser Ile Arg Trp Val Ser Asn Gln
 85 90 95

Lys Gly Arg Trp Gly Ser Cys Thr Val Ala Thr Ala Glu Ile Arg Ile
 100 105 110

Ser Asp Arg Leu Lys His Val Pro Asp Tyr Val Leu Asp Ala Val Leu
 115 120 125

Val His Glu Leu Thr His Thr Phe Ile Ala Gly His Ser Ala Glu Phe
 130 135 140

Trp Glu Trp Ala Asp Lys Thr Pro Leu Ala Glu Arg Ala Lys Gly Tyr
 145 150 155 160

Leu Glu Ala Tyr Gln Arg Trp Gly
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<210> 765

<211> 627

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(604)

<223> FRXA01742

<400> 765

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 Met Gln Glu Lys Pro
 1 5

gag atg cca gcg att gag gtc atc cgt tca gcg aaa cgc acc aaa act 163
 Glu Met Pro Ala Ile Glu Val Ile Arg Ser Ala Lys Arg Thr Lys Thr
 10 15 20

gtt caa gct cga att gtg gac ggg caa atc cag gtg cgc atc cct gcg 211
 Val Gln Ala Arg Ile Val Asp Gly Gln Ile Gln Val Arg Ile Pro Ala
 25 30 35

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agg atg tct aaa gcg gag gaa gaa aaa gcg gtg ggg gag atc gtc gca 259
Arg Met Ser Lys Ala Glu Glu Glu Lys Ala Val Gly Ile Val Ala
      40              45              50

aag cta aag cga cgc acc caa tcg gcc gtc tca agc gac gct gac ctg 307
Lys Leu Lys Lys Arg Arg Thr Gln Ser Ala Val Ser Ser Asp Ala Asp Leu
      55              60              65

att gag cgc gcc cat aag ttg aac aag act gtg ttg gag ggg cgg gcg 355
Ile Glu Arg Ala His Lys Leu Asn Lys Thr Val Leu Glu Gly Arg Ala
      70              75              80              85

cgg gtg gaa agt att cgg tgg gtg agt aat cag aag ggg cgg tgg ggg 403
Arg Val Glu Ser Ile Arg Trp Val Ser Asn Gln Lys Gly Arg Trp Gly
      90              95              100

tcg tgc acg gtg gcg act gcg gag att cgg att tcg gat cgt tta aag 451
Ser Cys Thr Val Ala Thr Ala Glu Ile Arg Ile Ser Asp Arg Leu Lys
      105              110              115

cac gtg ccg gat tat gtg ttg gat gcg gtg ttg gtg cat gag ctg acg 499
His Val Pro Asp Tyr Val Leu Asp Ala Val Leu Val His Glu Leu Thr
      120              125              130

cat acg ttt att gcg ggg cat tcg gcg gag ttt tgg gag tgg gca gac 547
His Thr Phe Ile Ala Gly His Ser Ala Glu Phe Trp Glu Trp Ala Asp
      135              140              145

aaa acg ccc ctg gca gag agg gcc aag ggc tat ttg gag gcg tat cag 595
Lys Thr Pro Leu Ala Glu Arg Ala Lys Gly Tyr Leu Glu Ala Tyr Gln
      150              155              160              165

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Arg Trp Gly

<210> 766
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 766
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  1              5              10              15

Lys Arg Thr Lys Thr Val Gln Ala Arg Ile Val Asp Gly Gln Ile Gln
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Val Arg Ile Pro Ala Arg Met Ser Lys Ala Glu Glu Glu Lys Ala Val
      35              40              45

Gly Glu Ile Val Ala Lys Leu Lys Arg Arg Thr Gln Ser Ala Val Ser
      50              55              60

Ser Asp Ala Asp Leu Ile Glu Arg Ala His Lys Leu Asn Lys Thr Val
      65              70              75              80

Leu Glu Gly Arg Ala Arg Val Glu Ser Ile Arg Trp Val Ser Asn Gln
      85              90              95

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Lys Gly Arg Trp Gly Ser Cys Thr Val Ala Thr Ala Glu Ile Arg Ile
 100 105 110
 Ser Asp Arg Leu Lys His Val Pro Asp Tyr Val Leu Asp Ala Val Leu
 115 120 125
 Val His Glu Leu Thr His Thr Phe Ile Ala Gly His Ser Ala Glu Phe
 130 135 140
 Trp Glu Trp Ala Asp Lys Thr Pro Leu Ala Glu Arg Ala Lys Gly Tyr
 145 150 155 160
 Leu Glu Ala Tyr Gln Arg Trp Gly
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<210> 767

<211> 2064

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(2041)

<223> RXN01754

<400> 767

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 cccctttttt ttgatgtgaa agttgaatcg gtaagctcct gtg aaa att aaa tcc 115
 Val Lys Ile Lys Ser
 1 5
 gta ttt ttg agc acc gct tta agc gct tcc tta ctg ctc gga atc acc 163
 Val Phe Leu Ser Thr Ala Leu Ser Ala Ser Leu Leu Gly Ile Thr
 10 15 20
 cca ccc gtg ctg gga gca acg atc aac ccc agt ttg cct ctt tct gcg 211
 Pro Pro Val Leu Gly Ala Thr Ile Asn Pro Ser Leu Pro Leu Ser Ala
 25 30 35
 ttg agc tcc tcg gac gat atc gcc gta ccc aac ttc gcc aaa gaa tta 259
 Leu Ser Ser Ser Asp Asp Ile Ala Val Pro Asn Phe Ala Lys Glu Leu
 40 45 50
 ccg tta gct ttt gat gta cca gca ggc act gtt ccc caa agc ttg agt 307
 Pro Leu Ala Phe Asp Val Pro Ala Gly Thr Val Pro Gln Ser Leu Ser
 55 60 65
 gga acg ctg cag att cct gcc gag ttt tct ggc ggc gtc gtg gag ttt 355
 Gly Thr Leu Gln Ile Pro Ala Glu Phe Ser Gly Gly Val Val Glu Phe
 70 75 80 85
 tat gac ggt gac cgg ctc ttt cac acc ctg cgc cta gaa gtt aat gat 403
 Tyr Asp Gly Asp Arg Leu Phe His Thr Leu Arg Leu Glu Val Asn Asp
 90 95 100
 tcc cga gca cac att gag gtt ccg ctg caa agc gtt cct gtc gaa gac 451
 Ser Arg Ala His Ile Glu Val Pro Leu Gln Ser Val Pro Val Glu Asp
 105 110 115

ggc cgc gcc acc ttt tgg ttg cgc gcc atg ttg gat cct gta aac aac Gly Arg Ala Thr Phe Trp Leu Arg Ala Met Leu Asp Pro Val Asn Asn 120 125 130	499
cag tgg tgc tac gag gag cag gaa gtc cgc ttc tta gac gga aac gtc Gln Trp Cys Tyr Glu Glu Gln Glu Val Arg Phe Leu Asp Gly Asn Val 135 140 145	547
acc ttt gaa ggg cgc acg att aac cca gct gtg gtg gct gat tac ttc Thr Phe Glu Gly Ala Thr Ile Asn Pro Ala Val Val Ala Asp Tyr Phe 150 155 160 165	595
ccg tca gtg ctg cgc gcg ttg aca att tac gtc ccg gaa aac ccc tct Pro Ser Val Leu Arg Ala Leu Thr Ile Tyr Val Pro Glu Asn Pro Ser 170 175 180	643
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gac gag ctt tac gat caa gcg cgc ttg ctt acc gac gca acc ctg cca Asp Glu Leu Tyr Asp Gln Ala Arg Leu Leu Thr Asp Ala Thr Leu Pro 265 270 275	931
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atc att gac cgt gag ttc aac gtt cct gga gac ttg gtc aac cgc tac	1267
Ile Ile Asp Arg Glu Phe Asn Val Pro Gly Asp Leu Val Asn Arg Tyr	
375 380 385	
acg gcg atc gtc gtg gaa ttc acc agc acc ggc gac gtt aat tgt ggg	1315
Thr Ala Ile Val Val Glu Phe Thr Ser Thr Gly Asp Val Asn Cys Gly	
390 395 400 405	
gtc acc cag ccc gta ggc ctc aac att gat tcc gac agc ctt gtc acc	1363
Val Thr Gln Pro Val Gly Leu Asn Ile Asp Ser Asp Ser Leu Val Thr	
410 415 420	
tcc caa cat tca gat gtt cct gta ctc aac ggc ttc cgg tcc cta ccg	1411
Ser Gln His Ser Asp Val Pro Val Leu Asn Gly Phe Arg Ser Leu Pro	
425 430 435	
cag tcc ttc caa cct cgt gtg gac gtg gcg ttt gct gat ccc agc gtg	1459
Gln Ser Phe Gln Pro Arg Val Asp Val Ala Phe Ala Asp Pro Ser Val	
440 445 450	
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Gln Glu Leu Ser Arg Ala Val Ser Val Val Leu Gly Ile Gln Ser Met	
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Ala Ser Glu Arg Pro Thr Ile Phe Ile Asp Ala Ala Gly Ala Lys Thr	
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Asp Gln Val Pro Ser Tyr Leu Ala Gln Gln Gly Gln Thr Leu Glu Ile	
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Thr Ser Lys Asn Asp Gln Asn Ala Asp Gly Glu Gln Leu Thr Arg Ser	
520 525 530	
ctg caa acc aac gct gcg ctt gtt gtc ggt tcc att cag gcc gtg tgg	1747
Leu Gln Thr Asn Ala Ala Leu Val Val Gly Ser Ile Gln Ala Val Trp	
535 540 545	
gat gcc gat aag aag cgc acg gtg att gtg gca agt tcc cag gac aac	1795
Asp Ala Asp Lys Lys Arg Thr Val Ile Val Ala Ser Ser Gln Asp Asn	
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Pro Pro Asp Leu Asp Ala Leu Ile Ser Trp Met Gly Glu Asp Arg Glu	
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Arg Trp Ser Asp Leu Asn Gly Asp Leu Ile Val Lys Val Arg Asp Arg	
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gaa cct gtg caa ttg acc acc gtg gaa gcc cca gat cag cct ggt cga	1939
Glu Pro Val Gln Leu Thr Thr Val Glu Ala Pro Asp Gln Pro Gly Arg	

600	605	610	
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Ser Ala Thr Ala Phe Ile Ala Ile Gly Val Ser Leu Val Val Ile Ala			
615	620	625	
ctg att gtc gca gcc gtg gtg tca gtg tcc agg cgt tcg caa aaa gga			2035
Leu Ile Val Ala Ala Val Val Ser Val Ser Arg Arg Ser Gln Lys Gly			
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Tyr Lys			

<210> 768

<211> 647

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 768

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Leu Pro Leu Ser Ala Leu Ser Ser Ser Asp Asp Ile Ala Val Pro Asn			
35	40	45	

Phe Ala Lys Glu Leu Pro Leu Ala Phe Asp Val Pro Ala Gly Thr Val			
50	55	60	

Pro Gln Ser Leu Ser Gly Thr Leu Gln Ile Pro Ala Glu Phe Ser Gly			
65	70	75	80

Gly Val Val Glu Phe Tyr Asp Gly Asp Arg Leu Phe His Thr Leu Arg			
85	90	95	

Leu Glu Val Asn Asp Ser Arg Ala His Ile Glu Val Pro Leu Gln Ser			
100	105	110	

Val Pro Val Glu Asp Gly Arg Ala Thr Phe Trp Leu Arg Ala Met Leu			
115	120	125	

Asp Pro Val Asn Asn Gln Trp Cys Tyr Glu Glu Gln Glu Val Arg Phe			
130	135	140	

Leu Asp Gly Asn Val Thr Phe Glu Gly Ala Thr Ile Asn Pro Ala Val			
145	150	155	160

Val Ala Asp Tyr Phe Pro Ser Val Leu Arg Ala Leu Thr Ile Tyr Val			
165	170	175	

Pro Glu Asn Pro Ser Glu Ala Val Gln Glu Ala Thr Leu Glu Val Ala			
180	185	190	

Thr Ser Leu Asp Ser Val Tyr Arg Arg Ser Gly Leu Asp Val Asn Val			
195	200	205	

Glu Thr Leu Pro Thr Gly Thr Asp Ala Pro Pro Thr Arg Pro Gln Asp			
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210					215					220					
Phe	Glu	Arg	Gln	Ile	Val	Leu	Val	Asp	Glu	Ala	Thr	Glu	Ser	Asn	Thr
225					230					235					240
Gln	Lys	Thr	Glu	Leu	Val	Asn	Pro	Gly	Gln	Asp	Asn	Ala	Phe	Leu	Arg
				245					250					255	
Leu	Asn	Gly	Asn	Ala	Asp	Glu	Leu	Tyr	Asp	Gln	Ala	Arg	Leu	Leu	Thr
			260					265					270		
Asp	Ala	Thr	Leu	Pro	Leu	Ala	Val	Asp	Thr	Glu	Val	Thr	Ala	Ser	Gly
			275					280					285		
Phe	Gly	Asp	Val	Pro	Asn	Leu	Ser	Thr	Asp	Val	Ala	Thr	Leu	Gln	Glu
	290					295					300				
Leu	Gly	Ile	Thr	Gln	Leu	Thr	Ser	Glu	Ser	Val	Ala	Arg	Thr	Ser	Val
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Thr	Leu	Gly	Ile	Glu	Arg	Ser	Arg	Leu	Arg	Thr	Tyr	Ser	Gln	Ser	Met
				325					330					335	
Asp	Leu	His	Ile	Thr	Gly	Thr	Tyr	Thr	Pro	Leu	Pro	Pro	Gln	Asn	Ala
			340					345						350	
Gly	Gln	Ile	Thr	Phe	Ser	Ile	Gly	Asp	Thr	Val	Leu	Asp	Ser	Leu	Thr
			355				360					365			
Thr	Asp	Asp	Thr	Gly	Ile	Ile	Asp	Arg	Glu	Phe	Asn	Val	Pro	Gly	Asp
	370					375					380				
Leu	Val	Asn	Arg	Tyr	Thr	Ala	Ile	Val	Val	Glu	Phe	Thr	Ser	Thr	Gly
385						390					395				400
Asp	Val	Asn	Cys	Gly	Val	Thr	Gln	Pro	Val	Gly	Leu	Asn	Ile	Asp	Ser
			405						410					415	
Asp	Ser	Leu	Val	Thr	Ser	Gln	His	Ser	Asp	Val	Pro	Val	Leu	Asn	Gly
			420					425					430		
Phe	Arg	Ser	Leu	Pro	Gln	Ser	Phe	Gln	Pro	Arg	Val	Asp	Val	Ala	Phe
			435				440						445		
Ala	Asp	Pro	Ser	Val	Gln	Glu	Leu	Ser	Arg	Ala	Val	Ser	Val	Val	Leu
	450					455					460				
Gly	Ile	Gln	Ser	Met	Ser	Ser	Gln	Arg	Ile	Arg	Pro	His	Leu	Val	Asn
465						470					475				480
Trp	Asp	Glu	Ala	Val	Ala	Ser	Glu	Arg	Pro	Thr	Ile	Phe	Ile	Asp	Ala
				485					490					495	
Ala	Gly	Ala	Lys	Thr	Asp	Gln	Val	Pro	Ser	Tyr	Leu	Ala	Gln	Gln	Gly
			500					505					510		
Gln	Thr	Leu	Glu	Ile	Thr	Ser	Lys	Asn	Asp	Gln	Asn	Ala	Asp	Gly	Glu
			515				520						525		
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Ile Gln Ala Val Trp Asp Ala Asp Lys Lys Arg Thr Val Ile Val Ala
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Ser Ser Gln Asp Asn Pro Pro Asp Leu Asp Ala Leu Ile Ser Trp Met
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Gly Glu Asp Arg Glu Arg Trp Ser Asp Leu Asn Gly Asp Leu Ile Val
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Lys Val Arg Asp Arg Glu Pro Val Gln Leu Thr Thr Val Glu Ala Pro
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Asp Gln Pro Gly Arg Ser Ala Thr Ala Phe Ile Ala Ile Gly Val Ser
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                                     Val Lys Ile Lys Ser
                                     1                               5

gta ttt ttg agc acc gct tta agc gct tcc tta ctg ctc gga atc acc 163
Val Phe Leu Ser Thr Ala Leu Ser Ala Ser Leu Leu Leu Gly Ile Thr
                        10                      15                      20

cca ccc gtg ctg gga gca acg atc aac ccc agt ttg cct ctt tct gcg 211
Pro Pro Val Leu Gly Ala Thr Ile Asn Pro Ser Leu Pro Leu Ser Ala
                        25                      30                      35

ttg agc tcc tcg gac gat atc gcc gta ccc aac ttc gcc aaa gaa tta 259
Leu Ser Ser Ser Asp Asp Ile Ala Val Pro Asn Phe Ala Lys Glu Leu
                        40                      45                      50

ccg tta gct ttt gat gta cca gca ggc act gtt ccc caa agc ttg agt 307
Pro Leu Ala Phe Asp Val Pro Ala Gly Thr Val Pro Gln Ser Leu Ser
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gga acg ctg cag att cct gcc gag ttt tct ggc ggc gtc gtg gag ttt 355
Gly Thr Leu Gln Ile Pro Ala Glu Phe Ser Gly Gly Val Val Glu Phe
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tat gac ggt gac cgg ctc ttt cac acc ctg cgc cta gaa gtt aat gat 403

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Ser	Arg	Ala	His 105	Ile	Glu	Val	Pro	Leu 110	Gln	Ser	Val	Pro	Val 115	Glu	Asp	
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Gly	Arg	Ala	Thr 120	Phe	Trp	Leu	Arg 125	Ala	Met	Leu	Asp	Pro	Val 130	Asn	Asn	
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Gln	Trp	Cys	Tyr	Glu	Glu	Gln	Glu 140	Val	Arg	Phe	Leu 145	Asp	Gly	Asn	Val	
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Thr	Phe	Glu	Gly	Ala	Thr	Ile	Asn 155	Pro	Ala	Val	Val 160	Ala	Asp	Tyr	Phe 165	
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Pro	Ser	Val	Leu 170	Arg	Ala	Leu	Thr 175	Ile	Tyr	Val	Pro	Glu	Asn 180	Pro	Ser	
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Glu	Ala	Val	Gln 185	Glu	Ala	Thr	Leu 190	Glu	Val	Ala	Thr	Ser	Leu 195	Asp	Ser	
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Val	Tyr	Arg	Arg 200	Ser	Gly	Leu	Asp 205	Val	Asn	Val	Glu 210	Thr	Leu	Pro	Thr	
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Gly	Thr	Asp	Ala 215	Pro	Pro	Thr	Arg 220	Pro	Gln	Asp	Phe 225	Glu	Arg	Gln	Ile	
gtg	ctg	gtt	gac	gag	gca	aca	gaa	agt	aac	acg	caa	aaa	acc	gaa	ttg	835
Val	Leu	Val	Asp	Glu	Ala	Thr	Glu 235	Ser	Asn	Thr	Gln 240	Lys	Thr	Glu	Leu 245	
gtc	aat	ccc	ggc	caa	gac	aat	gca	ttc	ttg	cgc	ctg	aac	ggc	aac	gcc	883
Val	Asn	Pro	Gly 250	Gln	Asp	Asn	Ala 255	Phe	Leu	Arg	Leu	Asn	Gly 260	Asn	Ala	
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Asp	Glu	Leu	Tyr 265	Asp	Gln	Ala	Arg 270	Leu	Leu	Thr	Asp	Ala 275	Thr	Leu	Pro	
ctt	gcc	gta	gac	acc	gaa	gta	acg	gcc	tca	ggt	ttt	ggt	gat	gtg	ccc	979
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Asn	Leu	Ser	Thr 295	Asp	Val	Ala	Thr 300	Leu	Gln	Glu	Leu 305	Gly	Ile	Thr	Gln	
ctc	acc	tct	gaa	tca	gtt	gcg	cgc	aca	agc	gtc	acc	ttg	ggc	att	gaa	1075
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cgc	tcc	cgc	ctg	cgg	acc	tac	tcg	cag	tcc	atg	gac	ctg	cac	ata	acg	1123
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	tcc att ggt gac acc gtg ttg gac tcc ttg acc acc gat gac act ggc			1219
	Ser Ile Gly Asp Thr Val Leu Asp Ser Ser Leu Thr Thr Asp Asp Thr Gly			
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	atc att gac cgt gag ttg aac gtt cct gga gac ttg gtc aac cgc tac			1267
	Ile Ile Asp Arg Glu Phe Asn Val Pro Gly Asp Leu Val Asn Arg Tyr			
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	acg gcg atc gtc gtg gaa ttc acc agc acc ggc gac gtt aat tgt ggg			1315
	Thr Ala Ile Val Val Glu Phe Thr Ser Thr Thr Gly Asp Val Asn Cys Gly			
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	gtc acc cag ccc gta ggc ctc aac att gat tcc gac agc ctt gtc acc			1363
	Val Thr Gln Pro Val Gly Leu Asn Ile Asp Ser Asp Ser Leu Val Thr			
	410	415	420	
	tcc caa cat tca gat gtt cct gta ctc aac ggc ttc cgg tcc cta ccg			1411
	Ser Gln His Ser Asp Val Pro Val Leu Asn Gly Phe Arg Ser Leu Pro			
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	cag tcc ttc caa cct cgt gtg gac gtg gcg ttt gct gat ccc agc gtg			1459
	Gln Ser Phe Gln Pro Arg Val Asp Val Ala Phe Ala Asp Pro Ser Val			
	440	445	450	
	cag gaa ctc tcc cgc gct gtc agc gta gtg ttg gga att caa tct atg			1507
	Gln Glu Leu Ser Arg Ala Val Ser Val Val Leu Gly Ile Gln Ser Met			
	455	460	465	
	agc tcc cag cgc atc cgc cca cac ctg gtt aac tgg gat gaa gcc gta			1555
	Ser Ser Gln Arg Ile Arg Pro His Leu Val Asn Trp Asp Glu Ala Val			
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	gcc agc gag cgc cca aca att ttc att gat gct gcg gcc gca aag act			1603
	Ala Ser Glu Arg Pro Thr Ile Phe Ile Asp Ala Ala Gly Ala Lys Thr			
	490	495	500	
	gat caa gtg cca agc tac ctc gcc caa caa gcc caa acc cta gag atc			1651
	Asp Gln Val Pro Ser Tyr Leu Ala Gln Gln Gly Gln Thr Leu Glu Ile			
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	acc agc aag aac gac caa aat gcg gac ggc gaa caa ctc acc cga tcc			1699
	Thr Ser Lys Asp Asn Asp Gln Asn Ala Asp Gly Glu Gln Leu Thr Arg Ser			
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	ctg caa acc aac gct gcg ctt gtt gtc ggt tcc att cag gcc gtg tgg			1747
	Leu Gln Thr Asn Ala Ala Leu Val Val Gly Ser Ile Gln Ala Val Trp			
	535	540	545	
	gat gcc gat aag aag cgc acg gtg att gtg gca agt tcc cag gac aac			1795
	Asp Ala Asp Lys Lys Arg Thr Val Ile Val Ala Ser Ser Gln Asp Asn			
	550	555	560	565
	ccc ccc gat ttg gat gcc ttg att tgg tgg atg gga gaa gac cgc gaa			1843
	Pro Pro Asp Leu Asp Ala Leu Ile Ser Trp Met Gly Glu Asp Arg Glu			
	570	575	580	

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 Arg Trp Ser Asp Leu Asn Gly Asp Leu Ile Val Lys Val Arg Asp Arg
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 gaa cct gtg caa ttg acc acc gtg gaa gcc cca gat cag cct ggt cga 1939
 Glu Pro Val Gln Leu Thr Thr Val Glu Ala Pro Asp Gln Pro Gly Arg
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 tcg gcc aca gcc ttt att gcg atc ggc gtc agc ctt gtg gtc att gcc 1987
 Ser Ala Thr Ala Phe Ile Ala Ile Gly Val Ser Leu Val Val Ile Ala
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 Pro Gln Ser Leu Ser Gly Thr Leu Gln Ile Pro Ala Glu Phe Ser Gly
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 Gly Val Val Glu Phe Tyr Asp Gly Asp Arg Leu Phe His Thr Leu Arg
 85 90 95
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 100 105 110
 Val Pro Val Glu Asp Gly Arg Ala Thr Phe Trp Leu Arg Ala Met Leu
 115 120 125
 Asp Pro Val Asn Asn Gln Trp Cys Tyr Glu Glu Gln Glu Val Arg Phe
 130 135 140
 Leu Asp Gly Asn Val Thr Phe Glu Gly Ala Thr Ile Asn Pro Ala Val
 145 150 155 160
 Val Ala Asp Tyr Phe Pro Ser Val Leu Arg Ala Leu Thr Ile Tyr Val
 165 170 175

Pro Glu Asn Pro Ser Glu Ala Val Gln Glu Ala Thr Leu Glu Val Ala
 180 185 190
 Thr Ser Leu Asp Ser Val Tyr Arg Arg Ser Gly Leu Asp Val Asn Val
 195 200 205
 Glu Thr Leu Pro Thr Gly Thr Asp Ala Pro Pro Thr Arg Pro Gln Asp
 210 215 220
 Phe Glu Arg Gln Ile Val Leu Val Asp Glu Ala Thr Glu Ser Asn Thr
 225 230 235 240
 Gln Lys Thr Glu Leu Val Asn Pro Gly Gln Asp Asn Ala Phe Leu Arg
 245 250 255
 Leu Asn Gly Asn Ala Asp Glu Leu Tyr Asp Gln Ala Arg Leu Leu Thr
 260 265 270
 Asp Ala Thr Leu Pro Leu Ala Val Asp Thr Glu Val Thr Ala Ser Gly
 275 280 285
 Phe Gly Asp Val Pro Asn Leu Ser Thr Asp Val Ala Thr Leu Gln Glu
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 Leu Gly Ile Thr Gln Leu Thr Ser Glu Ser Val Ala Arg Thr Ser Val
 305 310 315 320
 Thr Leu Gly Ile Glu Arg Ser Arg Leu Arg Thr Tyr Ser Gln Ser Met
 325 330 335
 Asp Leu His Ile Thr Gly Thr Tyr Thr Pro Leu Pro Pro Gln Asn Ala
 340 345 350
 Gly Gln Ile Thr Phe Ser Ile Gly Asp Thr Val Leu Asp Ser Leu Thr
 355 360 365
 Thr Asp Asp Thr Gly Ile Ile Asp Arg Glu Phe Asn Val Pro Gly Asp
 370 375 380
 Leu Val Asn Arg Tyr Thr Ala Ile Val Val Glu Phe Thr Ser Thr Gly
 385 390 395 400
 Asp Val Asn Cys Gly Val Thr Gln Pro Val Gly Leu Asn Ile Asp Ser
 405 410 415
 Asp Ser Leu Val Thr Ser Gln His Ser Asp Val Pro Val Leu Asn Gly
 420 425 430
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 Ala Asp Pro Ser Val Gln Glu Leu Ser Arg Ala Val Ser Val Val Leu
 450 455 460
 Gly Ile Gln Ser Met Ser Ser Gln Arg Ile Arg Pro His Leu Val Asn
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 Trp Asp Glu Ala Val Ala Ser Glu Arg Pro Thr Ile Phe Ile Asp Ala
 485 490 495
 Ala Gly Ala Lys Thr Asp Gln Val Pro Ser Tyr Leu Ala Gln Gln Gly

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Ile Gln Ala Val Trp Asp Ala Asp Lys Lys Arg Thr Val Ile Val Ala
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Ser Ser Gln Asp Asn Pro Pro Asp Leu Asp Ala Leu Ile Ser Trp Met
565          570          575
Gly Glu Asp Arg Glu Arg Trp Ser Asp Leu Asn Gly Asp Leu Ile Val
580          585          590
Lys Val Arg Asp Arg Glu Pro Val Gln Leu Thr Thr Val Glu Ala Pro
595          600          605
Asp Gln Pro Gly Arg Ser Ala Thr Ala Phe Ile Ala Ile Gly Val Ser
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Val Thr Ala Thr Val
1 5
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Leu Glu Pro Gln Pro Val Gln Leu Ser Glu Gln Asp Val Asp Ala Glu
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Ile Ala Arg Met Glu Leu Lys His Asn Arg His Lys Thr Trp Arg Arg
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Arg Thr Met Ala Val Val Met Thr Leu Leu Ile Ser Val Gly Leu Ser
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Phe Gly Ala Phe Gly Asn Lys Glu Arg Glu Ala Asn Ala Phe Ala Ser

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Ala Ile Cys Pro Ser Asp Gly Asp Thr Glu Met Leu Leu Lys Cys Ile			
	90	95	100
acc gag aac tta ggt gaa atg cac att atc gag aag tgt ctc gaa gca			451
Thr Glu Asn Leu Gly Glu Met His Ile Ile Glu Lys Cys Leu Glu Ala			
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gaa gat gtc ttg aag tgc ttc tac gat gcg aaa aac gaa gag caa cgt			499
Glu Asp Val Leu Lys Cys Phe Tyr Asp Ala Lys Asn Glu Glu Gln Arg			
	120	125	130
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Lys Glu Gln Asn Leu Asp Lys Ala Pro Asp Tyr Ser Met Tyr Arg Met			
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Ala Ser Ala Met Ala Ser Phe Tyr Gly Asn Gly Arg Ala Ala Thr Ala			
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Gly Val Glu Glu Gly Gly Pro Asn Glu Phe Leu Asp Ser Glu Asp Ala			
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Gly Leu Lys Val Trp Glu Gly Ile Leu Ser Lys Ala Ala Asn Gly Gly			
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Asn Val Leu Gly Tyr Ala Asp Ala Lys His Asn Glu Asp Ser Gly Trp			
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Phe Phe Gly Asn Gly Val Ala Asn Asn Glu Lys Thr Tyr Ser Tyr Asp			
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Gly Ala Thr Leu Ser Ser Gly Leu Gly Phe Asp Ser Ser Lys Ala Glu Asp			
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Ser Gln Thr Asp Phe Ala Gln Arg Lys Gly Met Gly Tyr Ala Met Met			
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atc gcg tac atc atc tcc gga ggc att gat ctg gtt ttt aac act gtg			979
Ile Ala Tyr Ile Ile Ser Gly Gly Ile Asp Leu Val Phe Asn Thr Val			
	280	285	290
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Leu Asn Ile Leu Ser Thr Ile Asn Pro Phe Arg Leu Leu Val Gly Pro			
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 490 495 500

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 Asn Asp Ser Ile Ser Ser Gly Ser Phe Glu Thr Ser Ile Arg Ser Ala
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atc aca gtg gcc tca tcc atg ggg gtc atc atc ttc acg att att gcg	2611
Ile Thr Val Ala Ser Ser Met Gly Val Ile Ile Phe Thr Ile Ile Ala	
825 830 835	
atg aag gtg cgc gga tct ttg gta tca ggt gtc gat gaa acc gtg acc	2659
Met Lys Val Arg Gly Ser Leu Val Ser Gly Val Asp Glu Thr Val Thr	
840 845 850	
agt gtt att aac cgc ttc ttg gat aca cag gtc tct tct gca ggt gct	2707
Ser Val Ile Asn Arg Phe Leu Asp Thr Gln Val Ser Ser Ala Gly Ala	
855 860 865	
acc tct ggt gac ggc atg atg cgt cgt gca gcc gca acg ggt ctt ggt	2755
Thr Ser Gly Asp Gly Met Met Arg Arg Ala Ala Ala Thr Gly Leu Gly	
870 875 880 885	
att ggt gcg aca cat atg gta ctc aac cgt gat ggt gac ggt ggt gga	2803
Ile Gly Ala Thr His Met Val Leu Asn Arg Asp Gly Asp Gly Gly Gly	
890 895 900	
tct gat tca ggc tct ggt gga tca ggt ggc ggt agc gat tca ggc ttg	2851
Ser Asp Ser Gly Ser Gly Ser Gly Gly Gly Ser Asp Ser Gly Leu	
905 910 915	
ggg gag aag gct gct ggt ctg gcg aag gtt gtc aca act gtg gct ggt	2899
Gly Glu Lys Ala Ala Gly Leu Ala Lys Val Val Thr Thr Val Ala Gly	
920 925 930	
gcc gga tta gtc ggt aag tat gct acg gat gcg ctc gat aat tat gca	2947
Ala Gly Leu Val Gly Lys Tyr Ala Thr Asp Ala Leu Asp Asn Tyr Ala	
935 940 945	
gat ggc gtt atc aac ggc gac ggt gat ggt gcg ttc gca gca ggt ggt	2995
Asp Gly Val Ile Asn Gly Asp Gly Asp Gly Ala Phe Ala Ala Gly Gly	
950 955 960 965	
gac gct acc gtt gat ggc gac tat gta gca gat gga gat gca att gct	3043
Asp Ala Thr Val Asp Gly Asp Tyr Val Ala Asp Gly Asp Ala Ile Ala	
970 975 980	
tct gct gat gct aac gct gat ttt gta gac ggt gtt gtt gat ggt gct	3091
Ser Ala Asp Asn Ala Asp Phe Val Asp Gly Val Val Asp Gly Ala	
985 990 995	
ggg cgc gcg tca ttt agc aat gct gcg tat agc tcc gat gga acc act	3139
Gly Arg Ala Ser Phe Ser Asn Ala Ala Tyr Ser Ser Ser Asp Gly Thr Thr	
1000 1005 1010	
ctc gac ggt gag ggt gcg agc gtt gat gca cag ggt aac ccg ctt cat	3187
Leu Asp Gly Glu Gly Ala Ser Val Asp Ala Gln Gly Asn Pro Leu His	
1015 1020 1025	
gct gat ggc aca cca atg agt gct gct gaa gct gaa atg aag atg gct	3235
Ala Asp Gly Thr Pro Met Ser Ala Ala Glu Ala Glu Met Lys Met Ala	

1030	1035	1040	1045
ggt ctg agc tcg tca gga acc atg atg gag aaa tct ggt gtg aaa tcg			3283
Gly Leu Ser Ser Ser Gly Thr Met Met Glu Lys Ser Gly Val Lys Ser	1050	1055	1060
agt ggc att acc act gca gcg gat gtc atg gac gat cag tct ctg gca			3331
Ser Gly Ile Thr Thr Ala Ala Asp Val Met Asp Asp Gln Ser Leu Ala	1065	1070	1075
agc agt gtc act gag tct ggt ctg tcc aag att cca gac acc tat ggt			3379
Ser Ser Val Thr Glu Ser Gly Leu Ser Lys Ile Pro Asp Thr Tyr Gly	1080	1085	1090
gca gat gtc tcg ggt gct gcg ggc aca gtc gga act acc ggt gct gat			3427
Ala Asp Val Ser Gly Ala Ala Gly Thr Val Gly Thr Thr Gly Ala Asp	1095	1100	1105
tac agt gcg acc gat tca agc gca ggt ctg aac atg agc gag gct gca			3475
Tyr Ser Ala Thr Asp Ser Ser Ala Gly Leu Asn Met Ser Glu Ala Ala	1110	1115	1120
ttg cag agt ggc acc cca atg ggc gct ctc gct ggt gga tct gtg tcg			3523
Leu Gln Ser Gly Thr Pro Met Gly Ala Leu Ala Gly Gly Ser Val Ser	1130	1135	1140
agt tcc gat cag gcc atg aat gac gca gct ctt cag att gca gcg tct			3571
Ser Ser Asp Gln Ala Met Asn Asp Ala Ala Leu Gln Ile Ala Ala Ser	1145	1150	1155
cag ggt ctt gca cca gca ggt tcc ata gct ggt atg gag caa ctt agt			3619
Gln Gly Leu Ala Pro Ala Gly Ser Ile Ala Gly Met Glu Gln Leu Ser	1160	1165	1170
gct caa gcc act gaa gca cct gct gga aag gcc ggc aag cag ctt ggc			3667
Ala Gln Ala Thr Glu Ala Pro Ala Gly Lys Ala Gly Lys Gln Leu Gly	1175	1180	1185
gat ctt tct ggc tca gcg ctc aat act cag ctg gcg tcc atg gga cag			3715
Asp Leu Ser Gly Ser Ala Leu Asn Thr Gln Leu Ala Ser Met Gly Gln	1190	1195	1200
cag gta ggt gac agt gtg aac agc gct tat gct gca ggc ggt atg ggt			3763
Gln Val Gly Asp Ser Val Asn Ser Ala Tyr Ala Ala Gly Gly Met Gly	1210	1215	1220
ggt gtt gat gtg gct ggc aag gtc acc gag gca gca cag cac ttg tct			3811
Gly Val Asp Val Ala Gly Lys Val Thr Glu Ala Ala Gln His Leu Ser	1225	1230	1235
cag gtt cca ggt cag att cag aat gct gtg acc aat gcg gat gct ggt			3859
Gln Val Pro Gly Gln Ile Gln Asn Ala Val Thr Asn Ala Asp Ala Gly	1240	1245	1250
tcc tct ggc gca agc ttt ggt cag atg gca cag ggg gca gct ggt att			3907
Ser Ser Gly Ala Ser Phe Gly Gln Met Ala Gln Gly Ala Ala Gly Ile	1255	1260	1265
gcc ggt gtc gca ggt gtg atc ggt gca gcg ggc gca gca agc tct gca			3955
Ala Gly Val Ala Gly Val Ile Gly Ala Ala Gly Ala Ala Ser Ser Ala	1270	1275	1280
			1285

gca caa ggc gca ggt act gtc cag ggt gcg atg ggt aat gct gca gct 4003
Ala Gln Gly Ala Gly Thr Val Gln Gly Ala Met Gly Asn Ala Ala Ala
1290 1295 1300

ggt gcg gga atg atc aac aac gct gtt tcc ggt gga gct act ggc tca 4051
Gly Ala Gly Met Ile Asn Asn Ala Val Ser Gly Gly Ala Thr Gly Ser
1305 1310 1315

aca ggt gcc gca cat gtg gtc aat gca tca cat gga cca gtg gcg cct 4099
Thr Gly Ala Ala His Val Val Asn Ala Ser His Gly Pro Val Ala Pro
1320 1325 1330

ggt cag gct cac tac caa gag tct ggt cat gca caa gca ttt gtg cag 4147
Gly Gln Ala His Tyr Gln Glu Ser Gly His Ala Gln Phe Val Gln
1335 1340 1345

aac aac cag gcc aac acc gcg cac aca gca aac acg cgt gca ccg tca 4195
Asn Asn Gln Ala Asn Thr Ala His Thr Ala Asn Thr Arg Ala Pro Ser
1350 1355 1360 1365

tca gct caa att atg ggc gcg aac gtt gct ggc tca ctg gca tca cag 4243
Ser Ala Gln Ile Met Gly Ala Asn Val Ala Gly Ser Leu Ala Ser Gln
1370 1375 1380

gct gta cga gga atc ggt cag cct ggt cag atg ggt gct aat gtt cgc 4291
Ala Val Arg Gly Ile Gly Gln Pro Gly Gln Met Gly Ala Asn Val Arg
1385 1390 1395

gac gcg atg ggt ggc agc gga cgc tct ggt ggc cgt ggt gga gca act 4339
Asp Ala Met Gly Gly Ser Gly Arg Ser Gly Gly Arg Gly Gly Ala Thr
1400 1405 1410

caa ggc ggt cga ggc gca cag cgc agc ggt gtc agt gct aag aac ggt 4387
Gln Gly Gly Arg Gly Ala Gln Arg Ser Gly Val Ser Ala Lys Asn Gly
1415 1420 1425

atc cgt gca cag cga ggt cag aag cct tct gtg acc ggc cag gcg atg 4435
Ile Arg Ala Gln Arg Gly Gln Lys Pro Ser Val Thr Gly Gln Ala Met
1430 1435 1440 1445

aat gca gca atg cgt tca gca gcg gta agc ggt cgc atg gca aac atg 4483
Asn Ala Ala Met Arg Ser Ala Ala Val Ser Gly Arg Met Ala Asn Met
1450 1455 1460

gac ggc aac agt gta ggt ggc act gaa gca gat cca cag cag ggg agt 4531
Asp Gly Asn Ser Val Gly Gly Thr Glu Ala Asp Pro Gln Gln Gly Ser
1465 1470 1475

ggc gta acc gag aag ggt gat aaa ggc gtt aaa tagcgtgttaa aacacaatga 4584
Gly Val Thr Glu Lys Gly Asp Lys Gly Val Lys
1480 1485

ccg 4587

<210> 772

<211> 1488

<212> PRT

<213> Corynebacterium glutamicum

<400> 772

Val Thr Ala Thr Val Leu Glu Pro Gln Pro Val Gln Leu Ser Glu Gln
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Asp Val Asp Ala Glu Ile Ala Arg Met Glu Leu Lys His Asn Arg His
 20 25 30

Lys Thr Trp Arg Arg Arg Thr Met Ala Val Val Met Thr Leu Leu Ile
 35 40 45

Ser Val Gly Leu Ser Phe Gly Ala Phe Gly Asn Lys Glu Arg Glu Ala
 50 55 60

Asn Ala Phe Ala Ser Ala Ile Ile Ala Gln Val Val Gly Ala Met Gly
 65 70 75 80

Glu Val Ala Phe Glu Ala Ile Cys Pro Ser Asp Gly Asp Thr Glu Met
 85 90 95

Leu Leu Lys Cys Ile Thr Glu Asn Leu Gly Glu Met His Ile Ile Glu
 100 105 110

Lys Cys Leu Glu Ala Glu Asp Val Leu Lys Cys Phe Tyr Asp Ala Lys
 115 120 125

Asn Glu Glu Gln Arg Lys Glu Gln Asn Leu Asp Lys Ala Pro Asp Tyr
 130 135 140

Ser Met Tyr Arg Met Ala Ser Ala Met Ala Ser Phe Tyr Gly Asn Gly
 145 150 155 160

Arg Ala Ala Thr Ala Gly Val Glu Glu Gly Gly Pro Asn Glu Phe Leu
 165 170 175

Asp Ser Glu Asp Ala Gly Leu Lys Val Trp Glu Gly Ile Leu Ser Lys
 180 185 190

Ala Ala Asn Gly Gly Asn Val Leu Gly Tyr Ala Asp Ala Lys His Asn
 195 200 205

Glu Asp Ser Gly Trp Phe Phe Gly Asn Gly Val Ala Asn Asn Glu Lys
 210 215 220

Thr Tyr Ser Tyr Asp Ser Leu Ala Asp His Ala Phe Gln Gly Pro Tyr
 225 230 235 240

His Phe Ala Leu Phe Gly Ala Thr Leu Ser Gly Leu Gly Phe Asp Ser
 245 250 255

Ser Lys Ala Glu Asp Ser Gln Thr Asp Phe Ala Gln Arg Lys Gly Met
 260 265 270

Gly Tyr Ala Met Met Ile Ala Tyr Ile Ile Ser Gly Gly Ile Asp Leu
 275 280 285

Val Phe Asn Thr Val Leu Asn Ile Leu Ser Thr Ile Asn Pro Phe Arg
 290 295 300

Leu Leu Val Gly Pro Val Ser Gln Asn Thr Asn Lys Thr Phe Thr Glu
 305 310 315 320

Asn Met Ala Gly Gly Gln Thr Thr Glu Gly Thr Pro Phe Glu Gly Met
 325 330 335
 Thr Asp Phe Phe Gly Leu Ile Tyr Asn Trp Ser Val Thr Val Gly Trp
 340 345 350
 Leu Ile Gly Ile Pro Val Ser Ile Gly Leu Phe Met Met Gly Ala Leu
 355 360 365
 Met Phe Arg Arg Met Asp Lys Gly Ser Ala Phe Lys Lys Val Val Ile
 370 375 380
 Arg Val Val Tyr Gly Val Val Gly Leu Pro Leu Leu Gly Val Ser Tyr
 385 390 395 400
 Thr Gly Ala Leu Asp Ser Phe Leu Asp Ser Gly Ser Ser Thr Ser Ala
 405 410 415
 Gly Ser Asn Ala Thr Lys Ile Val Leu Ser Thr Tyr Val Asp Phe Gln
 420 425 430
 Ser Trp Ala Glu Asn Thr Arg Met Arg Val Pro Asp Lys Val Thr Leu
 435 440 445
 Ala Trp Ser Leu Glu Asp Gln Ala Pro Thr Gly Gln Ser Met Arg Met
 450 455 460
 Val Arg Asn Ser Ala Leu Glu Ile Asn Ala Gln Ser Asn Glu Ser Phe
 465 470 475 480
 Thr Thr Phe Lys Asn Pro Gly Ser Met Asp Leu Gly Tyr Ser Met Asp
 485 490 495
 Trp Met Glu Lys Met Ala Asp Pro Ala Asn Ser Gly Thr Asp Gly Thr
 500 505 510
 Ser Ser Ser Ser Ala Thr Thr Ile Phe Gln Gly Thr Ile Ala Leu Leu
 515 520 525
 Ser Arg Tyr Ile Asp Asn Asp Ser Ile Ser Ser Gly Ser Phe Glu Thr
 530 535 540
 Ser Ile Arg Ser Ala Met Glu Ser Leu Thr Ser Lys Glu Gly Ser Gly
 545 550 555 560
 Glu Ala Val Ala Gly Gly Asp Val Met Ala Trp Val Thr Gly Tyr Asn
 565 570 575
 Thr Ala Ser Gly Leu Asn Glu Ile Thr Ala Ala Glu Leu Ala Asp Ala
 580 585 590
 Asn Asn Pro Leu Leu Glu Val Ser Asp Ser Ala Gly Leu Gln Gly Arg
 595 600 605
 Pro Ile Asp Arg Asn Ala Val Ser Phe Lys Ser Gly Asp Ala Thr Ala
 610 615 620
 Ser Cys Asn Asn Ser Val Val Thr Gly Ser Arg Ala Val Val Gly Asp
 625 630 635 640
 Tyr Arg Ser Asp Cys Asn Met Ser Pro Leu Thr Met Tyr Asn Phe Leu

645										650					655				
Asn	Thr	Ser	Phe	His	Pro	Ala	Asp	Ala	Ser	Val	Phe	Ser	Thr	Ser	Thr				
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Ser	Ala	Ser	Ser	Tyr	Thr	Arg	Ala	Ser	His	Ser	Ala	Val	Ser	Leu	Ile				
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Gly	Ser	Gly	Ala	Met	Asn	Phe	Val	Tyr	Trp	Phe	Ser	Ala	Met	Ser	Leu				
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Met	Gly	Ser	Phe	Ile	Val	Ile	Gly	Ile	Gly	Tyr	Ala	Gly	Ala	Met	Leu				
705					710					715					720				
Phe	Asn	Thr	Ile	Arg	Arg	Thr	Leu	Ser	Leu	Ile	Gly	Ala	Val	Pro	Phe				
				725					730					735					
Ala	Ala	Met	Gly	Phe	Ile	Ala	Gly	Val	Ala	Lys	Val	Ile	Val	Tyr	Thr				
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Ile	Ala	Met	Leu	Val	Glu	Val	Ile	Gly	Thr	Ile	Ile	Leu	Tyr	Gln	Leu				
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Ile	Thr	Arg	Phe	Leu	Met	Ala	Val	Pro	Ala	Leu	Phe	Glu	Gln	Pro	Leu				
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Ala	Asp	Ser	Leu	Ser	Ser	Asn	Glu	Ser	Ala	Glu	Leu	Val	Ala	Gly	Ala				
785					790					795					800				
Gly	Met	Gly	Leu	Val	Gly	Met	Ala	Leu	Ala	Thr	Ser	Gly	Asn	Trp	Ala				
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Ile	Ala	Gly	Met	Val	Ile	Thr	Val	Ala	Ser	Ser	Met	Gly	Val	Ile	Ile				
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Phe	Thr	Ile	Ile	Ala	Met	Lys	Val	Arg	Gly	Ser	Leu	Val	Ser	Gly	Val				
			835				840					845							
Asp	Glu	Thr	Val	Thr	Ser	Val	Ile	Asn	Arg	Phe	Leu	Asp	Thr	Gln	Val				
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Ser	Ser	Ala	Gly	Ala	Thr	Ser	Gly	Asp	Gly	Met	Met	Arg	Arg	Ala	Ala				
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Ala	Thr	Gly	Leu	Gly	Ile	Gly	Ala	Thr	His	Met	Val	Leu	Asn	Arg	Asp				
				885					890					895					
Gly	Asp	Gly	Gly	Gly	Ser	Asp	Ser	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Gly				
			900					905					910						
Ser	Asp	Ser	Gly	Leu	Gly	Glu	Lys	Ala	Ala	Gly	Leu	Ala	Lys	Val	Val				
			915				920					925							
Thr	Thr	Val	Ala	Gly	Ala	Gly	Leu	Val	Gly	Lys	Tyr	Ala	Thr	Asp	Ala				
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Leu	Asp	Asn	Tyr	Ala	Asp	Gly	Val	Ile	Asn	Gly	Asp	Gly	Asp	Gly	Ala				
945					950					955					960				
Phe	Ala	Ala	Gly	Gly	Asp	Ala	Thr	Val	Asp	Gly	Asp	Tyr	Val	Ala	Asp				
				965					970						975				

Gly Asp Ala Ile Ala Ser Ala Asp Ala Asn Ala Asp Phe Val Asp Gly
 980 985 990
 Val Val Asp Gly Ala Gly Arg Ala Ser Phe Ser Asn Ala Ala Tyr Ser
 995 1000 1005
 Ser Asp Gly Thr Thr Leu Asp Gly Glu Gly Ala Ser Val Asp Ala Gln
 1010 1015 1020
 Gly Asn Pro Leu His Ala Asp Gly Thr Pro Met Ser Ala Ala Glu Ala
 1025 1030 1035 1040
 Glu Met Lys Met Ala Gly Leu Ser Ser Ser Gly Thr Met Met Glu Lys
 1045 1050 1055
 Ser Gly Val Lys Ser Ser Gly Ile Thr Thr Ala Ala Asp Val Met Asp
 1060 1065 1070
 Asp Gln Ser Leu Ala Ser Ser Val Thr Glu Ser Gly Leu Ser Lys Ile
 1075 1080 1085
 Pro Asp Thr Tyr Gly Ala Asp Val Ser Gly Ala Ala Gly Thr Val Gly
 1090 1095 1100
 Thr Thr Gly Ala Asp Tyr Ser Ala Thr Asp Ser Ser Ala Gly Leu Asn
 1105 1110 1115 1120
 Met Ser Glu Ala Ala Leu Gln Ser Gly Thr Pro Met Gly Ala Leu Ala
 1125 1130 1135
 Gly Gly Ser Val Ser Ser Ser Asp Gln Ala Met Asn Asp Ala Ala Leu
 1140 1145 1150
 Gln Ile Ala Ala Ser Gln Gly Leu Ala Pro Ala Gly Ser Ile Ala Gly
 1155 1160 1165
 Met Glu Gln Leu Ser Ala Gln Ala Thr Glu Ala Pro Ala Gly Lys Ala
 1170 1175 1180
 Gly Lys Gln Leu Gly Asp Leu Ser Gly Ser Ala Leu Asn Thr Gln Leu
 1185 1190 1195 1200
 Ala Ser Met Gly Gln Gln Val Gly Asp Ser Val Asn Ser Ala Tyr Ala
 1205 1210 1215
 Ala Gly Gly Met Gly Gly Val Asp Val Ala Gly Lys Val Thr Glu Ala
 1220 1225 1230
 Ala Gln His Leu Ser Gln Val Pro Gly Gln Ile Gln Asn Ala Val Thr
 1235 1240 1245
 Asn Ala Asp Ala Gly Ser Ser Gly Ala Ser Phe Gly Gln Met Ala Gln
 1250 1255 1260
 Gly Ala Ala Gly Ile Ala Gly Val Ala Gly Val Ile Gly Ala Ala Gly
 1265 1270 1275 1280
 Ala Ala Ser Ser Ala Ala Gln Gly Ala Gly Thr Val Gln Gly Ala Met
 1285 1290 1295

Gly Asn Ala Ala Ala Gly Ala Gly Met Ile Asn Asn Ala Val Ser Gly
1300 1305 1310

Gly Ala Thr Gly Ser Thr Gly Ala Ala His Val Val Asn Ala Ser His
1315 1320 1325

Gly Pro Val Ala Pro Gly Gln Ala His Tyr Gln Glu Ser Gly His Ala
1330 1335 1340

Gln Ala Phe Val Gln Asn Asn Gln Ala Asn Thr Ala His Thr Ala Asn
1345 1350 1355 1360

Thr Arg Ala Pro Ser Ser Ala Gln Ile Met Gly Ala Asn Val Ala Gly
1365 1370 1375

Ser Leu Ala Ser Gln Ala Val Arg Gly Ile Gly Gln Pro Gly Gln Met
1380 1385 1390

Gly Ala Asn Val Arg Asp Ala Met Gly Gly Ser Gly Arg Ser Gly Gly
1395 1400 1405

Arg Gly Gly Ala Thr Gln Gly Gly Arg Gly Ala Gln Arg Ser Gly Val
1410 1415 1420

Ser Ala Lys Asn Gly Ile Arg Ala Gln Arg Gly Gln Lys Pro Ser Val
1425 1430 1435 1440

Thr Gly Gln Ala Met Asn Ala Ala Met Arg Ser Ala Ala Val Ser Gly
1445 1450 1455

Arg Met Ala Asn Met Asp Gly Asn Ser Val Gly Gly Thr Glu Ala Asp
1460 1465 1470

Pro Gln Gln Gly Ser Gly Val Thr Glu Lys Gly Asp Lys Gly Val Lys
1475 1480 1485

<210> 773

<211> 916

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(916)

<223> FRXA00739

<400> 773

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agcaattgtt taaaacgaat attgaggggg tggcgggcaa gtg act gcg aca gtt 115
Val Thr Ala Thr Val
1 5

tta gaa ccg caa cct gta cag ctt agt gag cag gac gta gat gct gag 163
Leu Glu Pro Gln Pro Val Gln Leu Ser Glu Gln Asp Val Asp Ala Glu
10 15 20

att gcg cgc atg gag ctt aaa cac aac cga cac aag acg tgg cga cgc 211
 Ile Ala Arg Met Glu Leu Lys His Asn Arg His Lys Thr Trp Arg Arg
 25 30 35

cga acg atg gct gtt gtc atg acg ctc ttg atc tca gtg ggt ttg agc 259
 Arg Thr Met Ala Val Val Met Thr Leu Leu Ile Ser Val Gly Leu Ser
 40 45 50

ttt ggt gcg ttt ggt aac aag gaa cgt gaa gct aat gct ttc gcc agc 307
 Phe Gly Ala Phe Gly Asn Lys Glu Arg Glu Ala Asn Ala Phe Ala Ser
 55 60 65

gct att att gcc cag gtt gtc ggt gct atg ggc gag gtt gcc ttt gaa 355
 Ala Ile Ile Ala Gln Val Val Gly Ala Met Gly Glu Val Ala Phe Glu
 70 75 80 85

gcg att tgt ccc agt gat ggt gac acc gag atg ctt ctt aag tgc atc 403
 Ala Ile Cys Pro Ser Asp Gly Asp Thr Glu Met Leu Leu Lys Cys Ile
 90 95 100

acc gag aac tta ggt gaa atg cac att atc gag aag tgt ctc gaa gca 451
 Thr Glu Asn Leu Gly Glu Met His Ile Ile Glu Lys Cys Leu Glu Ala
 105 110 115

gaa gat gtc ttg aag tgc ttc tac gat gcg aaa aac gaa gag caa cgt 499
 Glu Asp Val Leu Lys Cys Phe Tyr Asp Ala Lys Asn Glu Glu Gln Arg
 120 125 130

aaa gaa cag aac ctt gat aaa gcc cct gat tac tcc atg tac cgt atg 547
 Lys Glu Gln Asn Leu Asp Lys Ala Pro Asp Tyr Ser Met Tyr Arg Met
 135 140 145

gcc tct gcg atg gca tgc ttc tat ggc aat ggt cgg gca gct act gcc 595
 Ala Ser Ala Met Ala Ser Phe Tyr Gly Asn Gly Arg Ala Ala Thr Ala
 150 155 160 165

ggt gta gag gaa ggc gga ccg aac gag ttc ctc gat tct gag gac gcc 643
 Gly Val Glu Glu Gly Gly Pro Asn Glu Phe Leu Asp Ser Glu Asp Ala
 170 175 180

ggt ctt aag gtg tgg gag ggc att ctc agt aag gcc gcc aac gga ggc 691
 Gly Leu Lys Val Trp Glu Gly Ile Leu Ser Lys Ala Ala Asn Gly Gly
 185 190 195

aat gtc ctt ggt tat gct gac gcg aaa cac aac gag gac tct ggt tgg 739
 Asn Val Leu Gly Tyr Ala Asp Ala Lys His Asn Glu Asp Ser Gly Trp
 200 205 210

ttc ttt ggt aat ggt gtt gcc aac aac gag aaa acg tac tcc tat gat 787
 Phe Phe Gly Asn Gly Val Ala Asn Asn Glu Lys Thr Tyr Ser Tyr Asp
 215 220 225

tct cta gct gat cat gcc ttt caa ggg cct tat cac ttt gca tta ttt 835
 Ser Leu Ala Asp His Ala Phe Gln Gly Pro Tyr His Phe Ala Leu Phe
 230 235 240 245

ggc gcg aca ctg agt ggc tta ggc ttt gat agc tca aag gcg gag gat 883
 Gly Ala Thr Leu Ser Gly Leu Gly Phe Asp Ser Ser Lys Ala Glu Asp
 250 255 260

tcg cag act gat ttt gct cag cgt aag ggc atg 916

Ser Gln Thr Asp Phe Ala Gln Arg Lys Gly Met
265 270

<210> 774

<211> 272

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 774

Val Thr Ala Thr Val Leu Glu Pro Gln Pro Val Gln Leu Ser Glu Gln
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Asp Val Asp Ala Glu Ile Ala Arg Met Glu Leu Lys His Asn Arg His
20 25 30

Lys Thr Trp Arg Arg Arg Thr Met Ala Val Val Met Thr Leu Leu Ile
35 40 45

Ser Val Gly Leu Ser Phe Gly Ala Phe Gly Asn Lys Glu Arg Glu Ala
50 55 60

Asn Ala Phe Ala Ser Ala Ile Ile Ala Gln Val Val Gly Ala Met Gly
65 70 75 80

Glu Val Ala Phe Glu Ala Ile Cys Pro Ser Asp Gly Asp Thr Glu Met
85 90 95

Leu Leu Lys Cys Ile Thr Glu Asn Leu Gly Glu Met His Ile Ile Glu
100 105 110

Lys Cys Leu Glu Ala Glu Asp Val Leu Lys Cys Phe Tyr Asp Ala Lys
115 120 125

Asn Glu Glu Gln Arg Lys Glu Gln Asn Leu Asp Lys Ala Pro Asp Tyr
130 135 140

Ser Met Tyr Arg Met Ala Ser Ala Met Ala Ser Phe Tyr Gly Asn Gly
145 150 155 160

Arg Ala Ala Thr Ala Gly Val Glu Glu Gly Gly Pro Asn Glu Phe Leu
165 170 175

Asp Ser Glu Asp Ala Gly Leu Lys Val Trp Glu Gly Ile Leu Ser Lys
180 185 190

Ala Ala Asn Gly Gly Asn Val Leu Gly Tyr Ala Asp Ala Lys His Asn
195 200 205

Glu Asp Ser Gly Trp Phe Phe Gly Asn Gly Val Ala Asn Asn Glu Lys
210 215 220

Thr Tyr Ser Tyr Asp Ser Leu Ala Asp His Ala Phe Gln Gly Pro Tyr
225 230 235 240

His Phe Ala Leu Phe Gly Ala Thr Leu Ser Gly Leu Gly Phe Asp Ser
245 250 255

Ser Lys Ala Glu Asp Ser Gln Thr Asp Phe Ala Gln Arg Lys Gly Met
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<210> 775

<211> 2083

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(2083)

<223> FRXA01587

<400> 775

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 Met Thr Asp Phe Phe
 1 5

ggg ttg atc tat aac tgg tca gtg act gtg ggc tgg ctc atc ggt att 163
 Gly Leu Ile Tyr Asn Trp Ser Val Thr Val Gly Trp Leu Ile Gly Ile
 10 15 20

cct gtc tcc att ggt ctg ttt atg atg ggt gcg ttg atg ttt cga cgc 211
 Pro Val Ser Ile Gly Leu Phe Met Met Gly Ala Leu Met Phe Arg Arg
 25 30 35

atg gac aag gga tca gcg ttt aaa aag gtt gtt atc cgc gtc gtg tac 259
 Met Asp Lys Gly Ser Ala Phe Lys Lys Val Val Ile Arg Val Val Tyr
 40 45 50

ggt gtc gtt ggc ctg cca ctg ctt ggt gtc tct tat acc ggt gcg ctg 307
 Gly Val Val Gly Leu Pro Leu Leu Gly Val Ser Tyr Thr Gly Ala Leu
 55 60 65

gat tcc ttc ctc gac agc ggt agt tcc aca agt gct gga tca aat gcg 355
 Asp Ser Phe Leu Asp Ser Gly Ser Ser Thr Ser Ala Gly Ser Asn Ala
 70 75 80 85

aca aag att gtg ttg tcc acc tac gtg gat ttc caa tca tgg gca gaa 403
 Thr Lys Ile Val Leu Ser Thr Tyr Val Asp Phe Gln Ser Trp Ala Glu
 90 95 100

aac acc cgt atg cgt gtt cct gac aaa gta aca ctg gcg tgg agt ctg 451
 Asn Thr Arg Met Arg Val Pro Asp Lys Val Thr Leu Ala Trp Ser Leu
 105 110 115

gag gat cag gcg cca aca ggg cag tcc atg cgg atg gta cgc aat tcg 499
 Glu Asp Gln Ala Pro Thr Gly Gln Ser Met Arg Met Val Arg Asn Ser
 120 125 130

gcg ttg gaa att aat gct caa tca aat gag agt ttt act act ttt aag 547
 Ala Leu Glu Ile Asn Ala Gln Ser Asn Glu Ser Phe Thr Thr Phe Lys
 135 140 145

aat cca ggt tcc atg gat cta ggc tat agc atg gac tgg atg gaa aag 595
 Asn Pro Gly Ser Met Asp Leu Gly Tyr Ser Met Asp Trp Met Glu Lys
 150 155 160 165

atg gcg gat cca gcc aat tct ggc acc gat ggg acc tca tca agt tgc	643
Met Ala Asp Pro Ala Asn Ser Gly Thr Asp Gly Thr Ser Ser Ser Ser	
170 175 180	
gcg acg act att ttc cag gga acc atc gcg cta ctg agt cgt tat atc	691
Ala Thr Thr Ile Phe Gln Gly Thr Ile Ala Leu Leu Ser Arg Tyr Ile	
185 190 195	
gac aac gac agt atc tcc tct ggc agt ttc gaa acc tct att cga agt	739
Asp Asn Asp Ser Ile Ser Ser Gly Ser Phe Glu Thr Ser Ile Arg Ser	
200 205 210	
gcg atg gaa tct ttg acc tcg aaa gag gga agt ggc gaa gct gtt gcc	787
Ala Met Glu Ser Leu Thr Ser Lys Glu Gly Ser Gly Glu Ala Val Ala	
215 220 225	
ggc ggt gat gta atg gcc tgg gtt act ggt tac aac aca gcc tct ggt	835
Gly Gly Asp Val Met Ala Trp Val Thr Gly Tyr Asn Thr Ala Ser Gly	
230 235 240 245	
ctt aat gag atc act gct gct gaa tta gct gat gcg aac aat cca ttg	883
Leu Asn Glu Ile Thr Ala Ala Glu Leu Ala Asp Ala Asn Asn Pro Leu	
250 255 260	
ctt gag gtc agc gac tca gct ggt ctg cag gga cga cct att gac cgc	931
Leu Glu Val Ser Asp Ser Ala Gly Leu Gln Gly Arg Pro Ile Asp Arg	
265 270 275	
aat gcg gtg tca ttt aaa tct ggt gat gcg aca gcg tca tgc aac aac	979
Asn Ala Val Ser Phe Lys Ser Gly Asp Ala Thr Ala Ser Cys Asn Asn	
280 285 290	
tca gtc gtg aca ggt tct cgt gct gtg gtc ggg gac tac cga agt gac	1027
Ser Val Val Thr Gly Ser Arg Ala Val Val Gly Asp Tyr Arg Ser Asp	
295 300 305	
tgc aat atg tcg ccc ttg acg atg tac aac ttc ctc aac acc tca ttc	1075
Cys Asn Met Ser Pro Leu Thr Met Tyr Asn Phe Leu Asn Thr Ser Phe	
310 315 320 325	
cat cca gct gat gca agt gtc ttt tct acg tcc act tct gcg tca agc	1123
His Pro Ala Asp Ala Ser Val Phe Ser Thr Ser Thr Ser Ala Ser Ser	
330 335 340	
tac acc cgt gca tcg cat agc gca gtg agt ctt atc ggt tct ggt gcc	1171
Tyr Thr Arg Ala Ser His Ser Ala Val Ser Leu Ile Gly Ser Gly Ala	
345 350 355	
atg aac ttt gtg tac tgg ttc tct gca atg tcc ctg atg ggt agc ttc	1219
Met Asn Phe Val Tyr Trp Phe Ser Ala Met Ser Leu Met Gly Ser Phe	
360 365 370	
atc gtg atc ggt atc ggt tac gcc ggt gcc atg ctg ttt aat acg att	1267
Ile Val Ile Gly Ile Gly Tyr Ala Gly Ala Met Leu Phe Asn Thr Ile	
375 380 385	
cga cgc acg ctg tcg ctc att ggt gcc gtt cct ttt gct gcg atg ggc	1315
Arg Arg Thr Leu Ser Leu Ile Gly Ala Val Pro Phe Ala Ala Met Gly	
390 395 400 405	
ttt att gct ggt gtt gcc aag gtc att gtg tac acc atc gct atg ctc	1363

Phe Ile Ala Gly Val Ala Lys Val Ile Val Tyr Thr Ile Ala Met Leu	
410 415 420	
gta gag gtt atc gga acg atc att ttg tac cag ctc att acc cgg ttc	1411
Val Glu Val Ile Gly Thr Ile Ile Leu Tyr Gln Leu Ile Thr Arg Phe	
425 430 435	
ttg atg gct gta cca gca ctc ttt gaa caa cct ttg gct gat tcc tta	1459
Leu Met Ala Val Pro Ala Leu Phe Glu Gln Pro Leu Ala Asp Ser Leu	
440 445 450	
agt agt aac gag agt gct gag ctg gtt gcc ggt gct ggt atg ggg cta	1507
Ser Ser Asn Glu Ser Ala Glu Leu Val Ala Gly Ala Gly Met Gly Leu	
455 460 465	
gtc ggt atg gca cta gct acc tca gcc aac tgg gcg att gcc ggc atg	1555
Val Gly Met Ala Leu Ala Thr Ser Gly Asn Trp Ala Ile Ala Gly Met	
470 475 480 485	
gtg atc aca gtg gcc tca tcc atg ggg gtc atc atc ttc acg att att	1603
Val Ile Thr Val Ala Ser Ser Met Gly Val Ile Ile Phe Thr Ile Ile	
490 495 500	
gcg atg aag gtg cgc gga tct ttg gta tca ggt gtc gat gaa acc gtg	1651
Ala Met Lys Val Arg Gly Ser Leu Val Ser Gly Val Asp Glu Thr Val	
505 510 515	
acc agt gtt att aac cgc ttc ttg gat aca cag gtc tct tct gca ggt	1699
Thr Ser Val Ile Asn Arg Phe Leu Asp Thr Gln Val Ser Ser Ala Gly	
520 525 530	
gct acc tct ggt gac ggc atg atg cgt cgt gca gcc gca acg ggt ctt	1747
Ala Thr Ser Gly Asp Gly Met Met Arg Arg Ala Ala Thr Gly Leu	
535 540 545	
ggt att ggt gcg aca cat atg gta ctc aac cgt gat ggt gac ggt ggt	1795
Gly Ile Gly Ala Thr His Met Val Leu Asn Arg Asp Gly Asp Gly Ile	
550 555 560 565	
gga tct gat tca gcc tct ggt gga tca ggt gcc ggt agc gat tca gcc	1843
Gly Ser Asp Ser Gly Ser Gly Gly Ser Gly Gly Ser Asp Ser Gly	
570 575 580	
ttg ggt gag aag gct gct ggt ctg gcg aag gtt gtc aca act gtg gct	1891
Leu Gly Glu Lys Ala Ala Gly Leu Ala Lys Val Val Thr Thr Val Ala	
585 590 595	
ggt gcc gga tta gtc ggt aag tat gct acg gat gcg ctc gat aat tat	1939
Gly Ala Gly Leu Val Gly Lys Tyr Ala Thr Asp Ala Leu Asp Asn Tyr	
600 605 610	
gca gat gcc gtt atc aac gcc gac ggt gat ggt gcg ttc gca gca ggt	1987
Ala Asp Gly Val Ile Asn Gly Asp Gly Asp Gly Ala Phe Ala Ala Gly	
615 620 625	
ggt gac gct acc gtt gat gcc gac tat gta gca gat gga gat gca att	2035
Gly Asp Ala Thr Val Asp Gly Asp Tyr Val Ala Asp Gly Asp Ala Ile	
630 635 640 645	
gct tct gct gat gct aac gct gat ttt gta gac ggg gtt gct gat ggt	2083
Ala Ser Ala Asp Ala Asn Ala Asp Phe Val Asp Gly Val Ala Asp Gly	

650

655

660

<210> 776

<211> 661

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 776

Met Thr Asp Phe Phe Gly Leu Ile Tyr Asn Trp Ser Val Thr Val Gly
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Trp Leu Ile Gly Ile Pro Val Ser Ile Gly Leu Phe Met Met Gly Ala
 20 25 30

Leu Met Phe Arg Arg Met Asp Lys Gly Ser Ala Phe Lys Lys Val Val
 35 40 45

Ile Arg Val Val Tyr Gly Val Val Gly Leu Pro Leu Leu Gly Val Ser
 50 55 60

Tyr Thr Gly Ala Leu Asp Ser Phe Leu Asp Ser Gly Ser Ser Thr Ser
 65 70 75 80

Ala Gly Ser Asn Ala Thr Lys Ile Val Leu Ser Thr Tyr Val Asp Phe
 85 90 95

Gln Ser Trp Ala Glu Asn Thr Arg Met Arg Val Pro Asp Lys Val Thr
 100 105 110

Leu Ala Trp Ser Leu Glu Asp Gln Ala Pro Thr Gly Gln Ser Met Arg
 115 120 125

Met Val Arg Asn Ser Ala Leu Glu Ile Asn Ala Gln Ser Asn Glu Ser
 130 135 140

Phe Thr Thr Phe Lys Asn Pro Gly Ser Met Asp Leu Gly Tyr Ser Met
 145 150 155 160

Asp Trp Met Glu Lys Met Ala Asp Pro Ala Asn Ser Gly Thr Asp Gly
 165 170 175

Thr Ser Ser Ser Ser Ala Thr Thr Ile Phe Gln Gly Thr Ile Ala Leu
 180 185 190

Leu Ser Arg Tyr Ile Asp Asn Asp Ser Ile Ser Ser Gly Ser Phe Glu
 195 200 205

Thr Ser Ile Arg Ser Ala Met Glu Ser Leu Thr Ser Lys Glu Gly Ser
 210 215 220

Gly Glu Ala Val Ala Gly Gly Asp Val Met Ala Trp Val Thr Gly Tyr
 225 230 235 240

Asn Thr Ala Ser Gly Leu Asn Glu Ile Thr Ala Ala Glu Leu Ala Asp
 245 250 255

Ala Asn Asn Pro Leu Leu Glu Val Ser Asp Ser Ala Gly Leu Gln Gly
 260 265 270

Arg Pro Ile Asp Arg Asn Ala Val Ser Phe Lys Ser Gly Asp Ala Thr

275					280					285					
Ala	Ser	Cys	Asn	Asn	Ser	Val	Val	Thr	Gly	Ser	Arg	Ala	Val	Val	Gly
290						295					300				
Asp	Tyr	Arg	Ser	Asp	Cys	Asn	Met	Ser	Pro	Leu	Thr	Met	Tyr	Asn	Phe
305					310					315					320
Leu	Asn	Thr	Ser	Phe	His	Pro	Ala	Asp	Ala	Ser	Val	Phe	Ser	Thr	Ser
				325					330					335	
Thr	Ser	Ala	Ser	Ser	Tyr	Thr	Arg	Ala	Ser	His	Ser	Ala	Val	Ser	Leu
				340				345					350		
Ile	Gly	Ser	Gly	Ala	Met	Asn	Phe	Val	Tyr	Trp	Phe	Ser	Ala	Met	Ser
			355				360					365			
Leu	Met	Gly	Ser	Phe	Ile	Val	Ile	Gly	Ile	Gly	Tyr	Ala	Gly	Ala	Met
	370					375					380				
Leu	Phe	Asn	Thr	Ile	Arg	Arg	Thr	Leu	Ser	Leu	Ser	Ile	Gly	Ala	Val
385					390					395					400
Phe	Ala	Ala	Met	Gly	Phe	Ile	Ala	Gly	Val	Ala	Lys	Val	Ile	Val	Tyr
				405					410					415	
Thr	Ile	Ala	Met	Leu	Val	Glu	Val	Ile	Gly	Thr	Ile	Ile	Leu	Tyr	Gln
			420					425					430		
Leu	Ile	Thr	Arg	Phe	Leu	Met	Ala	Val	Pro	Ala	Leu	Phe	Glu	Gln	Pro
			435				440					445			
Leu	Ala	Asp	Ser	Leu	Ser	Ser	Asn	Glu	Ser	Ala	Glu	Leu	Val	Ala	Gly
						455					460				
Ala	Gly	Met	Gly	Leu	Val	Gly	Met	Ala	Leu	Ala	Thr	Ser	Gly	Asn	Trp
465					470					475					480
Ala	Ile	Ala	Gly	Met	Val	Ile	Thr	Val	Ala	Ser	Ser	Met	Gly	Val	Ile
				485					490					495	
Ile	Phe	Thr	Ile	Ile	Ala	Met	Lys	Val	Arg	Gly	Ser	Leu	Val	Ser	Gly
			500					505					510		
Val	Asp	Glu	Thr	Val	Thr	Ser	Val	Ile	Asn	Arg	Phe	Leu	Asp	Thr	Gln
			515				520					525			
Val	Ser	Ser	Ala	Gly	Ala	Thr	Ser	Gly	Asp	Gly	Met	Met	Arg	Arg	Ala
			530				535				540				
Ala	Ala	Thr	Gly	Leu	Gly	Ile	Gly	Ala	Thr	His	Met	Val	Leu	Asn	Arg
545					550					555					560
Asp	Gly	Asp	Gly	Gly	Gly	Ser	Asp	Ser	Gly	Ser	Gly	Gly	Ser	Gly	Gly
				565					570					575	
Gly	Ser	Asp	Ser	Gly	Leu	Gly	Glu	Lys	Ala	Ala	Gly	Leu	Ala	Lys	Val
			580					585					590		
Val	Thr	Thr	Val	Ala	Gly	Ala	Gly	Leu	Val	Gly	Lys	Tyr	Ala	Thr	Asp
			595				600					605			

Ala Leu Asp Asn Tyr Ala Asp Gly Val Ile Asn Gly Asp Gly Asp Gly
610 615 620

Ala Phe Ala Ala Gly Gly Asp Ala Thr Val Asp Gly Asp Tyr Val Ala
625 630 635 640

Asp Gly Asp Ala Ile Ala Ser Ala Asp Ala Asn Ala Asp Phe Val Asp
645 650 655

Gly Val Ala Asp Gly
660

<210> 777

<211> 1541

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1518)

<223> FRXA01761

<400> 777

gct gat gct aac gct gat ttt gta gac ggt gtt gtt gat ggt gct ggt 48
Ala Asp Ala Asn Ala Asp Phe Val Asp Gly Val Val Asp Gly Ala Gly
1 5 10 15

cgc gcg tca ttt agc aat gct gcg tat agc tcc gat gga acc act ctc 96
Arg Ala Ser Phe Ser Asn Ala Ala Tyr Ser Ser Asp Gly Thr Thr Leu
20 25 30

gac ggt gag ggt gcg agc gtt gat gca cag ggt aac cgc ctt cat gct 144
Asp Gly Glu Gly Ala Ser Val Asp Ala Gln Gly Asn Pro Leu His Ala
35 40 45

gat ggc aca cca atg agt gct gct gaa gct gaa atg aag atg gct ggt 192
Asp Gly Thr Pro Met Ser Ala Ala Glu Ala Glu Met Lys Met Ala Gly
50 55 60

ctg agc tcg tca gga acc atg atg gag aaa tct ggt gtg aaa tcg agt 240
Leu Ser Ser Ser Gly Thr Met Met Glu Lys Ser Gly Val Lys Ser Ser
65 70 75 80

ggc att acc act gca gcg gat gtc atg gac gat cag tct ctg gca agc 288
Gly Ile Thr Thr Ala Ala Asp Val Met Asp Asp Gln Ser Leu Ala Ser
85 90 95

agt gtc act gag tct ggt ctg tcc aag att cca gac acc tat ggt gca 336
Ser Val Thr Glu Ser Gly Leu Ser Lys Ile Pro Asp Thr Tyr Gly Ala
100 105 110

gat gtc tcg ggt gct gcg ggc aca gtc gga act acc ggt gct gat tac 384
Asp Val Ser Gly Ala Ala Gly Thr Val Gly Thr Thr Gly Ala Asp Tyr
115 120 125

agt gcg acc gat tca agc gca ggt ctg aac atg agc gag gct gca ttg 432
Ser Ala Thr Asp Ser Ser Ala Gly Leu Asn Met Ser Glu Ala Ala Leu
130 135 140

cag agt ggc acc cca atg ggc gct ctc gct ggt gga tct gtg tcg agt Gln Ser Gly Thr Pro Met Gly Ala Leu Ala Gly Ser Val Ser Ser 145 150 155 160	480
tcc gat cag gcc atg aat gac gca gct ctt cag att gca gcg tct cag Ser Asp Gln Ala Met Asn Asp Ala Ala Leu Gln Ile Ala Ala Ser Gln 165 170 175	528
ggc ctt gca cca gca ggt tcc ata gct ggt atg gag caa ctt agt gct Gly Leu Ala Pro Ala Gly Ser Ile Ala Gly Met Glu Gln Leu Ser Ala 180 185 190	576
caa gcc act gaa gca cct gct gga aag gcc ggc aag cag ctt ggc gat Gln Ala Thr Glu Ala Pro Ala Gly Lys Ala Gly Lys Gln Leu Gly Asp 195 200 205	624
ctt tct ggc tca gcg ctc aat act cag ctg gcg tcc atg gga cag cag Leu Ser Gly Ser Ala Leu Asn Thr Gln Leu Ala Ser Met Gly Gln Gln 210 215 220	672
gta ggt gac agt gtg aac agc gct tat gct gca ggc ggt atg ggt ggt Val Gly Asp Ser Val Asn Ser Ala Tyr Ala Ala Gly Gly Met Gly Gly 225 230 235 240	720
gtt gat gtg gct ggc aag gtc acc gag gca gca cag cac ttg tct cag Val Asp Val Ala Gly Lys Val Thr Glu Ala Ala Gln His Leu Ser Gln 245 250 255	768
gtt cca ggt cag att cag aat gct gtg acc aat gcg gat gct ggt tcc Val Pro Gly Gln Ile Gln Asn Ala Val Thr Asn Ala Asp Ala Gly Ser 260 265 270	816
tct ggc gca agc ttt ggt cag atg gca cag ggg gca gct ggt att gcc Ser Gly Ala Ser Phe Gly Gln Met Ala Gln Gly Ala Ala Gly Ile Ala 275 280 285	864
ggc gtc gca ggt gtg atc ggt gca gcg ggc gca gca agc tct gca gca Gly Val Ala Gly Val Ile Gly Ala Ala Gly Ala Ala Ser Ser Ala Ala 290 295 300	912
caa ggc gca ggt act gtc cag ggt gcg atg ggt aat gct gca gct ggt Gln Gly Ala Gly Thr Val Gln Gly Ala Met Gly Asn Ala Ala Ala Gly 305 310 315 320	960
gcg gga atg atc aac aac gct gtt tcc ggt gga gct act ggc tca aca Ala Gly Met Ile Asn Asn Ala Val Ser Gly Gly Ala Thr Gly Ser Thr 325 330 335	1008
ggc gcc gca cat gtg gtc aat gca tca cat gga cca gtg gcg cct ggt Gly Ala Ala His Val Val Asn Ala Ser His Gly Pro Val Ala Pro Gly 340 345 350	1056
cag gct cac tac caa gag tct ggt cat gca caa gca ttt gtg cag aac Gln Ala His Tyr Gln Glu Ser Gly His Ala Gln Ala Phe Val Gln Asn 355 360 365	1104
aac cag gcc aac acc gcg cac aca gca aac acg cgt gca ccg tca tca Asn Gln Ala Asn Thr Ala His Thr Ala Asn Thr Arg Ala Pro Ser Ser 370 375 380	1152
gct caa att atg ggc gcg aac gtt gct ggc tca ctg gca tca cag gct	1200

Ala Gln Ile Met Gly Ala Asn Val Ala Gly Ser Leu Ala Ser Gln Ala
385 390 395 400

gta cga gga atc ggt cag cct ggt cag atg ggt gct aat gtt cgc gac 1248
Val Arg Gly Ile Gly Gln Pro Gly Gln Met Gly Ala Asn Val Arg Asp
405 410 415

gcg atg ggt ggc agc gga cgc tct ggt ggc cgt ggt gga gca act caa 1296
Ala Met Gly Gly Ser Gly Arg Ser Gly Gly Arg Gly Gly Ala Thr Gln
420 425 430

ggc ggt cga ggc gca cag cgc agc ggt gtc agt gct aag aac ggt atc 1344
Gly Gly Arg Gly Ala Gln Arg Ser Gly Val Ser Ala Lys Asn Gly Ile
435 440 445

cgt gca cag cga ggt cag aag cct tct gtg acc ggc cag gcg atg aat 1392
Arg Ala Gln Arg Gly Gln Lys Pro Ser Val Thr Thr Gln Ala Met Asn
450 455 460

gca gca atg cgt tca gca gcg gta agc ggt cgc atg gca aac atg gac 1440
Ala Ala Met Arg Ser Ala Ala Val Ser Gly Arg Met Ala Asn Met Asp
465 470 475 480

ggc aac agt gta ggt ggc act gaa gca gat cca cag cag ggg agt ggc 1488
Gly Asn Ser Val Gly Gly Thr Glu Ala Asp Pro Gln Gln Gly Ser Gly
485 490 495

gta acc gag aag ggt gat aaa ggc gtt aaa tagcgtgtaa aacacaatga 1538
Val Thr Glu Lys Gly Asp Lys Gly Val Lys
500 505

ccg 1541

<210> 778
<211> 506
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 778
Ala Asp Ala Asn Ala Asp Phe Val Asp Gly Val Val Asp Gly Ala Gly
1 5 10 15

Arg Ala Ser Phe Ser Asn Ala Ala Tyr Ser Ser Asp Gly Thr Thr Leu
20 25 30

Asp Gly Glu Gly Ala Ser Val Asp Ala Gln Gly Asn Pro Leu His Ala
35 40 45

Asp Gly Thr Pro Met Ser Ala Ala Glu Ala Glu Met Lys Met Ala Gly
50 55 60

Leu Ser Ser Ser Gly Thr Met Met Glu Lys Ser Gly Val Lys Ser Ser
65 70 75 80

Gly Ile Thr Thr Ala Ala Asp Val Met Asp Asp Gln Ser Leu Ala Ser
85 90 95

Ser Val Thr Glu Ser Gly Leu Ser Lys Ile Pro Asp Thr Tyr Gly Ala
100 105 110

Asp Val Ser Gly Ala Ala Gly Thr Val Gly Thr Thr Gly Ala Asp Tyr
 115 120 125
 Ser Ala Thr Asp Ser Ser Ala Gly Leu Asn Met Ser Glu Ala Ala Leu
 130 135 140
 Gln Ser Gly Thr Pro Met Gly Ala Leu Ala Gly Gly Ser Val Ser Ser
 145 150 155 160
 Ser Asp Gln Ala Met Asn Asp Ala Ala Leu Gln Ile Ala Ala Ser Gln
 165 170 175
 Gly Leu Ala Pro Ala Gly Ser Ile Ala Gly Met Glu Gln Leu Ser Ala
 180 185 190
 Gln Ala Thr Glu Ala Pro Ala Gly Lys Ala Gly Lys Gln Leu Gly Asp
 195 200 205
 Leu Ser Gly Ser Ala Leu Asn Thr Gln Leu Ala Ser Met Gly Gln Gln
 210 215 220
 Val Gly Asp Ser Val Asn Ser Ala Tyr Ala Ala Gly Gly Met Gly Gly
 225 230 235 240
 Val Asp Val Ala Gly Lys Val Thr Glu Ala Ala Gln His Leu Ser Gln
 245 250 255
 Val Pro Gly Gln Ile Gln Asn Ala Val Thr Asn Ala Asp Ala Gly Ser
 260 265 270
 Ser Gly Ala Ser Phe Gly Gln Met Ala Gln Gly Ala Ala Gly Ile Ala
 275 280 285
 Gly Val Ala Gly Val Ile Gly Ala Ala Gly Ala Ala Ser Ser Ala Ala
 290 295 300
 Gln Gly Ala Gly Thr Val Gln Gly Ala Met Gly Asn Ala Ala Ala Gly
 305 310 315 320
 Ala Gly Met Ile Asn Asn Ala Val Ser Gly Gly Ala Thr Gly Ser Thr
 325 330 335
 Gly Ala Ala His Val Val Asn Ala Ser His Gly Pro Val Ala Pro Gly
 340 345 350
 Gln Ala His Tyr Gln Glu Ser Gly His Ala Gln Ala Phe Val Gln Asn
 355 360 365
 Asn Gln Ala Asn Thr Ala His Thr Ala Asn Thr Arg Ala Pro Ser Ser
 370 375 380
 Ala Gln Ile Met Gly Ala Asn Val Ala Gly Ser Leu Ala Ser Gln Ala
 385 390 395 400
 Val Arg Gly Ile Gly Gln Pro Gly Gln Met Gly Ala Asn Val Arg Asp
 405 410 415
 Ala Met Gly Gly Ser Gly Arg Ser Gly Gly Arg Gly Gly Ala Thr Gln
 420 425 430
 Gly Gly Arg Gly Ala Gln Arg Ser Gly Val Ser Ala Lys Asn Gly Ile

435 440 445

Arg Ala Gln Arg Gly Gln Lys Pro Ser Val Thr Gly Gln Ala Met Asn
450 455 460

Ala Ala Met Arg Ser Ala Ala Val Ser Gly Arg Met Ala Asn Met Asp
465 470 475 480

Gly Asn Ser Val Gly Gly Thr Glu Ala Asp Pro Gln Gln Gly Ser Gly
485 490 495

Val Thr Glu Lys Gly Asp Lys Gly Val Lys
500 505

<210> 779
<211> 1065
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(1042)
<223> RXN01765

<400> 779
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caaggcataa caccgcacac caagaatttt aggaggggtc atg agc aac aac gta 115
Met Ser Asn Asn Val
1 5

gtg aaa tat gag tgc gcg gtc gac gcc gac aac att gtc gca gtc gat 163
Val Lys Tyr Glu Cys Ala Val Asp Ala Asp Asn Ile Val Ala Val Asp
10 15 20

atg cat gtg cac ttg gaa gtc gac agc tgc gga cac aaa tcg atg ccg 211
Met His Val His Leu Thr Glu Val Asp Ser Cys Gly His Lys Ser Met Pro
25 30 35

gca gac atc atg gcg gca tcc tcg aag tac ttt aag acc gcg gaa cga 259
Ala Asp Ile Met Ala Ala Ser Ser Lys Tyr Phe Lys Thr Ala Glu Arg
40 45 50

act ccc tca gca gat gcc att gct gat att tat agg gaa cac aag atg 307
Thr Pro Ser Ala Asp Ala Ile Ala Asp Ile Tyr Arg Glu His Lys Met
55 60 65

gcg gcg gtg gtt ttc acc atc gat gcg cgg acc caa atg ggg cat ctg 355
Ala Ala Val Val Phe Thr Ile Asp Ala Arg Thr Gln Met Gly His Leu
70 75 80 85

ccg aac tcg att gat gat ttg gtg gca agc tgt gcc cgc aac aat gac 403
Pro Asn Ser Ile Asp Asp Leu Val Ala Ser Cys Ala Arg Asn Asn Asp
90 95 100

gtg ctg atc cct ttt ggc agt gtg gat cct cgt acc ggc gag gac gcg 451
Val Leu Ile Pro Phe Gly Ser Val Asp Pro Arg Thr Gly Glu Asp Ala
105 110 115

ctg gtg gaa gct cgc cga cag gtg gaa gaa ctc ggg gtg cga ggc ttc 499

Leu Val Glu Ala Arg Arg Gln Val Glu Glu Leu Gly Val Arg Gly Phe
 120 125 130
 aaa ttc cat cca tcg gtt caa gga ttc gac cca tcc gcg cca gag ttc 547
 Lys Phe His Pro Ser Val Gln Gly Phe Asp Pro Ser Ala Pro Glu Phe
 135 140 145
 tac cca ctg tgg gaa ttg ctc gaa agt ttt gga ttg cca tgc gtg ttc 595
 Tyr Pro Leu Trp Glu Leu Leu Glu Ser Phe Gly Leu Pro Cys Val Phe
 150 155 160 165
 cat acc gga caa aac ggc atg ggt gca ggt ctt cca ggt ggt cga ggc 643
 His Thr Gly Gln Asn Gly Met Gly Ala Gly Leu Pro Gly Gly Arg Gly
 170 175 180
 att aag ctg cgc ttc tcc aac cca atg ttg ctt gat gat gtt gcg gcg 691
 Ile Lys Leu Arg Phe Ser Asn Pro Met Leu Leu Asp Asp Val Ala Ala
 185 190 195
 gac ttc ccg aac ctg acc atc atc atg gcg cac cct tct gtt cct tgg 739
 Asp Phe Pro Asn Leu Thr Ile Ile Met Ala His Pro Ser Val Pro Trp
 200 205 210
 cag gat gag gct aac tcg att gcc acc cac aag gcc aat gtg ttc att 787
 Gln Asp Glu Ala Asn Ser Ile Ala Thr His Lys Ala Asn Val Phe Ile
 215 220 225
 gat ctt tcc ggc tgg tcg ccg aag tat ttc cca gag tct ttg gtc aga 835
 Asp Leu Ser Gly Trp Ser Pro Lys Tyr Phe Pro Glu Ser Leu Val Arg
 230 235 240 245
 cag tcc aat aac gtg cta tcc aag aag gtg ctg ttt ggc acg gac ttc 883
 Gln Ser Asn Asn Val Leu Ser Lys Lys Val Leu Phe Gly Thr Asp Phe
 250 255 260
 ccg ctg att acc cca gag aaa tgg ctt gcg gct ttc gcg aat ctg cca 931
 Pro Leu Ile Thr Pro Glu Lys Trp Leu Ala Ala Phe Ala Asn Leu Pro
 265 270 275
 ctg aag gat gag gtt cgt ccg gga atc ctc aaa gac aat gcg gtg aag 979
 Leu Lys Asp Glu Val Arg Pro Gly Ile Leu Lys Asp Asn Ala Val Lys
 280 285 290
 gta ctt ggc cta gcc gct agc act gag cgc gga tct caa gca gaa aag 1027
 Val Leu Gly Leu Ala Ala Ser Thr Glu Arg Gly Ser Gln Ala Glu Lys
 295 300 305
 gtc gtg caa cat gcg tgatccatt caaggtgctg tta 1065
 Val Val Gln His Ala
 310

<210> 780

<211> 314

<212> PRT

<213> Corynebacterium glutamicum

<400> 780

Met Ser Asn Asn Val Val Lys Tyr Glu Cys Ala Val Asp Ala Asp Asn
 1 5 10 15

Ile Val Ala Val Asp Met His Val His Leu Glu Val Asp Ser Cys Gly
 20 25 30
 His Lys Ser Met Pro Ala Asp Ile Met Ala Ala Ser Ser Lys Tyr Phe
 35 40 45
 Lys Thr Ala Glu Arg Thr Pro Ser Ala Asp Ala Ile Ala Asp Ile Tyr
 50 55 60
 Arg Glu His Lys Met Ala Ala Val Val Phe Thr Ile Asp Ala Arg Thr
 65 70 75 80
 Gln Met Gly His Leu Pro Asn Ser Ile Asp Asp Leu Val Ala Ser Cys
 85 90 95
 Ala Arg Asn Asn Asp Val Leu Ile Pro Phe Gly Ser Val Asp Pro Arg
 100 105 110
 Thr Gly Glu Asp Ala Leu Val Glu Ala Arg Arg Gln Val Glu Glu Leu
 115 120 125
 Gly Val Arg Gly Phe Lys Phe His Pro Ser Val Gln Gly Phe Asp Pro
 130 135 140
 Ser Ala Pro Glu Phe Tyr Pro Leu Trp Glu Leu Leu Glu Ser Phe Gly
 145 150 155 160
 Leu Pro Cys Val Phe His Thr Gly Gln Asn Gly Met Gly Ala Gly Leu
 165 170 175
 Pro Gly Gly Arg Gly Ile Lys Leu Arg Phe Ser Asn Pro Met Leu Leu
 180 185 190
 Asp Asp Val Ala Ala Asp Phe Pro Asn Leu Thr Ile Ile Met Ala His
 195 200 205
 Pro Ser Val Pro Trp Gln Asp Glu Ala Asn Ser Ile Ala Thr His Lys
 210 215 220
 Ala Asn Val Phe Ile Asp Leu Ser Gly Trp Ser Pro Lys Tyr Phe Pro
 225 230 235 240
 Glu Ser Leu Val Arg Gln Ser Asn Asn Val Leu Ser Lys Lys Val Leu
 245 250 255
 Phe Gly Thr Asp Phe Pro Leu Ile Thr Pro Glu Lys Trp Leu Ala Ala
 260 265 270
 Phe Ala Asn Leu Pro Leu Lys Asp Glu Val Arg Pro Gly Ile Leu Lys
 275 280 285
 Asp Asn Ala Val Lys Val Leu Gly Leu Ala Ala Ser Thr Glu Arg Gly
 290 295 300
 Ser Gln Ala Glu Lys Val Val Gln His Ala
 305 310

<210> 781

<211> 1065

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1042)

<223> FRXA01765

<400> 781

gcagtcgcgc ggtgtcgttt tccctgaact gcgggcagag cttcagccac aaatccagc 60

caaggcataa caccgcacac caagaatattt agggaggggtc atg agc aac aac gta 115
 Met Ser Asn Asn Val
 1 5

gtg aaa tat gag tgc gcg gtc gac gcc gac aac att gtc gca gtc gat 163
 Val Lys Tyr Glu Cys Ala Val Asp Ala Asp Asn Ile Val Ala Val Asp
 10 15 20

atg cat gtg cac ttg gaa gtc gac agc tgc gga cac aaa tcg atg ccg 211
 Met His Val His Leu Glu Val Asp Ser Cys Gly His Lys Ser Met Pro
 25 30 35

gca gac atc atg gcg gca tcc tcg aag tac ttt aag acc gcg gaa cga 259
 Ala Asp Ile Met Ala Ala Ser Ser Lys Tyr Phe Lys Thr Ala Glu Arg
 40 45 50

act ccc tca gca gat gcc att gct gat att tat agg gaa cac aag atg 307
 Thr Pro Ser Ala Asp Ala Ile Ala Asp Ile Tyr Arg Glu His Lys Met
 55 60 65

gcg gcg gtg gtt ttc acc atc gat gcg cgg acc caa atg ggg cat ctg 355
 Ala Ala Val Val Phe Thr Ile Asp Ala Arg Thr Gln Met Gly His Leu
 70 75 80 85

ccg aac tcg att gat gat ttg gtg gca agc tgt gcc cgc aac aat gac 403
 Pro Asn Ser Ile Asp Asp Leu Val Ala Ser Cys Ala Arg Asn Asn Asp
 90 95 100

gtg ctg atc cct ttt ggc agt gtg gat cct cgt acc ggc gag gac gcg 451
 Val Leu Ile Pro Phe Gly Ser Val Asp Pro Arg Thr Gly Glu Asp Ala
 105 110 115

ctg gtg gaa gct cgc cga cag gtg gaa gaa ctc ggg gtg cga ggc ttc 499
 Leu Val Glu Ala Arg Arg Gln Val Glu Glu Leu Gly Val Arg Gly Phe
 120 125 130

aaa ttc cat cca tcg gtt caa gga ttc gac cca tcc gcg cca gag ttc 547
 Lys Phe His Pro Ser Val Gln Gly Phe Asp Pro Ser Ala Pro Glu Phe
 135 140 145

tac cca ctg tgg gaa ttg ctc gaa agt ttt gga ttg cca tgc gtg ttc 595
 Tyr Pro Leu Trp Glu Leu Leu Glu Ser Phe Gly Leu Pro Cys Val Phe
 150 155 160 165

cat acc gga caa aac ggc atg ggt gca ggt ctt cca ggt ggt cga ggc 643
 His Thr Gly Gln Asn Gly Met Gly Ala Gly Leu Pro Gly Gly Arg Gly
 170 175 180

att aag ctg cgc ttc tcc aac cca atg ttg ctt gat gat gtt gcg gcg 691
 Ile Lys Leu Arg Phe Ser Asn Pro Met Leu Leu Asp Asp Val Ala Ala
 185 190 195

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gac ttc ccg aac ctg acc atc atc atg gcg cac cct tct gtt cct tgg 739
Asp Phe Pro Asn Leu Thr Ile Ile Met Ala His Pro Ser Val Pro Trp
      200                      205                      210

cag gat gag gct aac tcg att gcc acc cac aag gcc aat gtg ttc att 787
Gln Asp Glu Ala Asn Ser Ile Ala Thr His Lys Ala Asn Val Phe Ile
      215                      220                      225

gat ctt tcc ggc tgg tcg ccg aag tat ttc cca gag tct ttg gtc aga 835
Asp Leu Ser Gly Trp Ser Pro Lys Tyr Phe Pro Glu Ser Leu Val Arg
      230                      235                      240                      245

cag tcc aat aac gtg cta tcc aag aag gtg ctg ttt ggc acg gac ttc 883
Gln Ser Asn Asn Val Leu Ser Lys Lys Val Leu Phe Gly Thr Asp Phe
      250                      255                      260

ccg ctg att acc cca gag aaa tgg ctt gcg gct ttc gcg aat ctg cca 931
Pro Leu Ile Thr Pro Glu Lys Trp Leu Ala Ala Phe Ala Asn Leu Pro
      265                      270                      275

ctg aag gat gag gtt cgt ccg gga atc ctc aaa gac aat gcg gtg aag 979
Leu Lys Asp Glu Val Arg Pro Gly Ile Leu Lys Asp Asn Ala Val Lys
      280                      285                      290

gta ctt ggc cta gcc gct agc act gag cgc gga tct caa gca gaa aag 1027
Val Leu Gly Leu Ala Ala Ser Thr Glu Arg Gly Ser Gln Ala Glu Lys
      295                      300                      305

gtc gtg caa cat gcg tgatccatt caagggtctg tta 1065
Val Val Gln His Ala
      310

<210> 782
<211> 314
<212> PRT
<213> Corynebacterium glutamicum

<400> 782
Met Ser Asn Asn Val Val Lys Tyr Glu Cys Ala Val Asp Ala Asp Asn
  1                      5                      10                      15

Ile Val Ala Val Asp Met His Val His Leu Glu Val Asp Ser Cys Gly
                      20                      25                      30

His Lys Ser Met Pro Ala Asp Ile Met Ala Ala Ser Ser Lys Tyr Phe
      35                      40                      45

Lys Thr Ala Glu Arg Thr Pro Ser Ala Asp Ala Ile Ala Asp Ile Tyr
      50                      55                      60

Arg Glu His Lys Met Ala Ala Val Val Phe Thr Ile Asp Ala Arg Thr
      65                      70                      75                      80

Gln Met Gly His Leu Pro Asn Ser Ile Asp Asp Leu Val Ala Ser Cys
      85                      90                      95

Ala Arg Asn Asn Asp Val Leu Ile Pro Phe Gly Ser Val Asp Pro Arg
      100                      105                      110

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Thr Gly Glu Asp Ala Leu Val Glu Ala Arg Arg Gln Val Glu Glu Leu
 115 120 125
 Gly Val Arg Gly Phe Lys Phe His Pro Ser Val Gln Gly Phe Asp Pro
 130 135 140
 Ser Ala Pro Glu Phe Tyr Pro Leu Trp Glu Leu Leu Glu Ser Phe Gly
 145 150 155 160
 Leu Pro Cys Val Phe His Thr Gly Gln Asn Gly Met Gly Ala Gly Leu
 165 170 175
 Pro Gly Gly Arg Gly Ile Lys Leu Arg Phe Ser Asn Pro Met Leu Leu
 180 185 190
 Asp Asp Val Ala Ala Asp Phe Pro Asn Leu Thr Ile Ile Met Ala His
 195 200 205
 Pro Ser Val Pro Trp Gln Asp Glu Ala Asn Ser Ile Ala Thr His Lys
 210 215 220
 Ala Asn Val Phe Ile Asp Leu Ser Gly Trp Ser Pro Lys Tyr Phe Pro
 225 230 235 240
 Glu Ser Leu Val Arg Gln Ser Asn Asn Val Leu Ser Lys Lys Val Leu
 245 250 255
 Phe Gly Thr Asp Phe Pro Leu Ile Thr Pro Glu Lys Trp Leu Ala Ala
 260 265 270
 Phe Ala Asn Leu Pro Leu Lys Asp Glu Val Arg Pro Gly Ile Leu Lys
 275 280 285
 Asp Asn Ala Val Lys Val Leu Gly Leu Ala Ala Ser Thr Glu Arg Gly
 290 295 300
 Ser Gln Ala Glu Lys Val Val Gln His Ala
 305 310

<210> 783

<211> 588

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(565)

<223> RXN01767

<400> 783

acaccagccc tccacaagag cgtcgaagca atctacgctt cgacgctctt tttttcacta 60

cctactcatt cccacataa gaaaaaaga cgacaccacc atg att gac cat aaa 115
 Met Ile Asp His Lys 5
 1

ctg tgg ttt aac aca gta acc aac aac gcc tct gtc cga gaa gct gca 163
 Leu Trp Phe Asn Thr Val Thr Asn Asn Ala Ser Val Arg Glu Ala Ala
 10 15 20

gga aaa tgc gac ata ccc atc aga acg ctc aac gag cag ctt aac cgt 211
 Gly Lys Cys Asp Ile Pro Ile Arg Thr Leu Asn Glu Gln Leu Asn Arg
 25 30 35

cga ata ctc cct gaa aag acc gtc atc gct cta gca cgc gct tat gat 259
 Arg Ile Leu Pro Glu Lys Thr Val Ile Ala Leu Ala Arg Ala Tyr Asp
 40 45 50

ctc tca cct gtt gat gcg ctc gtt cgc acc gga cac ctc acc gaa gaa 307
 Leu Ser Pro Val Asp Ala Leu Val Arg Thr Gly His Leu Thr Glu Glu
 55 60 65

gag gct ggt agt cgt gaa gaa gat gcc agc cca gat tca gct gac gac 355
 Glu Ala Gly Ser Arg Glu Glu Asp Ala Ser Pro Asp Ser Ala Asp Asp
 70 75 80 85

tac cct acc tgg gca ctg aac tcg cac ctt gac tat ggc att ctc gga 403
 Tyr Pro Thr Trp Ala Leu Asn Ser His Leu Asp Tyr Gly Ile Leu Gly
 90 95 100

gct ttt ggc gac atc gct gaa gaa gta aac agc gaa aga gtt aac cgc 451
 Ala Phe Gly Asp Ile Ala Glu Glu Val Asn Ser Glu Arg Val Asn Arg
 105 110 115

gac aac gcc ata gag caa att cgc gca tgg ctc gac gag ctt cca ggc 499
 Asp Asn Ala Ile Glu Gln Ile Arg Ala Trp Leu Asp Glu Leu Pro Gly
 120 125 130

agc cta ttc aac aac ctc cgc agc act aaa aca ggc tac atc gaa cta 547
 Ser Leu Phe Asn Asn Leu Arg Ser Thr Lys Thr Gly Tyr Ile Glu Leu
 135 140 145

ttc gag acc tat ctc gat taaacccaac cagcacaaca ata 588
 Phe Glu Thr Tyr Leu Asp
 150 155

<210> 784
 <211> 155
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 784
 Met Ile Asp His Lys Leu Trp Phe Asn Thr Val Thr Asn Asn Ala Ser
 1 5 10 15

Val Arg Glu Ala Ala Gly Lys Cys Asp Ile Pro Ile Arg Thr Leu Asn
 20 25 30

Glu Gln Leu Asn Arg Arg Ile Leu Pro Glu Lys Thr Val Ile Ala Leu
 35 40 45

Ala Arg Ala Tyr Asp Leu Ser Pro Val Asp Ala Leu Val Arg Thr Gly
 50 55 60

His Leu Thr Glu Glu Glu Ala Gly Ser Arg Glu Glu Asp Ala Ser Pro
 65 70 75 80

Asp Ser Ala Asp Asp Tyr Pro Thr Trp Ala Leu Asn Ser His Leu Asp
 85 90 95

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Tyr Gly Ile Leu Gly Ala Phe Gly Asp Ile Ala Glu Glu Val Asn Ser
      100                      105                      110

Glu Arg Val Asn Arg Asp Asn Ala Ile Glu Gln Ile Arg Ala Trp Leu
      115                      120                      125

Asp Glu Leu Pro Gly Ser Leu Phe Asn Asn Leu Arg Ser Thr Lys Thr
      130                      135                      140

Gly Tyr Ile Glu Leu Phe Glu Thr Tyr Leu Asp
      145                      150                      155

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<210> 785

<211> 436

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(436)

<223> FRXA01767

<400> 785

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acaccagccc tccacaagag cgctcgaagca atctacgctt cgacgctctt tttttcacta 60
cctactcatc cccacataa gaaaaaaga cgacaccacc atg att gac cat aaa 115
Met Ile Asp His Lys
      1                      5

ctg tgg ttt aac aca gta acc aac aac gcc tct gtc cga gaa gct gca 163
Leu Trp Phe Asn Thr Val Thr Asn Asn Ala Ser Val Arg Glu Ala Ala
      10                      15                      20

gga aaa tgc gac ata ccc atc aga acg ctc aac gag cag ctt aac cgt 211
Gly Lys Cys Asp Ile Pro Ile Arg Thr Leu Asn Glu Gln Leu Asn Arg
      25                      30                      35

cga ata ctc cct gaa aag acc gtc atc gct cta gca cgc gct tat gat 259
Arg Ile Leu Pro Glu Lys Thr Val Ile Ala Leu Ala Arg Ala Tyr Asp
      40                      45                      50

ctc tca cct gtt gat gcg ctc gtt cgc acc gga cac ctc acc gaa gaa 307
Leu Ser Pro Val Asp Ala Leu Val Arg Thr Gly His Leu Thr Glu Glu
      55                      60                      65

gag gct ggt agt cgt gaa gaa gat gcc agc cca gat tca gct gac gac 355
Glu Ala Gly Ser Arg Glu Glu Asp Ala Ser Pro Asp Ser Ala Asp Asp
      70                      75                      80                      85

tac cct acc tgg gca ctg aac tcg cac ctt gac tat ggc att ctc gga 403
Tyr Pro Thr Trp Ala Leu Asn Ser His Leu Asp Tyr Gly Ile Leu Gly
      90                      95                      100

gct ttt ggc gac atc gct gaa gaa gta aac agc 436
Ala Phe Gly Asp Ile Ala Glu Glu Val Asn Ser
      105                      110

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<210> 786

<211> 112

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 786

Met	Ile	Asp	His	Lys	Leu	Trp	Phe	Asn	Thr	Val	Thr	Asn	Asn	Ala	Ser
1				5					10					15	

Val	Arg	Glu	Ala	Ala	Gly	Lys	Cys	Asp	Ile	Pro	Ile	Arg	Thr	Leu	Asn
			20					25					30		

Glu	Gln	Leu	Asn	Arg	Arg	Ile	Leu	Pro	Glu	Lys	Thr	Val	Ile	Ala	Leu
			35				40					45			

Ala	Arg	Ala	Tyr	Asp	Leu	Ser	Pro	Val	Asp	Ala	Leu	Val	Arg	Thr	Gly
	50					55					60				

His	Leu	Thr	Glu	Glu	Glu	Ala	Gly	Ser	Arg	Glu	Glu	Asp	Ala	Ser	Pro
	65				70					75					80

Asp	Ser	Ala	Asp	Asp	Tyr	Pro	Thr	Trp	Ala	Leu	Asn	Ser	His	Leu	Asp
			85						90					95	

Tyr	Gly	Ile	Leu	Gly	Ala	Phe	Gly	Asp	Ile	Ala	Glu	Glu	Val	Asn	Ser
			100					105					110		

<210> 787

<211> 564

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(541)

<223> RXN01769

<400> 787

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caca	accccg	ttgc	gcac	cacc	agc	ataa	atc	tat	att	cgct	gtg	acg	ggg	ttg	ttg	115
											Val	Thr	Gly	Leu	Leu	
											1				5	

ggg	cgc	gcc	cca	cat	tca	ctc	ttt	ttc	cgc	att	ggt	ttc	tac	tac	aca	163
Gly	Arg	Ala	Pro	His	Ser	Leu	Phe	Phe	Pro	Ile	Gly	Phe	Tyr	Tyr	Thr	
				10					15					20		

ccc	atg	acc	tct	att	act	act	acc	gat	acc	cgc	cta	tat	aca	gca	ctg	211
Pro	Met	Thr	Ser	Ile	Thr	Thr	Thr	Asp	Thr	Pro	Leu	Tyr	Thr	Ala	Leu	
			25					30					35			

ccc	cat	acc	cgt	atc	tct	gat	gcg	gaa	ttg	ttg	aca	cca	aca	aca	act	259
Pro	His	Thr	Arg	Ile	Ser	Asp	Ala	Glu	Leu	Leu	Thr	Pro	Thr	Thr	Thr	
		40				45					50					

gtg	cac	gag	att	ctc	gtt	tac	gga	cgc	gct	gag	tgc	cca	ggg	tgt	aca	307
Val	His	Glu	Ile	Leu	Val	Tyr	Gly	Pro	Ala	Glu	Cys	Pro	Gly	Cys	Thr	
		55				60					65					

gca acg ctt gac ttc ttt gca cgc aaa aac atg ccg gcc acc aaa gtc 355
 Ala Thr Leu Asp Phe Phe Ala Arg Lys Asn Met Pro Ala Thr Lys Val
 70 75 80 85

act gta gct gcc ggt gat gta gca cat acc tac atc acc caa gac tta 403
 Thr Val Ala Ala Gly Asp Val Ala His Thr Tyr Ile Thr Gln Asp Leu
 90 95 100

ggt tat ctc caa gca ccg att gtc act gtc cgt atc agt tcc tct gct 451
 Gly Tyr Leu Gln Ala Pro Ile Val Thr Val Arg Ile Ser Ser Ser Ala
 105 110 115

tct aac cac gac aac gaa cac aac acc cag atc ctg cac tgg tcc ggc 499
 Ser Asn His Asp Asn Glu His Asn Thr Gln Ile Leu His Trp Ser Gly
 120 125 130

gtt aat cgc tac ctc atg cag gca ctc tcc cgt act cat ttc 541
 Val Asn Arg Tyr Leu Met Gln Ala Leu Ser Arg Thr His Phe
 135 140 145

tagaaagggtt tttcccggtca tgt 564

<210> 788

<211> 147

<212> PRT

<213> Corynebacterium glutamicum

<400> 788

Val Thr Gly Leu Leu Gly Arg Ala Pro His Ser Leu Phe Phe Pro Ile
 1 5 10 15

Gly Phe Tyr Tyr Thr Pro Met Thr Ser Ile Thr Thr Thr Asp Thr Pro
 20 25 30

Leu Tyr Thr Ala Leu Pro His Thr Arg Ile Ser Asp Ala Glu Leu Leu
 35 40 45

Thr Pro Thr Thr Thr Val His Glu Ile Leu Val Tyr Gly Pro Ala Glu
 50 55 60

Cys Pro Gly Cys Thr Ala Thr Leu Asp Phe Phe Ala Arg Lys Asn Met
 65 70 75 80

Pro Ala Thr Lys Val Thr Val Ala Ala Gly Asp Val Ala His Thr Tyr
 85 90 95

Ile Thr Gln Asp Leu Gly Tyr Leu Gln Ala Pro Ile Val Thr Val Arg
 100 105 110

Ile Ser Ser Ser Ala Ser Asn His Asp Asn Glu His Asn Thr Gln Ile
 115 120 125

Leu His Trp Ser Gly Val Asn Arg Tyr Leu Met Gln Ala Leu Ser Arg
 130 135 140

Thr His Phe
 145

<210> 789
 <211> 552
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(529)
 <223> FRXA01769

<400> 789
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 gcagcaccag cataaatcta tattcgctgt gacgggggtg ttg ggg cgc gcc cca 115
 Leu Gly Arg Ala Pro
 1 5
 cat tca ctc ttt ttc ccg att ggt ttc tac tac aca ccc atg acc tct 163
 His Ser Leu Phe Phe Pro Ile Gly Phe Tyr Thr Pro Met Thr Ser
 10 15 20
 att act act acc gat acc ccg cta tat aca gca ctg ccc cat acc cgt 211
 Ile Thr Thr Thr Asp Thr Pro Leu Tyr Thr Ala Leu Pro His Thr Arg
 25 30 35
 atc tct gat gcg gaa ttg ttg aca cca aca aca act gtg cac gag att 259
 Ile Ser Asp Ala Glu Leu Leu Thr Pro Thr Thr Thr Val His Glu Ile
 40 45 50
 ctc gtt tac gga ccg gct gag tgc cca ggg tgt aca gca acg ett gac 307
 Leu Val Tyr Gly Pro Ala Glu Cys Pro Gly Cys Thr Ala Thr Leu Asp
 55 60 65
 ttc ttt gca cgc aaa aac atg ccg gcc acc aaa gtc act gta gct gcc 355
 Phe Phe Ala Arg Lys Asn Met Pro Ala Thr Lys Val Thr Val Ala Ala
 70 75 80 85
 ggt gat gta gca cat acc tac atc acc caa gac tta ggt tat ctc caa 403
 Gly Asp Val Ala His Thr Tyr Ile Thr Gln Asp Leu Gly Tyr Leu Gln
 90 95 100
 gca ccg att gtc act gtc cgt atc agt tcc tct gct tct aac cac gac 451
 Ala Pro Ile Val Thr Val Arg Ile Ser Ser Ser Ala Ser Asn His Asp
 105 110 115
 aac gaa cac aac acc cag atc ctg cac tgg tcc ggc gtt aat cgc tac 499
 Asn Glu His Asn Thr Gln Ile Leu His Trp Ser Gly Val Asn Arg Tyr
 120 125 130
 ctc atg cag gca ctc tcc cgt act cat ttc tagaaagggt tttcccgctca 549
 Leu Met Gln Ala Leu Ser Arg Thr His Phe
 135 140
 tgt 552

<210> 790
 <211> 143
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 790

Leu Gly Arg Ala Pro His Ser Leu Phe Phe Pro Ile Gly Phe Tyr Tyr
1 5 10 15

Thr Pro Met Thr Ser Ile Thr Thr Thr Asp Thr Pro Leu Tyr Thr Ala
20 25 30

Leu Pro His Thr Arg Ile Ser Asp Ala Glu Leu Leu Thr Pro Thr Thr
35 40 45

Thr Val His Glu Ile Leu Val Tyr Gly Pro Ala Glu Cys Pro Gly Cys
50 55 60

Thr Ala Thr Leu Asp Phe Phe Ala Arg Lys Asn Met Pro Ala Thr Lys
65 70 75 80

Val Thr Val Ala Ala Gly Asp Val Ala His Thr Tyr Ile Thr Gln Asp
85 90 95

Leu Gly Tyr Leu Gln Ala Pro Ile Val Thr Val Arg Ile Ser Ser Ser
100 105 110

Ala Ser Asn His Asp Asn Glu His Asn Thr Gln Ile Leu His Trp Ser
115 120 125

Gly Val Asn Arg Tyr Leu Met Gln Ala Leu Ser Arg Thr His Phe
130 135 140

<210> 791

<211> 825

<212> DNA

<213> *Corynebacterium glutamicum*

 $\langle 220 \rangle$

<221> CDS

<222> (101) .. (802)

<223> RXN01771

<400> 791

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gggtattttc aggtcgcggt cgcaggattt tgggtgggagc atg cac cag gct ggc 115
Met His Gln Ala Gly
1 5

cag ctc atc aat gat ccc agt cag ggt ctg tgg cgc act tct gcc ctg 163
Gln Leu Ile Asn Asp Pro Ser Gln Gly Leu Trp Arg Thr Ser Ala Leu
10 15 20

cgc tgc ccg gtt gct cgg gtt gga cat gcc gtg ttg cgc cag cgt gcc 211
Arg Ser Pro Val Ala Arg Val Gly His Ala Val Leu Arg Gln Arg Ala
25 30 35

ggt gag atc tcg cgc atg caa ggt cgt gag ttt tct cgc cct ggg gat 259
Gly Glu Ile Ser Arg Met Gln Gly Arg Glu Phe Ser Arg Pro Gly Asp
40 45 50

cag ttc cga cag gta gat ttg cgc agg cga ctg att cag gtc cat ccc 307
Gln Phe Arg Gln Val Asp Leu Arg Arg Arg Leu Ile Gln Val His Pro
55 60 65

caa tca att cct aca gcg gat gcg atg gcc gta acc atc acc atg gcg 355
 Gln Ser Ile Pro Thr Ala Asp Ala Met Ala Val Thr Ile Thr Met Ala
 70 75 80 85
 ctc acc gct gcc acg att gat ccg gtg aag ttc gtc gcg gat tca cag 403
 Leu Thr Ala Ala Thr Ile Asp Pro Val Lys Phe Val Ala Asp Ser Gln
 90 95 100
 aac ccg gat gaa gag att tat ttg gca gct cag atc gca ttg cgg gaa 451
 Asn Pro Asp Glu Glu Ile Tyr Leu Ala Ala Gln Ile Ala Leu Arg Glu
 105 110 115
 atg gtt atc gct atg cct ttg gag gat ttc atc ggg gtg cgc att gat 499
 Met Val Ile Ala Met Pro Leu Glu Asp Phe Ile Gly Val Arg Ile Asp
 120 125 130
 cta gag cct gtt ttg gtg gct gct caa gct gct gcg aag aat gtg ggc 547
 Leu Glu Pro Val Leu Val Ala Ala Gln Ala Ala Lys Asn Val Gly
 135 140 145
 gtg gaa gtc tcg tca atc ttg ctg aag gat ctg aat ctt ccc cag gag 595
 Val Glu Val Ser Ser Ile Leu Leu Lys Asp Leu Asn Leu Pro Gln Glu
 150 155 160 165
 tac tcg gga gcg ttg cag gaa tcg atc gtt gcg aaa att caa gcc gaa 643
 Tyr Ser Gly Ala Leu Gln Glu Ser Ile Val Ala Lys Ile Gln Ala Glu
 170 175 180
 act gat ctg gaa cgt gca cga aat gaa gtg aaa act acc cgt gct cga 691
 Thr Asp Leu Glu Arg Ala Arg Asn Glu Val Lys Thr Thr Arg Ala Arg
 185 190 195
 ctt gcc agc gcg aaa gtg ttg gag caa aat ccg att ctt gcc aaa att 739
 Leu Ala Ser Ala Lys Val Leu Glu Gln Asn Pro Ile Leu Ala Lys Ile
 200 205 210
 cgg atg att gaa gcg ctc cca ccg gga tcc aca att gag gtt cgg gag 787
 Arg Met Ile Glu Ala Leu Pro Pro Gly Ser Thr Ile Glu Val Arg Glu
 215 220 225
 ggt gac tca aag gca taaagttgcc catttcggtg ccc 825
 Gly Asp Ser Lys Ala
 230

<210> 792

<211> 234

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 792

Met His Gln Ala Gly Gln Leu Ile Asn Asp Pro Ser Gln Gly Leu Trp
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 Arg Thr Ser Ala Leu Arg Ser Pro Val Ala Arg Val Gly His Ala Val
 20 25 30
 Leu Arg Gln Arg Ala Gly Glu Ile Ser Arg Met Gln Gly Arg Glu Phe
 35 40 45

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Ser Arg Pro Gly Asp Gln Phe Arg Gln Val Asp Leu Arg Arg Arg Leu
 50                      55                      60

Ile Gln Val His Pro Gln Ser Ile Pro Thr Ala Asp Ala Met Ala Val
 65                      70                      75                      80

Thr Ile Thr Met Ala Leu Thr Ala Ala Thr Ile Asp Pro Val Lys Phe
 85                      90                      95

Val Ala Asp Ser Gln Asn Pro Asp Glu Glu Ile Tyr Leu Ala Ala Gln
100                      105                      110

Ile Ala Leu Arg Glu Met Val Ile Ala Met Pro Leu Glu Asp Phe Ile
115                      120                      125

Gly Val Arg Ile Asp Leu Glu Pro Val Leu Val Ala Ala Gln Ala Ala
130                      135                      140

Ala Lys Asn Val Gly Val Glu Val Ser Ser Ile Leu Leu Lys Asp Leu
145                      150                      155                      160

Asn Leu Pro Gln Glu Tyr Ser Gly Ala Leu Gln Glu Ser Ile Val Ala
165                      170                      175

Lys Ile Gln Ala Glu Thr Asp Leu Glu Arg Ala Arg Asn Glu Val Lys
180                      185                      190

Thr Thr Arg Ala Arg Leu Ala Ser Ala Lys Val Leu Glu Gln Asn Pro
195                      200                      205

Ile Leu Ala Lys Ile Arg Met Ile Glu Ala Leu Pro Pro Gly Ser Thr
210                      215                      220

Ile Glu Val Arg Glu Gly Asp Ser Lys Ala
225                      230

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<210> 793

<211> 825

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(802)

<223> FRXA01771

<400> 793

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gggtattttc aggtgcgcgt cgcaggattt tgggtggagc atg cac cag gct ggc 115
                                   Met His Gln Ala Gly
                                   1                      5

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cag ctc atc aat gat ccc agt cag ggt ctg tgg cgc act tct gcc ctg 163
Gln Leu Ile Asn Asp Pro Ser Gln Gly Leu Trp Arg Thr Ser Ala Leu
                      10                      15                      20

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cgc tcg cag gtt gct cgg gtt gga cat gcc gtg ttg cgc cag cgt gcc 211
Arg Ser Pro Val Ala Arg Val Gly His Ala Val Leu Arg Gln Arg Ala
                      25                      30                      35

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ggt gag atc tcg cgc atg caa ggt cgt gag ttt tct cgc cct ggg gat 259
 Gly Glu Ile Ser Arg Met Gln Gly Arg Glu Phe Ser Arg Pro Gly Asp
 40 45 50
 cag ttc cga cag gta gat ttg cgc agg cga ctg att cag gtc cat ccc 307
 Gln Phe Arg Gln Val Asp Leu Arg Arg Arg Leu Ile Gln Val His Pro
 55 60 65
 caa tca att cct aca gcg gat gcg atg gcc gta acc atc acc atg gcg 355
 Gln Ser Ile Pro Thr Ala Asp Ala Met Ala Val Thr Ile Thr Met Ala
 70 75 80 85
 ctg acc gct gcc acg att gat ccg gtg aag ttc gtc gcg gat tca cag 403
 Leu Thr Ala Ala Thr Ile Asp Pro Val Lys Phe Val Ala Asp Ser Gln
 90 95 100
 aac ccg gat gaa gag att tat ttg gca gct cag atc gca ttg cgg gaa 451
 Asn Pro Asp Glu Ile Tyr Leu Ala Ala Gln Ile Ala Leu Arg Glu
 105 110 115
 atg gtt atc gct atg cct ttg gag gat ttc atc ggg gtg cgc att gat 499
 Met Val Ile Ala Met Pro Leu Glu Asp Phe Ile Gly Val Arg Ile Asp
 120 125 130
 cta gag cct gtt ttg gtg gct gct caa gct gct gcg aag aat gtg ggc 547
 Leu Glu Pro Val Leu Val Ala Ala Gln Ala Ala Lys Asn Val Gly
 135 140 145
 gtg gaa gtc tcg tca atc ttg ctg aag gat ctg aat ctt ccc cag gag 595
 Val Glu Val Ser Ser Ile Leu Leu Lys Asp Leu Asn Leu Pro Gln Glu
 150 155 160 165
 tac tcg gga gcg ttg cag gaa tcg atc gtt gcg aaa att caa gcc gaa 643
 Tyr Ser Gly Ala Leu Gln Glu Ser Ile Val Ala Lys Ile Gln Ala Glu
 170 175 180
 act gat ctg gaa cgt gca cga aat gaa gtg aaa act acc cgt gct cga 691
 Thr Asp Leu Glu Arg Ala Arg Asn Glu Val Lys Thr Thr Arg Ala Arg
 185 190 195
 ctt gcc agc gcg aaa gtg ttg gag caa aat ccg att ctt gcc aaa att 739
 Leu Ala Ser Ala Lys Val Leu Glu Gln Asn Pro Ile Leu Ala Lys Ile
 200 205 210
 cgg atg att gaa gcg ctg cca ccg gga tcc aca att gag gtt cgg gag 787
 Arg Met Ile Glu Ala Leu Pro Pro Gly Ser Thr Ile Glu Val Arg Glu
 215 220 225
 ggt gac tca aag gca taaagttgcc catttcggtg ccc 825
 Gly Asp Ser Lys Ala
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<210> 794

<211> 234

<212> PRT

<213> Corynebacterium glutamicum

<400> 794

Met His Gln Ala Gly Gln Leu Ile Asn Asp Pro Ser Gln Gly Leu Trp

1	5	10	15
Arg Thr Ser Ala Leu Arg Ser Pro Val Ala Arg Val Gly His Ala Val	20	25	30
Leu Arg Gln Arg Ala Gly Glu Ile Ser Arg Met Gln Gly Arg Glu Phe	35	40	45
Ser Arg Pro Gly Asp Gln Phe Arg Gln Val Asp Leu Arg Arg Arg Leu	50	55	60
Ile Gln Val His Pro Gln Ser Ile Pro Thr Ala Asp Ala Met Ala Val	65	70	75
Thr Ile Thr Met Ala Leu Thr Ala Ala Thr Ile Asp Pro Val Lys Phe	85	90	95
Val Ala Asp Ser Gln Asn Pro Asp Glu Glu Ile Tyr Leu Ala Ala Gln	100	105	110
Ile Ala Leu Arg Glu Met Val Ile Ala Met Pro Leu Glu Asp Phe Ile	115	120	125
Gly Val Arg Ile Asp Leu Glu Pro Val Leu Val Ala Ala Gln Ala Ala	130	135	140
Ala Lys Asn Val Gly Val Glu Val Ser Ser Ile Leu Leu Lys Asp Leu	145	150	155
Asn Leu Pro Gln Glu Tyr Ser Gly Ala Leu Gln Glu Ser Ile Val Ala	165	170	175
Lys Ile Gln Ala Glu Thr Asp Leu Glu Arg Ala Arg Asn Glu Val Lys	180	185	190
Thr Thr Arg Ala Arg Leu Ala Ser Ala Lys Val Leu Glu Gln Asn Pro	195	200	205
Ile Leu Ala Lys Ile Arg Met Ile Glu Ala Leu Pro Pro Gly Ser Thr	210	215	220
Ile Glu Val Arg Glu Gly Asp Ser Lys Ala	225	230	

<210> 795

<211> 849

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(826)

<223> RXN01774

<400> 795

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cacacaccac tcttctctgag agaattcctga ggtcatcacc atg tca ccg aac ttc 115

Met Ser Pro Asn Phe
1 5

caa gct cgc ggt act act gcg ccc act gtt gct ttg tcc atg cgc cag 163
 Gln Ala Arg Gly Thr Ala Pro Thr Val Ala Leu Ser Met Arg Gln
 10 15 20

atc gcg cac atc cgt gaa gaa att aag aaa tca cca ctc gct gct tcc 211
 Ile Ala His Ile Arg Glu Glu Ile Lys Lys Ser Pro Leu Ala Ala Ser
 25 30 35

gtt ttc atc aca ccc acc acc aaa caa atg gtt gtc cga gat cta gaa 259
 Val Phe Ile Thr Pro Thr Thr Lys Gln Met Val Val Arg Asp Leu Glu
 40 45 50

tca ctg ttc cag cag ctc tac cac aca gat cta cct gaa cca tcc atc 307
 Ser Leu Phe Gln Gln Leu Tyr His Thr Asp Leu Pro Glu Pro Ser Ile
 55 60 65

aaa gac agt ggt ctt atc agt gct atc ggc tct agc gcc ggc aat acc 355
 Lys Asp Ser Gly Leu Ile Ser Ala Ile Gly Ser Ser Ala Gly Asn Thr
 70 75 80 85

aat aat cca gca ctc gcc cta gaa act cag atg gct tac cac ctg gtg 403
 Asn Asn Pro Ala Leu Ala Leu Glu Thr Gln Met Ala Tyr His Leu Val
 90 95 100

ctt gct atg cac cac acc gat gtt gct acc tgg cac aag gtg gtg acc 451
 Leu Ala Met His His Thr Asp Val Ala Thr Trp His Lys Val Val Thr
 105 110 115

aaa aac atc acc gaa tct gct gct gca caa gat gct gcg gtc gag cac 499
 Lys Asn Ile Thr Glu Ser Ala Ala Gln Asp Ala Ala Val Glu His
 120 125 130

agt gct aaa tac gat gct gtg tac gat gcc gca caa ctt atg ggc atc 547
 Ser Ala Lys Tyr Asp Ala Val Tyr Asp Ala Ala Gln Leu Met Gly Ile
 135 140 145

act gtt gag gaa ggt aat gtc ggt agc atc gct att gcc ttt agc aca 595
 Thr Val Glu Glu Gly Asn Val Gly Ser Ile Ala Ile Ala Phe Ser Thr
 150 155 160 165

gca cgt gca gac ggt aaa tct gat tgg tgt gtt tcc gcc atc agc cgc 643
 Ala Arg Ala Asp Gly Lys Ser Asp Trp Cys Val Ser Gly Ile Ser Arg
 170 175 180

tac atc gag gtc acc gaa gcc ttg gat gct gcg cga gct gtc act aaa 691
 Tyr Ile Glu Val Thr Glu Ala Leu Asp Ala Ala Arg Ala Val Thr Lys
 185 190 195

aat act gat gcg ctc aat aaa act gct cta cca gac gtg cag cgc gcg 739
 Asn Thr Asp Ala Leu Asn Lys Thr Ala Leu Pro Asp Val Gln Pro Ala
 200 205 210

ccg gtt gtg cat tca gca cag ttc atg aac aag tcc gca cac gat cat 787
 Pro Val Val His Ser Ala Gln Phe Met Asn Lys Ser Ala His Asp His
 215 220 225

ggg gtt aat act gcg gaa aaa gat caa cca acc ctg ttt taaaagactg 836
 Gly Val Asn Thr Ala Glu Lys Asp Gln Pro Thr Leu Phe
 230 235 240

tccatttaac aac

849

<210> 796

<211> 242

<212> FRT

<213> *Corynebacterium glutamicum*

<400> 796

Met Ser Pro Asn Phe Gln Ala Arg Gly Thr Thr Ala Pro Thr Val Ala
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Leu Ser Met Arg Gln Ile Ala His Ile Arg Glu Glu Ile Lys Lys Ser
 20 25 30

Pro Leu Ala Ala Ser Val Phe Ile Thr Pro Thr Thr Lys Gln Met Val
 35 40 45

Val Arg Asp Leu Glu Ser Leu Phe Gln Gln Leu Tyr His Thr Asp Leu
 50 55 60

Pro Glu Pro Ser Ile Lys Asp Ser Gly Leu Ile Ser Ala Ile Gly Ser
 65 70 75 80

Ser Ala Gly Asn Thr Asn Asn Pro Ala Leu Ala Leu Glu Thr Gln Met
 85 90 95

Ala Tyr His Leu Val Leu Ala Met His His Thr Asp Val Ala Thr Trp
 100 105 110

His Lys Val Val Thr Lys Asn Ile Thr Glu Ser Ala Ala Ala Gln Asp
 115 120 125

Ala Ala Val Glu His Ser Ala Lys Tyr Asp Ala Val Tyr Asp Ala Ala
 130 135 140

Gln Leu Met Gly Ile Thr Val Glu Glu Gly Asn Val Gly Ser Ile Ala
 145 150 155 160

Ile Ala Phe Ser Thr Ala Arg Ala Asp Gly Lys Ser Asp Trp Cys Val
 165 170 175

Ser Gly Ile Ser Arg Tyr Ile Glu Val Thr Glu Ala Leu Asp Ala Ala
 180 185 190

Arg Ala Val Thr Lys Asn Thr Asp Ala Leu Asn Lys Thr Ala Leu Pro
 195 200 205

Asp Val Gln Pro Ala Pro Val Val His Ser Ala Gln Phe Met Asn Lys
 210 215 220

Ser Ala His Asp His Gly Val Asn Thr Ala Glu Lys Asp Gln Pro Thr
 225 230 235 240

Leu Phe

<210> 797

<211> 883

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(883)

<223> FRXA01774

<400> 797

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cacacaccac tcttctctgag agaattctga ggtcatcacc atg tca ccg aac ttc 115
 Met Ser Pro Asn Phe
 1 5

caa gct cgc ggt act act gcg ccc act gtt gct ttg tcc atg cgc cag 163
 Gln Ala Arg Gly Thr Thr Ala Pro Thr Val Ala Leu Ser Met Arg Gln
 10 15 20

atc gcg cac atc cgt gaa gaa att aag aaa tca cca ctc gct gct tcc 211
 Ile Ala His Ile Arg Glu Glu Ile Lys Lys Ser Pro Leu Ala Ala Ser
 25 30 35

gtt ttc atc aca ccc acc acc aaa caa atg gtt gtc cga gat cta gaa 259
 Val Phe Ile Thr Pro Thr Thr Lys Gln Met Val Val Arg Asp Leu Glu
 40 45 50

tca ctg ttc cag cag ctc tac cac aca gat cta cct gaa cca tcc atc 307
 Ser Leu Phe Gln Gln Leu Tyr His Thr Asp Leu Pro Glu Pro Ser Ile
 55 60 65

aaa gac agt ggt ctt atc agt gct atc gcc tct agc gcc gcc aat acc 355
 Lys Asp Ser Gly Leu Ile Ser Ala Ile Gly Ser Ser Ala Gly Asn Thr
 70 75 80 85

aat aat cca gca ctc gcc cta gaa act cag atg gct tac cac ctg gtg 403
 Asn Asn Pro Ala Leu Ala Leu Glu Thr Gln Met Ala Tyr His Leu Val
 90 95 100

ctt gct atg cac cac acc gat gtt gct acc tgg cac aag gtg gtg acc 451
 Leu Ala Met His His Thr Asp Val Ala Thr Trp His Lys Val Val Thr
 105 110 115

aaa aac atc acc gaa tct gct gct gca caa gat gct gcg gtc gag cac 499
 Lys Asn Ile Thr Glu Ser Ala Ala Gln Asp Ala Val Glu His
 120 125 130

agt gct aaa tac gat gct gtg tac gat gcc gca caa ctt atg gcc atc 547
 Ser Ala Lys Tyr Asp Ala Val Tyr Asp Ala Ala Gln Leu Met Gly Ile
 135 140 145

act gtt gag gaa ggt aat gtc ggt agc atc gct att gcc ttt agc aca 595
 Thr Val Glu Glu Gly Asn Val Gly Ser Ile Ala Ile Ala Phe Ser Thr
 150 155 160 165

gca cgt gca gac ggt aaa tct gat tgg tgt gtt tcc gcc atc agc cgc 643
 Ala Arg Ala Asp Gly Lys Ser Asp Trp Cys Val Ser Gly Ile Ser Arg
 170 175 180

tac atc gag gtc acc gaa gcc ttg gat gct gcg cga gct gtc act aaa 691
 Tyr Ile Glu Val Thr Glu Ala Leu Asp Ala Arg Ala Val Thr Lys
 185 190 195

aat act gat gcg ctc aat aaa act gct cta cca gac gtg cag ccg gcg 739
 Asn Thr Asp Ala Leu Asn Lys Thr Ala Leu Pro Asp Val Gln Pro Ala
 200 205 210

ccg gtt gtg cat tca gca cag ttc atg aac aag tcc gca cac gat cat 787
 Pro Val Val His Ser Ala Gln Phe Met Asn Lys Ser Ala His Asp His
 215 220 225

ggg gtt aat act gcg gaa aaa gat caa cca acc tgt tta aag act gtg 835
 Gly Val Asn Thr Ala Glu Lys Asp Gln Pro Thr Cys Leu Lys Thr Val
 230 235 240 245

cat tta caa cca cat cgt tac ccc cga aca ggc ttt aag gct att caa 883
 His Leu Gln Pro His Arg Tyr Pro Arg Thr Gly Phe Lys Ala Ile Gln
 250 255 260

<210> 798

<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 798

Met Ser Pro Asn Phe Gln Ala Arg Gly Thr Thr Ala Pro Thr Val Ala
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Leu Ser Met Arg Gln Ile Ala His Ile Arg Glu Glu Ile Lys Lys Ser
 20 25 30

Pro Leu Ala Ala Ser Val Phe Ile Thr Pro Thr Thr Lys Gln Met Val
 35 40 45

Val Arg Asp Leu Glu Ser Leu Phe Gln Gln Leu Tyr His Thr Asp Leu
 50 55 60

Pro Glu Pro Ser Ile Lys Asp Ser Gly Leu Ile Ser Ala Ile Gly Ser
 65 70 75 80

Ser Ala Gly Asn Thr Asn Asn Pro Ala Leu Ala Leu Glu Thr Gln Met
 85 90 95

Ala Tyr His Leu Val Leu Ala Met His His Thr Asp Val Ala Thr Trp
 100 105 110

His Lys Val Val Thr Lys Asn Ile Thr Glu Ser Ala Ala Ala Gln Asp
 115 120 125

Ala Ala Val Glu His Ser Ala Lys Tyr Asp Ala Val Tyr Asp Ala Ala
 130 135 140

Gln Leu Met Gly Ile Thr Val Glu Glu Gly Asn Val Gly Ser Ile Ala
 145 150 155 160

Ile Ala Phe Ser Thr Ala Arg Ala Asp Gly Lys Ser Asp Trp Cys Val
 165 170 175

Ser Gly Ile Ser Arg Tyr Ile Glu Val Thr Glu Ala Leu Asp Ala Ala
 180 185 190

Arg Ala Val Thr Lys Asn Thr Asp Ala Leu Asn Lys Thr Ala Leu Pro

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195                200                205
Asp Val Gln Pro Ala Pro Val Val His Ser Ala Gln Phe Met Asn Lys
210                215                220

Ser Ala His Asp His Gly Val Asn Thr Ala Glu Lys Asp Gln Pro Thr
225                230                235                240

Cys Leu Lys Thr Val His Leu Gln Pro His Arg Tyr Pro Arg Thr Gly
245                250                255

Phe Lys Ala Ile Gln
260

<210> 799
<211> 816
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(793)
<223> RXN01787

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ttcacacccc cactccacac acaactcgcaa aggattcatc atg agc aac aat gct 115
Met Ser Asn Asn Ala
1 5

ctt tta gta gca aac gaa gcc gac atc ggt ctc tac ctc cac tgg aat 163
Leu Leu Val Ala Asn Glu Ala Asp Ile Gly Leu Tyr Leu His Trp Asn
10 15 20

ggt ggt cgc gac tcg att gag gcg ttt ctc gcc tac gcc gca tac gcg 211
Gly Gly Arg Asp Ser Ile Glu Ala Phe Leu Ala Tyr Ala Ala Tyr Ala
25 30 35

cag tta cca ccc atc aac gaa aat aac gat tgg ttg cca ccg ttt att 259
Gln Leu Pro Pro Ile Asn Glu Asn Asn Asp Trp Leu Pro Pro Phe Ile
40 45 50

act gtg ctg aag aac ttc ttc ggc aat gat ggt tct ggc gtc tac ctc 307
Thr Val Leu Lys Asn Phe Phe Gly Asn Asp Gly Ser Gly Val Tyr Leu
55 60 65

gaa cct gtc aat cag gat tat ctc gac gcc atc gac tat gac aac ggt 355
Glu Pro Val Asn Gln Asp Tyr Leu Asp Gly Ile Asp Tyr Asp Asn Gly
70 75 80 85

gtt tac atg ctt gac gat tat gag atc act gag cgt att aat cca ccc 403
Val Tyr Met Leu Asp Asp Tyr Glu Ile Thr Glu Arg Ile Asn Pro Pro
90 95 100

gct gtt gag caa gac tcc cac gat ctc cac gac atg ttg atc aaa att 451
Ala Val Glu Gln Asp Ser His Asp Leu His Asp Met Leu Ile Lys Ile
105 110 115

gat aaa gct caa cca cct gtc gat caa ctc ggg agt ttt ctc cat ggc 499

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Asp	Lys	Ala	Gln	Pro	Pro	Val	Asp	Gln	Leu	Gly	Ser	Phe	Leu	His	Gly		
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Leu	Glu	Thr	Ser	Val	Ala	Asp	Leu	Gly	Val	Gly	Asp	Arg	Val	Phe	Leu		
		135				140				145							
cca	cgt	ttt	agc	acc	ttt	gat	aag	aaa	ctc	ggt	cgc	tac	cgc	atc	cac	595	
Pro	Arg	Phe	Ser	Thr	Phe	Asp	Lys	Lys	Leu	Gly	Arg	Tyr	Arg	Ile	His		
		150			155				160					165			
act	gtt	ctc	gga	ttc	gct	gag	aac	gat	ccg	ttt	aac	cct	atg	acc	agc	643	
Thr	Val	Leu	Gly	Phe	Ala	Glu	Asn	Asp	Pro	Phe	Asn	Pro	Met	Thr	Ser		
			170						175					180			
agc	gag	cga	ttt	aaa	ggg	aag	ccc	tat	gtc	gat	atg	ttc	gac	aat	caa	691	
Ser	Glu	Arg	Phe	Lys	Gly	Lys	Pro	Tyr	Val	Asp	Met	Phe	Asp	Asn	Gln		
		185					190					195					
gac	aac	gcc	ttt	aac	cca	aat	tcc	tat	atc	act	aca	gat	acc	gtg	cgc	739	
Asp	Asn	Ala	Phe	Asn	Pro	Asn	Ser	Tyr	Ile	Thr	Thr	Asp	Thr	Val	Arg		
		200					205					210					
atc	gtt	gtc	gat	cct	gta	ccg	gaa	act	aat	ccc	gac	gat	gag	aaa	gca	787	
Ile	Val	Val	Asp	Pro	Val	Pro	Glu	Thr	Asn	Pro	Asp	Asp	Glu	Lys	Ala		
		215				220					225						
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Gly	Arg																
		230															

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<213>	Corynebacterium glutamicum																

<400>	800																
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	1			5					10					15			
Tyr	Leu	His	Trp	Asn	Gly	Gly	Arg	Asp	Ser	Ile	Glu	Ala	Phe	Leu	Ala		
			20					25					30				
Tyr	Ala	Ala	Tyr	Ala	Gln	Leu	Pro	Pro	Ile	Asn	Glu	Asn	Asn	Asp	Trp		
		35					40					45					
Leu	Pro	Pro	Phe	Ile	Thr	Val	Leu	Lys	Asn	Phe	Phe	Gly	Asn	Asp	Gly		
		50				55					60						
Ser	Gly	Val	Tyr	Leu	Glu	Pro	Val	Asn	Gln	Asp	Tyr	Leu	Asp	Gly	Ile		
		65			70				75					80			
Asp	Tyr	Asp	Asn	Gly	Val	Tyr	Met	Leu	Asp	Asp	Tyr	Glu	Ile	Thr	Glu		
			85						90					95			
Arg	Ile	Asn	Pro	Pro	Ala	Val	Glu	Gln	Asp	Ser	His	Asp	Leu	His	Asp		
		100					105						110				
Met	Leu	Ile	Lys	Ile	Asp	Lys	Ala	Gln	Pro	Pro	Val	Asp	Gln	Leu	Gly		
		115					120					125					

Ser Phe Leu His Gly Leu Glu Thr Ser Val Ala Asp Leu Gly Val Gly
 130 135 140

Asp Arg Val Phe Leu Pro Arg Phe Ser Thr Phe Asp Lys Lys Leu Gly
 145 150 155 160

Arg Tyr Arg Ile His Thr Val Leu Gly Phe Ala Glu Asn Asp Pro Phe
 165 170 175

Asn Pro Met Thr Ser Ser Glu Arg Phe Lys Gly Lys Pro Tyr Val Asp
 180 185 190

Met Phe Asp Asn Gln Asp Asn Ala Phe Asn Pro Asn Ser Tyr Ile Thr
 195 200 205

Thr Asp Thr Val Arg Ile Val Val Asp Pro Val Pro Glu Thr Asn Pro
 210 215 220

Asp Asp Glu Lys Ala Gly Arg
 225 230

<210> 801
 <211> 377
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 <213> Corynebacterium glutamicum

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 <222> (1)..(354)
 <223> FRXA01787

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 Thr Glu Lys Ile Asp Lys Ala Gln Pro Pro Val Asp Gln Leu Gly Ser
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ttt ctc cat ggc cta gag acc tct gtc gca gat ttg ggg gtt ggt gat 96
 Phe Leu His Gly Leu Glu Thr Ser Val Ala Asp Leu Gly Val Gly Asp
 20 25 30

cgc gta ttt ttg cca cgt ttt agc acc ttt gat aag aaa ctc ggt cgc 144
 Arg Val Phe Leu Pro Arg Phe Ser Thr Phe Asp Lys Lys Leu Gly Arg
 35 40 45

tac cgc atc cac act gtt ctc gga ttc gct gag aac gat ccg ttt aac 192
 Tyr Arg Ile His Thr Val Leu Gly Phe Ala Glu Asn Asp Pro Phe Asn
 50 55 60

cct atg acc agc agc gag cga ttt aaa ggt aag ccc tat gtc gat atg 240
 Pro Met Thr Ser Ser Glu Arg Phe Lys Gly Lys Pro Tyr Val Asp Met
 65 70 75 80

ttc gac aat caa gac aac gcc ttt aac cca aat tcc tat atc act aca 288
 Phe Asp Asn Gln Asp Asn Ala Phe Asn Pro Asn Ser Tyr Ile Thr Thr
 85 90 95

gat acc gtg cgc atc gtt gtc gat cct gta ccg gaa act aat ccc gac 336
 Asp Thr Val Arg Ile Val Val Asp Pro Val Pro Glu Thr Asn Pro Asp
 100 105 110

gat gag aaa gca gga cgc tagccatgtc tcgcagctac ccc 377
 Asp Glu Lys Ala Gly Arg
 115

<210> 802
 <211> 118
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 802
 Thr Glu Lys Ile Asp Lys Ala Gln Pro Pro Val Asp Gln Leu Gly Ser
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 Phe Leu His Gly Leu Glu Thr Ser Val Ala Asp Leu Gly Val Gly Asp
 20 25 30
 Arg Val Phe Leu Pro Arg Phe Ser Thr Phe Asp Lys Lys Leu Gly Arg
 35 40 45
 Tyr Arg Ile His Thr Val Leu Gly Phe Ala Glu Asn Asp Pro Phe Asn
 50 55 60
 Pro Met Thr Ser Ser Glu Arg Phe Lys Gly Lys Pro Tyr Val Asp Met
 65 70 75 80
 Phe Asp Asn Gln Asp Asn Ala Phe Asn Pro Asn Ser Tyr Ile Thr Thr
 85 90 95
 Asp Thr Val Arg Ile Val Val Asp Pro Val Pro Glu Thr Asn Pro Asp
 100 105 110
 Asp Glu Lys Ala Gly Arg
 115

<210> 803
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 <213> Corynebacterium glutamicum

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 <223> RXN01796

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 ttggtgcggc atcgggtggc tgctactagt cgggctcttc ttg ctc ctt ggc ggt 115
 Leu Leu Leu Gly Gly
 1 5
 aac cct gcc gag atc gac cag gtt tta ggt ggc gat caa acc cag atc 163
 Asn Pro Ala Glu Ile Asp Gln Val Leu Gly Gly Asp Gln Thr Gln Ile
 10 15 20
 gag tct gga gag tcc acc gga gcc ggc gac ttt gat cac tgc caa acc 211
 Glu Ser Gly Glu Ser Thr Gly Ala Gly Asp Phe Asp His Cys Gln Thr
 25 30 35

ggc gca gat gcc aac gcc agt gat gat tgt cgc ctt tac tac acc tca 259
 Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg Leu Tyr Thr Ser
 40 45 50

ttc tcc gtc aat gaa atg tgg cag act ttg ctt cca gct cag gct ggt 307
 Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu Pro Ala Gln Ala Gly
 55 60 65

atc gaa tac acc gag cgc aca ttg act ctt ttc aaa aac tcc acc caa 355
 Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe Lys Asn Ser Thr Gln
 70 75 80 85

acc ggc tgc ggt ttc gct tct gcg tcc act ggg cgc ttt tac tgt cgc 403
 Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly Pro Phe Tyr Cys Pro
 90 95 100

tca gac caa gat gct tat ttt gac ttg act ttc ttc gat cag atg cgt 451
 Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe Phe Asp Gln Met Arg
 105 110 115

cag ttc ggt gca gaa aac gcc cgc ctt gcc cag atg tac atc gtg gcg 499
 Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln Met Tyr Ile Val Ala
 120 125 130

cac gag tac ggc cac cac gtc caa aac ctc gag ggc aca ctc gga ctg 547
 His Glu Tyr Gly His His Val Gln Asn Leu Glu Gly Thr Leu Gly Leu
 135 140 145

tcc aat tac aac gat cgc ggc gct gat tcc aac gcc gtc aag atc gag 595
 Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn Ala Val Lys Ile Glu
 150 155 160 165

ttg cag gcc gat tgc tac gca ggc att tgg gct aat cac tcc agc gaa 643
 Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala Asn His Ser Ser Glu
 170 175 180

ggc cgc gat cgc cta ctc caa ccc atc acc gaa tct gag cta gat tcc 691
 Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu Ser Glu Leu Asp Ser
 185 190 195

gct ctc ctt gct gca agc gcc gtg gcc gac gac aat atc cag caa cga 739
 Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp Asn Ile Gln Gln Arg
 200 205 210

tcc ggt ggc gat gtc aat cct gaa agc tgg act cac ggc tca tog cag 787
 Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr His Gly Ser Ser Gln
 215 220 225

cag cgc aaa gac gcg ttc ctc gcc gcc tac aac acc ggc cag atg agc 835
 Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn Thr Gly Gln Met Ser
 230 235 240 245

gcc tgc gac ttc ctc gcc cgg gcc gtc tac aac gac gct taaagcattg 884
 Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn Asp Ala
 250 255

cttttgcagc tct 897

<210> 804

<211> 258

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 804

Leu Leu Leu Gly Gly Asn Pro Ala Glu Ile Asp Gln Val Leu Gly Gly
 1 5 10 15

Asp Gln Thr Gln Ile Glu Ser Gly Glu Ser Thr Gly Ala Gly Asp Phe
 20 25 30

Asp His Cys Gln Thr Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg
 35 40 45

Leu Tyr Tyr Thr Ser Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu
 50 55 60

Pro Ala Gln Ala Gly Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe
 65 70 75 80

Lys Asn Ser Thr Gln Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly
 85 90 95

Pro Phe Tyr Cys Pro Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe
 100 105 110

Phe Asp Gln Met Arg Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln
 115 120 125

Met Tyr Ile Val Ala His Glu Tyr Gly His His Val Gln Asn Leu Glu
 130 135 140

Gly Thr Leu Gly Leu Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn
 145 150 155 160

Ala Val Lys Ile Glu Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala
 165 170 175

Asn His Ser Ser Glu Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu
 180 185 190

Ser Glu Leu Asp Ser Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp
 195 200 205

Asn Ile Gln Gln Arg Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr
 210 215 220

His Gly Ser Ser Gln Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn
 225 230 235 240

Thr Gly Gln Met Ser Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn
 245 250 255

Asp Ala

<210> 805

<211> 506

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(483)

<223> FRXA01796

<400> 805

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Phe	Tyr	Cys	Pro	Ser	Asp	Gln	Asp	Ala	Tyr	Val	Asp	Leu	Thr	Leu	Phe	
1				5					10					15		

gat	cag	atg	cgt	cag	ttc	ggt	gca	gaa	aac	gcc	ccg	ctt	gcc	cag	atg	96
Asp	Gln	Met	Arg	Gln	Phe	Gly	Ala	Glu	Asn	Ala	Pro	Leu	Ala	Gln	Met	
			20				25					30				

tac	atc	gtg	gcg	cac	gag	tac	ggc	cac	cac	gtc	caa	aac	ctc	gag	ggc	144
Tyr	Ile	Val	Ala	His	Glu	Tyr	Gly	His	His	Val	Gln	Asn	Leu	Glu	Gly	
		35				40					45					

aca	ctc	gga	ctg	tcc	aat	tac	aac	gat	ccg	ggc	gct	gat	tcc	aac	gcc	192
Thr	Leu	Gly	Leu	Ser	Asn	Tyr	Asn	Asp	Pro	Gly	Ala	Asp	Ser	Asn	Ala	
	50				55					60						

gtc	aag	atc	gag	ttg	cag	gcc	gat	tgc	tac	gca	ggc	att	tgg	gct	aat	240
Val	Lys	Ile	Glu	Leu	Gln	Ala	Asp	Cys	Tyr	Ala	Gly	Ile	Trp	Ala	Asn	
65				70				75				80				

cac	tcc	agc	gaa	ggc	cgc	gat	ccg	cta	ctc	caa	ccc	atc	acc	gaa	tct	288
His	Ser	Ser	Glu	Gly	Pro	Asp	Pro	Leu	Leu	Gln	Pro	Ile	Thr	Gly	Ser	
			85					90				95				

gag	cta	gat	tcc	gct	ctc	ctt	gct	gca	agc	gcc	gtg	ggc	gac	gac	aat	336
Glu	Leu	Asp	Ser	Ala	Leu	Leu	Ala	Ala	Ser	Ala	Val	Gly	Asp	Asp	Asn	
			100				105					110				

atc	cag	caa	cga	tcc	ggt	ggc	gat	gtc	aat	cct	gaa	agc	tgg	act	cac	384
Ile	Gln	Gln	Arg	Ser	Gly	Gly	Asp	Val	Asn	Pro	Glu	Ser	Trp	Thr	His	
	115				120						125					

ggc	tca	tcg	cag	cag	cgc	aaa	gac	gcg	ttc	ctc	gcc	ggc	tac	aac	acc	432
Gly	Ser	Ser	Gln	Gln	Arg	Lys	Asp	Ala	Phe	Leu	Ala	Gly	Tyr	Asn	Thr	
	130				135					140						

ggc	cag	atg	agc	gcc	tgc	gac	ttc	ctc	ggc	cgg	ggc	gtc	tac	aac	gac	480
Gly	Gln	Met	Ser	Ala	Cys	Asp	Phe	Leu	Gly	Arg	Gly	Val	Tyr	Asn	Asp	
145				150					155			160				

gct	taaagcattg	cttttcgacg	tct													506
Ala																

<210> 806

<211> 161

<212> PRT

<213> Corynebacterium glutamicum

<400> 806

Phe	Tyr	Cys	Pro	Ser	Asp	Gln	Asp	Ala	Tyr	Val	Asp	Leu	Thr	Leu	Phe
1				5					10					15	

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Asp Gln Met Arg Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln Met
      20                      25                      30
Tyr Ile Val Ala His Glu Tyr Gly His His Val Gln Asn Leu Glu Gly
      35                      40                      45
Thr Leu Gly Leu Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn Ala
      50                      55                      60
Val Lys Ile Glu Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala Asn
      65                      70                      75                      80
His Ser Ser Glu Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu Ser
      85                      90                      95
Glu Leu Asp Ser Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp Asn
      100                     105                     110
Ile Gln Gln Arg Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr His
      115                     120                     125
Gly Ser Ser Gln Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn Thr
      130                     135                     140
Gly Gln Met Ser Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn Asp
      145                     150                     155                     160
Ala

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<210> 807

<211> 1083

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1060)

<223> RXN01803

<400> 807

ctagcggaaa ggcttttagcg acaaggcttt ttgcatgttt taatgcaggg aatattaact 60

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ttttgttaat ctctgaccat tgaccttgta cgcttaaaac atg cga aag aaa aaa 115
              Met Arg Lys Lys Lys
              1                      5

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gac ggt caa aat ctc cca gac ttc cgg aaa aat cgg cca aag ctg gat 163
Asp Gly Gln Asn Leu Pro Asp Phe Arg Lys Asn Pro Pro Lys Leu Asp
              10                      15                      20

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aaa aag gct tat gaa aaa gaa cta aaa aga ctt caa gcc gaa ctc gtc 211
Lys Lys Ala Tyr Glu Lys Glu Leu Lys Arg Leu Gln Ala Glu Leu Val
              25                      30                      35

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gat ttg caa caa tgg gtt gtg gaa acc ggt gcg cgc gtg gtc atc gtc 259
Asp Leu Gln Gln Trp Val Val Glu Thr Gly Ala Arg Val Val Ile Val
              40                      45                      50

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atg gaa ggc cgc gac gcc gct ggt aaa ggt tct gcg atc aag cgc att 307

Met	Glu	Gly	Arg	Asp	Ala	Ala	Gly	Lys	Gly	Ser	Ala	Ile	Lys	Arg	Ile	
	55					60					65					
acg	cag	tac	ctc	aac	ccc	cgg	tcc	gca	agg	atc	gaa	cgc	ctg	ccc	acc	355
Thr	Gln	Tyr	Leu	Asn	Pro	Arg	Ser	Ala	Arg	Ile	Glu	Ala	Leu	Pro	Thr	
	70				75				80					85		
cca	aac	tct	cgg	gaa	aaa	ggg	cag	tgg	tat	ttc	cag	cgc	tac	atc	gaa	403
Pro	Asn	Ser	Arg	Glu	Lys	Gly	Gln	Trp	Tyr	Phe	Gln	Arg	Tyr	Ile	Glu	
				90				95					100			
aaa	ttg	ccg	act	gct	ggc	gag	atc	gtt	atc	ttt	gac	cgc	tcc	tgg	tac	451
Lys	Leu	Pro	Thr	Ala	Gly	Glu	Ile	Val	Ile	Phe	Asp	Arg	Ser	Trp	Tyr	
			105				110						115			
aac	cgt	gca	gga	gtc	gag	cgc	gtc	atg	gga	ttt	tgc	acc	tcc	cag	gag	499
Asn	Arg	Ala	Gly	Val	Glu	Arg	Val	Met	Gly	Phe	Cys	Thr	Ser	Gln	Glu	
			120				125					130				
tac	cgc	cga	ttc	ctt	cac	cag	gca	cca	atc	ttt	gaa	cgc	ctg	ttg	gtg	547
Tyr	Arg	Arg	Phe	Leu	His	Gln	Ala	Pro	Ile	Phe	Glu	Arg	Leu	Leu	Val	
			135			140					145					
gaa	gat	ggc	att	cac	ctg	cgt	aaa	tac	tgg	ttc	tct	gta	tct	gat	gaa	595
Glu	Asp	Gly	Ile	His	Leu	Arg	Lys	Tyr	Trp	Phe	Ser	Val	Ser	Asp	Glu	
	150			155						160				165		
gag	cag	att	gag	cgt	ttc	gaa	gac	cgc	ctg	agc	gat	ccg	ctg	cgc	cgg	643
Glu	Gln	Ile	Glu	Arg	Phe	Glu	Asp	Arg	Leu	Ser	Asp	Pro	Leu	Arg	Arg	
			170					175					180			
tgg	aag	ttg	tgc	cca	atg	gat	tta	caa	tgc	atc	acc	cgc	tgg	gaa	gat	691
Trp	Lys	Leu	Ser	Pro	Met	Asp	Leu	Gln	Ser	Ile	Thr	Arg	Trp	Glu	Asp	
			185				190						195			
tac	tca	cgc	gca	aaa	gat	gag	atg	ttc	atc	cac	acg	gac	atc	ccg	tca	739
Tyr	Ser	Arg	Ala	Lys	Asp	Glu	Met	Phe	Ile	His	Thr	Asp	Ile	Pro	Ser	
			200				205					210				
gca	ccg	tgg	tac	acg	gtg	gaa	tct	gag	gac	aag	aag	cgt	tcc	cgc	atc	787
Ala	Pro	Trp	Tyr	Thr	Val	Glu	Ser	Glu	Asp	Lys	Lys	Arg	Ser	Arg	Ile	
	215				220						225					
aac	gtc	att	tgc	cat	ctg	ctc	tgc	acg	att	cct	tat	gag	aag	atc	gat	835
Asn	Val	Ile	Ser	His	Leu	Leu	Ser	Thr	Ile	Pro	Tyr	Glu	Lys	Ile	Asp	
	230			235					240					245		
cgt	cca	ttg	ccg	gaa	atc	cct	cat	cgc	cca	gat	tct	gaa	tct	gat	tat	883
Arg	Pro	Leu	Pro	Glu	Ile	Pro	His	Arg	Pro	Asp	Ser	Glu	Ser	Asp	Tyr	
			250						255					260		
gta	cgt	ccc	cct	cgc	gat	gag	ttc	cgt	tat	gtt	cca	gat	gtg	gca	gca	931
Val	Arg	Pro	Pro	Arg	Asp	Glu	Phe	Arg	Tyr	Val	Pro	Asp	Val	Ala	Ala	
			265				270						275			
cac	ttg	gaa	gaa	gag	cgc	atc	aag	aaa	gaa	gaa	aaa	gcc	aag	aag	gca	979
His	Leu	Glu	Glu	Glu	Arg	Ile	Lys	Lys	Glu	Glu	Lys	Ala	Lys	Lys	Ala	
			280			285					290					
aag	aag	cca	gct	aag	gct	gca	gga	aag	aac	tgc	gat	aag	cag	aag	tct	1027
Lys	Lys	Pro	Ala	Lys	Ala	Ala	Gly	Lys	Asn	Ser	Asp	Lys	Gln	Lys	Ser	

295

300

305

tcc gga gga aaa ggc aag aag aag tcc aag aaa tagaacgcct ttttaaggggt 1080
 Ser Gly Gly Lys Gly Lys Lys Ser Lys Lys
 310 315 320

tga

1083

<210> 808

<211> 320

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 808

Met Arg Lys Lys Lys Asp Gly Gln Asn Leu Pro Asp Phe Arg Lys Asn
 1 5 10 15

Pro Pro Lys Leu Asp Lys Lys Ala Tyr Glu Lys Glu Leu Lys Arg Leu
 20 25 30

Gln Ala Glu Leu Val Asp Leu Gln Gln Trp Val Val Glu Thr Gly Ala
 35 40 45

Arg Val Val Ile Val Met Glu Gly Arg Asp Ala Ala Gly Lys Gly Ser
 50 55 60

Ala Ile Lys Arg Ile Thr Gln Tyr Leu Asn Pro Arg Ser Ala Arg Ile
 65 70 75 80

Glu Ala Leu Pro Thr Pro Asn Ser Arg Glu Lys Gly Gln Trp Tyr Phe
 85 90 95

Gln Arg Tyr Ile Glu Lys Leu Pro Thr Ala Gly Glu Ile Val Ile Phe
 100 105 110

Asp Arg Ser Trp Tyr Asn Arg Ala Gly Val Glu Arg Val Met Gly Phe
 115 120 125

Cys Thr Ser Gln Glu Tyr Arg Arg Phe Leu His Gln Ala Pro Ile Phe
 130 135 140

Glu Arg Leu Leu Val Glu Asp Gly Ile His Leu Arg Lys Tyr Trp Phe
 145 150 155 160

Ser Val Ser Asp Glu Glu Gln Ile Glu Arg Phe Glu Asp Arg Leu Ser
 165 170 175

Asp Pro Leu Arg Arg Trp Lys Leu Ser Pro Met Asp Leu Gln Ser Ile
 180 185 190

Thr Arg Trp Glu Asp Tyr Ser Arg Ala Lys Asp Glu Met Phe Ile His
 195 200 205

Thr Asp Ile Pro Ser Ala Pro Trp Tyr Thr Val Glu Ser Glu Asp Lys
 210 215 220

Lys Arg Ser Arg Ile Asn Val Ile Ser His Leu Leu Ser Thr Ile Pro
 225 230 235 240

Tyr Glu Lys Ile Asp Arg Pro Leu Pro Glu Ile Pro His Arg Pro Asp

	245		250		255
Ser Glu Ser Asp Tyr Val Arg Pro Pro Arg Asp Glu Phe Arg Tyr Val	260	265	270		
Pro Asp Val Ala Ala His Leu Glu Glu Glu Arg Ile Lys Lys Glu Glu	275	280	285		
Lys Ala Lys Lys Ala Lys Lys Pro Ala Lys Ala Ala Gly Lys Asn Ser	290	295	300		
Asp Lys Gln Lys Ser Ser Gly Gly Lys Gly Lys Lys Ser Lys Lys	305	310	315	320	

<210> 809

<211> 1083

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1060)

<223> FRXA01803

<400> 809

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ttttgttaat ctctgacctg tgaccttgta cgcttaaaac atg cga aag aaa aaa	115
Met Arg Lys Lys Lys	
1 5	

gac ggt caa aat ctc cca gac ttc cgg aaa aat ccg cca aag ctg gat	163
Asp Gly Gln Asn Leu Pro Asp Phe Arg Lys Asn Pro Pro Lys Leu Asp	
10 15 20	

aaa aag gct tat gaa aaa gaa cta aaa aga ctt caa gcc gaa ctc gtc	211
Lys Lys Ala Tyr Glu Lys Glu Leu Lys Arg Leu Gln Ala Glu Leu Val	
25 30 35	

gat ttg caa caa tgg gtt gtg gaa acc ggt gcg cgc gtg gtc atc gtc	259
Asp Leu Gln Gln Trp Val Val Glu Thr Gly Ala Arg Val Val Ile Val	
40 45 50	

atg gaa ggc cgc gac gcc gct ggt aaa ggt tct gcg atc aag cgc att	307
Met Glu Gly Arg Asp Ala Ala Gly Lys Gly Ser Ala Ile Lys Arg Ile	
55 60 65	

acg cag tac ctc aac ccc cgg tcc gca agg atc gaa gcg ctg ccc acc	355
Thr Gln Tyr Leu Asn Pro Arg Ser Ala Arg Ile Glu Ala Leu Pro Thr	
70 75 80 85	

cca aac tct cgg gaa aaa ggg cag tgg tat ttc cag cgc tac atc gaa	403
Pro Asn Ser Arg Glu Lys Gly Gln Trp Tyr Phe Gln Arg Tyr Ile Glu	
90 95 100	

aaa ttg ccg act gct ggt gag atc gtt atc ttt gac cgc tcc tgg tac	451
Lys Leu Pro Thr Ala Gly Glu Ile Val Ile Phe Asp Arg Ser Trp Tyr	

	105	110	115	
aac cgt gca gga gtc gag cgc gtc atg gga ttt tgc acc tcc cag gag				499
Asn Arg Ala Gly Val Glu Arg Val Met Gly Phe Cys Thr Ser Gln Glu				
120		125	130	
tac cgc cga ttc ctt cac cag gca cca atc ttt gaa cgc ctg ttg gtg				547
Tyr Arg Arg Phe Leu His Leu Ala Pro Ile Phe Glu Arg Leu Leu Val				
135	140	145		
gaa gat ggc att cac ctg cgt aaa tac tgg ttc tct gta tct gat gaa				595
Glu Asp Gly Ile His Leu Arg Lys Tyr Trp Phe Ser Val Ser Asp Glu				
150	155	160	165	
gag cag att gag cgt ttc gaa gac cgc ctg agc gat ccg ctg cgc cgg				643
Glu Gln Ile Glu Arg Phe Glu Asp Arg Leu Ser Asp Pro Leu Arg Arg				
170	175	180		
tgg aag ttg tcg cca atg gat tta caa tcg atc acc cgc tgg gaa gat				691
Trp Lys Leu Ser Pro Met Asp Leu Gln Ser Ile Thr Arg Trp Glu Asp				
185	190	195		
tac tca cgc gca aaa gat gag atg ttc atc cac acg gac atc ccg tca				739
Tyr Ser Arg Ala Lys Asp Glu Met Phe Ile His Thr Asp Ile Pro Ser				
200	205	210		
gca ccg tgg tac acg gtg gaa tct gag gac aag aag cgt tcc cgc atc				787
Ala Pro Trp Tyr Thr Val Glu Ser Glu Asp Lys Lys Arg Ser Arg Ile				
215	220	225		
aac gtc att tcg cat ctg ctc tcg acg att cct tat gag aag atc gat				835
Asn Val Ile Ser His Leu Leu Ser Thr Ile Pro Tyr Glu Lys Ile Asp				
230	235	240	245	
cgt cca ttg ccg gaa atc cct cat cgc cca gat tct gaa tct gat tat				883
Arg Pro Leu Pro Glu Ile Pro His Arg Pro Asp Ser Glu Ser Asp Tyr				
250	255	260		
gta cgt ccc cct cgc gat gag ttc cgt tat gtt cca gat gtg gca gca				931
Val Arg Pro Pro Arg Asp Glu Phe Arg Tyr Val Pro Asp Val Ala Ala				
265	270	275		
cac ttg gaa gaa gag cgc atc aag aaa gaa gaa aaa gcc aag aag gca				979
His Leu Glu Glu Glu Arg Ile Lys Lys Glu Glu Lys Ala Lys Lys Ala				
280	285	290		
aag aag cca gct aag gct gca gga aag aac tcg gat aag cag aag tct				1027
Lys Lys Pro Ala Lys Ala Ala Gly Lys Asn Ser Asp Lys Gln Lys Ser				
295	300	305		
tcc gga gga aaa ggc aag aag aag tcc aag aaa tagaacgcct tttaaggggt				1080
Ser Gly Gly Lys Gly Lys Lys Lys Ser Lys Lys				
310	315	320		
tga				1083

<210> 810

<211> 320

<212> PRT

<213> Corynebacterium glutamicum

<400> 810

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Met Arg Lys Lys Lys Asp Gly Gln Asn Leu Pro Asp Phe Arg Lys Asn
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Pro Pro Lys Leu Asp Lys Lys Ala Tyr Glu Lys Glu Leu Lys Arg Leu
      20          25          30

Gln Ala Glu Leu Val Asp Leu Gln Gln Trp Val Val Glu Thr Gly Ala
      35          40          45

Arg Val Val Ile Val Met Glu Gly Arg Asp Ala Ala Gly Lys Gly Ser
      50          55          60

Ala Ile Lys Arg Ile Thr Gln Tyr Leu Asn Pro Arg Ser Ala Arg Ile
      65          70          75          80

Glu Ala Leu Pro Thr Pro Asn Ser Arg Glu Lys Gly Gln Trp Tyr Phe
      85          90          95

Gln Arg Tyr Ile Glu Lys Leu Pro Thr Ala Gly Glu Ile Val Ile Phe
      100          105          110

Asp Arg Ser Trp Tyr Asn Arg Ala Gly Val Glu Arg Val Met Gly Phe
      115          120          125

Cys Thr Ser Gln Glu Tyr Arg Arg Phe Leu His Gln Ala Pro Ile Phe
      130          135          140

Glu Arg Leu Leu Val Glu Asp Gly Ile His Leu Arg Lys Tyr Trp Phe
      145          150          155          160

Ser Val Ser Asp Glu Glu Gln Ile Glu Arg Phe Glu Asp Arg Leu Ser
      165          170          175

Asp Pro Leu Arg Arg Trp Lys Leu Ser Pro Met Asp Leu Gln Ser Ile
      180          185          190

Thr Arg Trp Glu Asp Tyr Ser Arg Ala Lys Asp Glu Met Phe Ile His
      195          200          205

Thr Asp Ile Pro Ser Ala Pro Trp Tyr Thr Val Glu Ser Glu Asp Lys
      210          215          220

Lys Arg Ser Arg Ile Asn Val Ile Ser His Leu Leu Ser Thr Ile Pro
      225          230          235          240

Tyr Glu Lys Ile Asp Arg Pro Leu Pro Glu Ile Pro His Arg Pro Asp
      245          250          255

Ser Glu Ser Asp Tyr Val Arg Pro Pro Arg Asp Glu Phe Arg Tyr Val
      260          265          270

Pro Asp Val Ala Ala His Leu Glu Glu Glu Arg Ile Lys Lys Glu Glu
      275          280          285

Lys Ala Lys Lys Ala Lys Lys Pro Ala Lys Ala Ala Gly Lys Asn Ser
      290          295          300

Asp Lys Gln Lys Ser Ser Gly Gly Lys Gly Lys Lys Lys Ser Lys Lys
      305          310          315          320

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<210> 811
<211> 1299
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1276)
<223> RXN01809

<400> 811
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Met Asn Glu Gln Glu
1 5

cga gaa gcc tta gag gat gct gcc ctt gag gaa gct gcc tta gcc gat 163
Arg Glu Ala Leu Glu Asp Ala Ala Leu Glu Ala Ala Leu Ala Asp
10 15 20

gaa tta gct gca tta gag gct gaa gct ggc gta caa ggg tca gtc gag 211
Glu Leu Ala Ala Leu Glu Ala Glu Ala Gly Val Gln Gly Ser Val Glu
25 30 35

cct tat gac tat gca gca gac ctt gat gat gag gac gag ttt gat gag 259
Pro Tyr Asp Tyr Ala Ala Asp Leu Asp Asp Glu Asp Glu Phe Asp Glu
40 45 50

gac cct ttt gct cag gat gaa ccc cgt gac gct ggt ccg cta ggt gag 307
Asp Pro Phe Ala Gln Asp Glu Pro Arg Asp Ala Gly Pro Leu Gly Glu
55 60 65

ttg agc agt gat aac cat gtc tct gag gct gtt gct gaa gac act ggg 355
Leu Ser Ser Asp Asn His Val Ser Glu Ala Val Ala Glu Asp Thr Gly
70 75 80 85

aca agt aca gaa gag tct gca caa gag ggc agt cac gaa gag tcg gta 403
Thr Ser Thr Glu Glu Ser Ala Gln Glu Gly Ser His Glu Glu Ser Val
90 95 100

gac aat ccc cgt gat ttc acc ggc act gcg aca gcg gtg cga tct ttt 451
Asp Asn Pro Arg Asp Phe Thr Gly Thr Ala Thr Ala Val Arg Ser Phe
105 110 115

cga ccc aga ctt ccc gta ccc aat gca ctg cga cca gga cca ccc atc 499
Arg Pro Arg Leu Pro Val Pro Asn Ala Leu Arg Pro Gly Pro Pro Ile
120 125 130

cga aca caa ccg gca gtg aac acc gac ata gat gat ggc ggg caa gag 547
Arg Thr Gln Pro Ala Val Asn Thr Asp Ile Asp Asp Gly Gly Gln Glu
135 140 145

aat aca gct ggc gcg act gcc gca gat gtg ggg gcg gga gtg ttt ttt 595
Asn Thr Ala Gly Ala Thr Ala Ala Asp Val Gly Ala Gly Val Phe Phe
150 155 160 165

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ggt acg cat ttt gag ctg gct ttt ggg cag gtt gat gtt cac cgc cac	643
Gly Thr His Phe Glu Leu Ala Phe Gly Gln Val Asp Val His Arg His	
170 175 180	
ata agg cat gag cag gct atg cga gat gga cac cag gat ctc agc gtc	691
Ile Arg His Glu Gln Ala Met Arg Asp Gly His Gln Asp Leu Ser Val	
185 190 195	
ttt gtc ggt gct gat ggg gcg atc atg ctg gaa gaa ctt aaa aat cgt	739
Phe Val Gly Ala Asp Gly Ala Ile Met Leu Glu Leu Lys Asn Arg	
200 205 210	
tac cag cgc cca ccg gag aac gag ccc cat gat gat gat gtc acc gaa	787
Tyr Gln Arg Pro Pro Glu Asn Glu Pro His Asp Asp Val Thr Glu	
215 220 225	
atg ata aag acc acc gag gaa aca gag aag gag aac gta gag atg gat	835
Met Ile Lys Thr Thr Glu Glu Thr Glu Lys Glu Asn Val Glu Met Asp	
230 235 240 245	
cag gat ata gct gta gta gac aac gtt gat gaa cag gtt gtg gtg aca	883
Gln Asp Ile Ala Val Val Asp Asn Val Asp Glu Gln Val Val Val Thr	
250 255 260	
cct gct cat gac gct gac agc gta gcg gtt gtt gct gaa cag gtc gtt	931
Pro Ala His Asp Ala Asp Ser Val Ala Val Val Ala Glu Gln Val Val	
265 270 275	
gcg tca gaa cca acg cca gag ccg gta ccc aag gtt gag cac gta gag	979
Ala Ser Glu Pro Thr Pro Glu Pro Val Pro Lys Val Glu His Val Glu	
280 285 290 295	
atg agt gtc gat cta gcg ggt gag act att aca ccg att gat cag gca	1027
Met Ser Val Asp Leu Ala Gly Glu Thr Ile Thr Pro Ile Asp Gln Ala	
295 300 305	
att cgg tct ttt atg cag ctc aac ggt att gag cac agc gtg gtg ttg	1075
Ile Arg Ser Phe Met Gln Leu Asn Gly Ile Glu His Ser Val Val Leu	
310 315 320 325	
cga cgc ttg ggg ctg atg act cag gtg gca cat aat aag gaa ctt gat	1123
Arg Arg Leu Gly Leu Met Thr Gln Val Ala His Asn Lys Glu Leu Asp	
330 335 340	
gag gtc tac gct aag gca ctt gcc gag ggt gaa tcc cat gct cag cag	1171
Glu Val Tyr Ala Lys Ala Leu Ala Glu Gly Glu Ser His Ala Gln Gln	
345 350 355	
cag cat gaa tta gaa gca gaa aat gaa ccg ctt aaa aaa gaa gtt gat	1219
Gln His Glu Leu Glu Ala Glu Asn Glu Arg Leu Lys Lys Glu Val Asp	
360 365 370	
gcg ctc gct gca gag ctt agt gct gcg ttg atg ggc gag ggt ggt ggt	1267
Ala Leu Ala Ala Glu Leu Ser Ala Ala Leu Met Gly Glu Gly Gly Gly	
375 380 385	
gat cat gac taaggccgtg acaccaattg tgg	1299
Asp His Asp	
390	

<210> 812

<211> 392

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 812

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 20 25 30

Gln Gly Ser Val Glu Pro Tyr Asp Tyr Ala Ala Asp Leu Asp Asp Glu
 35 40 45

Asp Glu Phe Asp Glu Asp Pro Phe Ala Gln Asp Glu Pro Arg Asp Ala
 50 55 60

Gly Pro Leu Gly Glu Leu Ser Ser Asp Asn His Val Ser Glu Ala Val
 65 70 75 80

Ala Glu Asp Thr Gly Thr Ser Thr Glu Glu Ser Ala Gln Glu Gly Ser
 85 90 95

His Glu Glu Ser Val Asp Asn Pro Arg Asp Phe Thr Gly Thr Ala Thr
 100 105 110

Ala Val Arg Ser Phe Arg Pro Arg Leu Pro Val Pro Asn Ala Leu Arg
 115 120 125

Pro Gly Pro Pro Ile Arg Thr Gln Pro Ala Val Asn Thr Asp Ile Asp
 130 135 140

Asp Gly Gly Gln Glu Asn Thr Ala Gly Ala Thr Ala Ala Asp Val Gly
 145 150 155 160

Ala Gly Val Phe Phe Gly Thr His Phe Glu Leu Ala Phe Gly Gln Val
 165 170 175

Asp Val His Arg His Ile Arg His Glu Ala Met Arg Asp Gly His
 180 185 190

Gln Asp Leu Ser Val Phe Val Gly Ala Asp Gly Ala Ile Met Leu Glu
 195 200 205

Glu Leu Lys Asn Arg Tyr Gln Arg Pro Pro Glu Asn Glu Pro His Asp
 210 215 220

Asp Asp Val Thr Glu Met Ile Lys Thr Thr Glu Thr Glu Lys Glu
 225 230 235 240

Asn Val Glu Met Asp Gln Asp Ile Ala Val Val Asp Asn Val Asp Glu
 245 250 255

Gln Val Val Val Thr Pro Ala His Asp Ala Asp Ser Val Ala Val Val
 260 265 270

Ala Glu Gln Val Val Ala Ser Glu Pro Thr Pro Glu Pro Val Pro Lys
 275 280 285

Val Glu His Val Glu Met Ser Val Asp Leu Ala Gly Glu Thr Ile Thr
290 295 300

Pro Ile Asp Gln Ala Ile Arg Ser Phe Met Gln Leu Asn Gly Ile Glu
305 310 315 320

His Ser Val Val Leu Arg Arg Leu Gly Leu Met Thr Gln Val Ala His
325 330 335

Asn Lys Glu Leu Asp Glu Val Tyr Ala Lys Ala Leu Ala Glu Gly Glu
340 345 350

Ser His Ala Gln Gln Gln His Glu Leu Glu Ala Glu Asn Glu Arg Leu
355 360 365

Lys Lys Glu Val Asp Ala Leu Ala Ala Glu Leu Ser Ala Ala Leu Met
370 375 380

Gly Glu Gly Gly Asp His Asp
385 390

<210> 813
<211> 586
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(586)
<223> FRXA01062

<400> 813
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Met Asn Glu Gln Glu
1 5
cga gaa gcc tta gag gat gct gcc ctt gag gaa gct gcc tta gcc gat 163
Arg Glu Ala Leu Glu Asp Ala Ala Leu Glu Glu Ala Ala Leu Ala Asp
10 15 20
gaa tta gct gca tta gag gct gaa gct ggc gta caa ggg tca gtc gag 211
Glu Leu Ala Ala Leu Glu Ala Glu Ala Gly Val Gln Gly Ser Val Glu
25 30 35
cct tat gac tat gca gca gac ctt gat gat gag gac gag ttt gat gag 259
Pro Tyr Asp Tyr Ala Ala Asp Leu Asp Asp Glu Asp Glu Phe Asp Glu
40 45 50
gac cct ttt gct cag gat gaa ccc cgt gac gct ggt ccg cta ggt gag 307
Asp Pro Phe Ala Gln Asp Glu Pro Arg Asp Ala Gly Pro Leu Gly Glu
55 60 65
ttg agc agt gat aac cat gtc tct gag gct gtt gct gaa gac act ggg 355
Leu Ser Ser Asp Asn His Val Ser Glu Ala Val Ala Glu Asp Thr Gly
70 75 80 85
aca agt aca gaa gag tct gca caa gag ggc agt cac gaa gag tcg gta 403
Thr Ser Thr Glu Glu Ser Ala Gln Glu Gly Ser His Glu Glu Ser Val

	90	95	100	
gac aat ccc cgt gat ttc acc ggc act gcg aca gcg gtg cga tct ttt				451
Asp Asn Pro Arg Asp Phe Thr Gly Thr Ala Thr Ala Val Arg Ser Phe				
	105	110	115	
cga ccc aga ctt ccc gta ccc aat gca ctg cga cca gga cca ccc atc				499
Arg Pro Arg Leu Pro Val Pro Asn Ala Leu Arg Pro Gly Pro Pro Ile				
	120	125	130	
cga aca caa ccg gca gtg aac acc gac ata tat gat ggc ggg caa gag				547
Arg Thr Gln Pro Ala Val Asn Thr Asp Ile Tyr Asp Gly Gly Gln Glu				
	135	140	145	
aat aca gct ggc gcg act gcc gca gat gtg ggg gcg gga				586
Asn Thr Ala Gly Ala Thr Ala Ala Asp Val Gly Ala Gly				
	150	155	160	

<210> 814

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 814

Met Asn Glu Gln Glu Arg Glu Ala Leu Glu Asp Ala Ala Leu Glu Glu			
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Ala Ala Leu Ala Asp Glu Leu Ala Ala Leu Glu Ala Glu Ala Gly Val			
20	25	30	

Gln Gly Ser Val Glu Pro Tyr Asp Tyr Ala Ala Asp Leu Asp Asp Glu			
35	40	45	

Asp Glu Phe Asp Glu Asp Pro Phe Ala Gln Asp Glu Pro Arg Asp Ala			
50	55	60	

Gly Pro Leu Gly Glu Leu Ser Ser Asp Asn His Val Ser Glu Ala Val			
65	70	75	80

Ala Glu Asp Thr Gly Thr Ser Thr Glu Glu Ser Ala Gln Glu Gly Ser			
85	90	95	

His Glu Glu Ser Val Asp Asn Pro Arg Asp Phe Thr Gly Thr Ala Thr			
100	105	110	

Ala Val Arg Ser Phe Arg Pro Arg Leu Pro Val Pro Asn Ala Leu Arg			
115	120	125	

Pro Gly Pro Pro Ile Arg Thr Gln Pro Ala Val Asn Thr Asp Ile Tyr			
130	135	140	

Asp Gly Gly Gln Glu Asn Thr Ala Gly Ala Thr Ala Ala Asp Val Gly			
145	150	155	160

Ala Gly

<210> 815

<211> 659

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(636)

<223> FRXA01809

<400> 815

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His	Ile	Arg	His	Glu	Gln	Ala	Met	Arg	Asp	Gly	His	Gln	Asp	Leu	Ser	
1				5					10					15		

gtc	ttt	gtc	ggg	gct	gat	ggg	gcg	atc	atg	ctg	gaa	gaa	ctt	aaa	aat	96
Val	Phe	Val	Gly	Ala	Asp	Gly	Ala	Ile	Met	Leu	Glu	Glu	Leu	Lys	Asn	
			20				25						30			

cgt	tac	cag	cgc	cca	ccg	gag	aac	gag	ccc	cat	gat	gat	gat	gtc	acc	144
Arg	Tyr	Gln	Arg	Pro	Pro	Glu	Asn	Glu	Pro	His	Asp	Asp	Asp	Val	Thr	
		35				40					45					

gaa	atg	ata	aag	acc	acc	gag	gaa	aca	gag	aag	gag	aac	gta	gag	atg	192
Glu	Met	Ile	Lys	Thr	Thr	Glu	Glu	Thr	Glu	Lys	Glu	Asn	Val	Glu	Met	
50						55					60					

gat	cag	gat	ata	gct	gta	gta	gac	aac	gtt	gat	gaa	cag	gtt	gtg	gtg	240
Asp	Gln	Asp	Ile	Ala	Val	Val	Asp	Asn	Val	Asp	Glu	Gln	Val	Val	Val	
65				70					75					80		

aca	cct	gct	cat	gac	gct	gac	agc	gta	gcg	gtt	gtt	gct	gaa	cag	gtc	288
Thr	Pro	Ala	His	Asp	Ala	Asp	Ser	Val	Ala	Ala	Val	Val	Ala	Glu	Gln	
				85				90						95		

gtt	gcg	tca	gaa	cca	acg	cca	gag	ccg	gta	ccc	aag	gtt	gag	cac	gta	336
Val	Ala	Ser	Glu	Pro	Thr	Pro	Glu	Pro	Val	Pro	Lys	Val	Glu	His	Val	
			100				105						110			

gag	atg	agt	gtc	gat	cta	gcg	ggg	gag	act	att	aca	ccg	att	gat	cag	384
Glu	Met	Ser	Val	Asp	Leu	Ala	Gly	Glu	Thr	Ile	Thr	Pro	Ile	Asp	Gln	
		115				120						125				

gca	att	cgg	tct	ttt	atg	cag	ctc	aac	ggg	att	gag	cac	agc	gtg	gtg	432
Ala	Ile	Arg	Ser	Phe	Met	Gln	Leu	Asn	Gly	Ile	Glu	His	Ser	Val	Val	
130						135					140					

ttg	cga	cgc	ttg	ggg	ctg	atg	act	cag	gtg	gca	cat	aat	aag	gaa	ctt	480
Leu	Arg	Arg	Leu	Gly	Leu	Met	Thr	Gln	Val	Ala	His	Asn	Lys	Glu	Leu	
145				150					155					160		

gat	gag	gtc	tac	gct	aag	gca	ctt	gcc	gag	ggg	gaa	tcc	cat	gct	cag	528
Asp	Glu	Val	Tyr	Ala	Lys	Ala	Leu	Ala	Glu	Gly	Glu	Ser	His	Ala	Gln	
			165					170						175		

cag	cag	cat	gaa	tta	gaa	gca	gaa	aat	gaa	cgg	ctt	aaa	aaa	gaa	gtt	576
Gln	Gln	His	Glu	Leu	Glu	Ala	Glu	Asn	Glu	Arg	Leu	Lys	Lys	Glu	Val	
			180				185						190			

gat	gcg	ctc	gct	gca	gag	ctt	agt	gct	gcg	ttg	atg	ggc	gag	ggg	ggg	624
Asp	Ala	Leu	Ala	Ala	Glu	Leu	Ser	Ala	Ala	Leu	Met	Gly	Glu	Gly	Gly	
		195				200						205				

ggt gat cat gac taaggccgtg acaccaattg tgg
 Gly Asp His Asp
 210

659

<210> 816
 <211> 212
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 816
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 Val Phe Val Gly Ala Asp Gly Ala Ile Met Leu Glu Glu Leu Lys Asn
 20 25 30
 Arg Tyr Gln Arg Pro Pro Glu Asn Glu Pro His Asp Asp Asp Val Thr
 35 40 45
 Glu Met Ile Lys Thr Thr Glu Thr Glu Lys Glu Asn Val Glu Met
 50 55 60
 Asp Gln Asp Ile Ala Val Val Asp Asn Val Asp Glu Gln Val Val Val
 65 70 75 80
 Thr Pro Ala His Asp Ala Asp Ser Val Ala Val Val Ala Glu Gln Val
 85 90 95
 Val Ala Ser Glu Pro Thr Pro Glu Pro Val Pro Lys Val Glu His Val
 100 105 110
 Glu Met Ser Val Asp Leu Ala Gly Glu Thr Ile Thr Pro Ile Asp Gln
 115 120 125
 Ala Ile Arg Ser Phe Met Gln Leu Asn Gly Ile Glu His Ser Val Val
 130 135 140
 Leu Arg Arg Leu Gly Leu Met Thr Gln Val Ala His Asn Lys Glu Leu
 145 150 155 160
 Asp Glu Val Tyr Ala Lys Ala Leu Ala Glu Gly Glu Ser His Ala Gln
 165 170 175
 Gln Gln His Glu Leu Glu Ala Glu Asn Glu Arg Leu Lys Lys Glu Val
 180 185 190
 Asp Ala Leu Ala Ala Glu Leu Ser Ala Ala Leu Met Gly Glu Gly Gly
 195 200 205
 Gly Asp His Asp
 210

<210> 817
 <211> 804
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS

<222> (101)..(781)

<223> RXN01811

<400> 817

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Val Phe Glu Phe Asp
1 5
gat acc ttg gca aaa gat ata caa gta gac cgt acg tcc atg caa gta 163
Asp Thr Leu Ala Lys Asp Ile Gln Val Asp Arg Thr Ser Met Gln Val
10 15 20
ttc gaa gct tca gaa acc gtc aaa gaa gcg ata aaa gct tcg att gaa 211
Phe Glu Ala Ser Glu Thr Val Lys Glu Ala Ile Lys Ala Ser Ile Glu
25 30 35
caa gga cat act cgc tat ccg gtt atc tta gaa tca aaa gac aat gtt 259
Gln Gly His Thr Arg Tyr Pro Val Ile Leu Glu Ser Lys Asp Asn Val
40 45 50
tta ggt tat gtc acc ttg cca gat ttg atc aag caa tct tat aaa gat 307
Leu Gly Tyr Val Thr Leu Pro Asp Leu Ile Lys Ser Tyr Lys Asp
55 60 65
gac cag ctg aca gta gaa cag ttg att gaa gag ccg atc gta aca act 355
Asp Gln Leu Thr Val Glu Gln Leu Ile Glu Glu Pro Ile Val Thr Thr
70 75 80 85
gaa acg atc cct ata aaa aaa tta ttg acg atc atg cga aaa aag gga 403
Glu Thr Ile Pro Ile Lys Lys Leu Leu Thr Thr Ile Met Arg Lys Lys Gly
90 95 100
aag cat att gct atc tta aaa gat gaa tac gga ggg aca agc ggc tta 451
Lys His Ile Ala Ile Leu Lys Asp Glu Tyr Gly Gly Thr Ser Gly Leu
105 110 115
gtg acg att gaa gat att tta gaa gaa atc gtc ggg gaa atc cga gat 499
Val Thr Ile Glu Asp Ile Leu Glu Glu Ile Val Gly Glu Ile Arg Asp
120 125 130
gag aca gat ttg gac gaa gca ttg ata gcg gaa cag tca gat ggc tct 547
Glu Thr Asp Leu Asp Glu Ala Leu Ile Ala Glu Ser Asp Gly Ser
135 140 145
tat atc atc tcc ggc aaa cta aca tta gat gat ttc cag cgt tat ttt 595
Tyr Ile Ile Ser Gly Lys Leu Thr Leu Asp Asp Phe Gln Arg Tyr Phe
150 155 160 165
cat gta gag att cca gag ttt gaa gaa acg aat ttt act aca ctt gcg 643
His Val Glu Ile Pro Glu Phe Glu Glu Thr Asn Phe Thr Thr Leu Ala
170 175 180
ggc ttt gct tct agc cga tat aaa gaa ata aaa gca gga aca atc att 691
Gly Phe Ala Ser Ser Arg Tyr Lys Glu Ile Lys Ala Gly Thr Ile Ile
185 190 195
gag att gca tca ttc cgt ttc acg gta tta gaa tac cag cat gca cat 739
Glu Ile Ala Ser Phe Arg Phe Thr Val Leu Glu Tyr Gln His Ala His
200 205 210

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atc gat tat ttc aaa gta gag tcc acg gaa aga aaa aca gaa 781
 Ile Asp Tyr Phe Lys Val Glu Ser Thr Glu Arg Lys Thr Glu
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taaaagaaaa aaggctgtga cat 804

<210> 818

<211> 227

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 818

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 20 25 30

Lys Ala Ser Ile Glu Gln Gly His Thr Arg Tyr Pro Val Ile Leu Glu
 35 40 45

Ser Lys Asp Asn Val Leu Gly Tyr Val Thr Leu Pro Asp Leu Ile Lys
 50 55 60

Gln Ser Tyr Lys Asp Asp Gln Leu Thr Val Glu Gln Leu Ile Glu Glu
 65 70 75 80

Pro Ile Val Thr Thr Glu Thr Ile Pro Ile Lys Lys Leu Leu Thr Ile
 85 90 95

Met Arg Lys Lys Gly Lys His Ile Ala Ile Leu Lys Asp Glu Tyr Gly
 100 105 110

Gly Thr Ser Gly Leu Val Thr Ile Glu Asp Ile Leu Glu Glu Ile Val
 115 120 125

Gly Glu Ile Arg Asp Glu Thr Asp Leu Asp Glu Ala Leu Ile Ala Glu
 130 135 140

Gln Ser Asp Gly Ser Tyr Ile Ile Ser Gly Lys Leu Thr Leu Asp Asp
 145 150 155 160

Phe Gln Arg Tyr Phe His Val Glu Ile Pro Glu Phe Glu Glu Thr Asn
 165 170 175

Phe Thr Thr Leu Ala Gly Phe Ala Ser Ser Arg Tyr Lys Glu Ile Lys
 180 185 190

Ala Gly Thr Ile Ile Glu Ile Ala Ser Phe Arg Phe Thr Val Leu Glu
 195 200 205

Tyr Gln His Ala His Ile Asp Tyr Phe Lys Val Glu Ser Thr Glu Arg
 210 215 220

Lys Thr Glu
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<210> 819

<211> 789
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> {101}..(766)
 <223> RXN01813

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 Met Val Ala Ile Val
 1 5
 gtc gtt gca atc gtc gtc gtc ggc ttc atc gtc atc caa ggc cag ggc 163
 Val Val Ala Ile Val Val Val Gly Phe Ile Val Ile Gln Gly Gln Gly
 10 15 20
 tca aaa gca gcc aag ctt ggt gac cgc gac tac gaa gac acc tct ttg 211
 Ser Lys Ala Ala Lys Leu Gly Asp Arg Asp Tyr Glu Asp Thr Ser Leu
 25 30 35
 gca atg gaa gta ggc tcc gac tcc atc acg ctg acc tcc gca aac acc 259
 Ala Met Glu Val Gly Ser Asp Ser Ile Thr Leu Thr Ser Ala Asn Thr
 40 45 50
 tcc gcc gac gca aag tcc gtg cag ctt ttt gaa gac ttc tcc tgc tct 307
 Ser Ala Asp Ala Lys Ser Val Gln Leu Phe Glu Asp Phe Ser Cys Ser
 55 60 65
 cac tgc tcc gag ctc tcc ctc gcc acc gac gct gac atg aag act cag 355
 His Cys Ser Glu Leu Ser Leu Ala Thr Asp Ala Asp Met Lys Thr Gln
 70 75 80 85
 atc gaa gac ggc aac ctg gtc gtc gaa atc aag cca ctg aac ttc ctt 403
 Ile Glu Asp Gly Asn Leu Val Val Glu Ile Lys Pro Leu Asn Phe Leu
 90 95 100
 gac cgc gaa aac atc gac ggc cac tcc acc cac gca ttg gca gca gcc 451
 Asp Arg Glu Asn Ile Asp Gly His Ser Thr His Ala Leu Ala Ala Ala
 105 110 115
 ctt gca gtg gca gac tcc aac gac gca acc ctc tac tgg aac ttc cgc 499
 Leu Ala Val Ala Asp Ser Asn Asp Ala Thr Leu Tyr Trp Asn Phe Arg
 120 125 130
 gca ttc ctc atg gaa gat cag tcc gag atc tac aac cag tgg tcc gat 547
 Ala Phe Leu Met Glu Asp Gln Ser Glu Ile Tyr Asn Gln Trp Ser Asp
 135 140 145
 gat gac ttc gca gac ggc gtt gaa gcc ctt ggc gca gac tcc tcc gta 595
 Asp Asp Phe Ala Asp Gly Val Glu Ala Leu Gly Ala Asp Ser Ser Val
 150 155 160 165
 gta gac gca atc cga aac ggc gac aac atc cag cgc gca tac gac ctg 643
 Val Asp Ala Ile Arg Asn Gly Asp Asn Ile Gln Arg Ala Tyr Asp Leu
 170 175 180
 gca acc gca aac ggt gaa gaa ctc act gaa gaa acc ggc agc ctg tcc 691

Ala Thr Ala Asn Gly Glu Glu Leu Thr Glu Glu Thr Gly Ser Leu Ser
 185 190 195

tca cca cgc gtc ctc cag gac ggc aag gat gtt gaa ggc aac atc tcc 739
 Ser Pro Arg Val Leu Gln Asp Gly Lys Asp Val Glu Gly Asn Ile Ser
 200 205 210

gac tgg atc acc act gtt cta gct tct taaagaactg atctagaagg 786
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 215 220

aaa 789

<210> 820

<211> 222

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 820

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Glu Asp Thr Ser Leu Ala Met Glu Val Gly Ser Asp Ser Ile Thr Leu
 35 40 45

Thr Ser Ala Asn Thr Ser Ala Asp Ala Lys Ser Val Gln Leu Phe Glu
 50 55 60

Asp Phe Ser Cys Ser His Cys Ser Glu Leu Ser Leu Ala Thr Asp Ala
 65 70 75 80

Asp Met Lys Thr Gln Ile Glu Asp Gly Asn Leu Val Val Glu Ile Lys
 85 90 95

Pro Leu Asn Phe Leu Asp Arg Glu Asn Ile Asp Gly His Ser Thr His
 100 105 110

Ala Leu Ala Ala Ala Leu Ala Val Ala Asp Ser Asn Asp Ala Thr Leu
 115 120 125

Tyr Trp Asn Phe Arg Ala Phe Leu Met Glu Asp Gln Ser Glu Ile Tyr
 130 135 140

Asn Gln Trp Ser Asp Asp Asp Phe Ala Asp Gly Val Glu Ala Leu Gly
 145 150 155 160

Ala Asp Ser Ser Val Val Asp Ala Ile Arg Asn Gly Asp Asn Ile Gln
 165 170 175

Arg Ala Tyr Asp Leu Ala Thr Ala Asn Gly Glu Glu Leu Thr Glu Glu
 180 185 190

Thr Gly Ser Leu Ser Ser Pro Arg Val Leu Gln Asp Gly Lys Asp Val
 195 200 205

Glu Gly Asn Ile Ser Asp Trp Ile Thr Thr Val Leu Ala Ser
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<222> (101)..(730)
<223> FRXA01813
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gtc gtt gca atc gtc gtc ggc ttc atc gtc atc caa ggc cag ggc	Val Val Ala Ile Val Val Val Gly Phe Ile Val Ile Gln Gly Gln Gly	163
tca aaa gca gcc aag ctt ggt gac cgc gac tac gaa gac acc tct ttg	Ser Lys Ala Ala Lys Leu Gly Asp Arg Asp Tyr Glu Asp Thr Ser Leu	211
gca atg gaa gta ggc tcc gac tcc atc acg ctg acc tcc gca aac acc	Ala Met Glu Val Gly Ser Asp Ser Ile Thr Leu Thr Ser Ala Asn Thr	259
tcc gcc gac gca aag tcc gtg cag ctt ttt gaa gac ttc tcc tgc tct	Ser Ala Asp Ala Lys Ser Val Gln Leu Phe Glu Asp Phe Ser Cys Ser	307
cac tgc tcc gag ctc tcc gcc gcc acc gac gct gac atg aag act cag	His Cys Ser Glu Leu Ser Leu Ala Thr Asp Ala Asp Met Lys Thr Gln	355
atc gaa gac ggc aac ctg gtc gtc gaa atc aag cca ctg aac ttc ctt	Ile Glu Asp Gly Asn Leu Val Val Glu Ile Lys Pro Leu Asn Phe Leu	403
gac cgc gaa aac atc gac ggc cac tcc acc cac gca ttg gca gca gcc	Asp Arg Glu Asn Ile Asp Gly His Ser Thr His Ala Leu Ala Ala Val	451
ctt gca gtg gca gac tcc aac gac gca acc ctc tac tgg aac ttc cgc	Leu Ala Val Ala Asp Ser Asn Asp Ala Thr Leu Tyr Trp Asn Phe Arg	499
gca ttc ctc atg gaa gat cag tcc gag atc tac aac cag tgg tcc gat	Ala Phe Leu Met Glu Asp Gln Ser Glu Ile Tyr Asn Gln Trp Ser Asp	547
gat gac ttc gca gac ggc gtt gaa gcc ctt ggc gca gac tcc gta	Asp Asp Phe Ala Asp Gly Val Glu Ala Leu Gly Ala Asp Ser Ser Val	595
gta gac gca atc cga acg gcg aca aca tcc agc gcg cat acg acc tgg	Val Asp Asp Ala Ile Arg Thr Ala Thr Ser Thr Ser Thr Ser Thr Trp	643

	170	175	180	
caa ccg caa acg gtg aag aac tca ctg aag aaa ccg gca gcc tgt tct				691
Gln Pro Gln Thr Val Lys Asn Ser Leu Lys Lys Pro Ala Ala Cys Ser				
	185	190	195	
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Tyr His Ala Phe Phe Lys Thr Ala Arg Met Leu Lys Ala				
	200	205	210	
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<212> PRT				
<213> <i>Corynebacterium glutamicum</i>				
 <400> 822				
Met Val Ala Ile Val Val Val Ala Ile Val Val Val Gly Phe Ile Val				
	1	5	10	15
Ile Gln Gly Gln Gly Ser Lys Ala Ala Lys Leu Gly Asp Arg Asp Tyr				
	20	25	30	
Glu Asp Thr Ser Leu Ala Met Glu Val Gly Ser Asp Ser Ile Thr Leu				
	35	40	45	
Thr Ser Ala Asn Thr Ser Ala Asp Ala Lys Ser Val Gln Leu Phe Glu				
	50	55	60	
Asp Phe Ser Cys Ser His Cys Ser Glu Leu Ser Leu Ala Thr Asp Ala				
	65	70	75	80
Asp Met Lys Thr Gln Ile Glu Asp Gly Asn Leu Val Val Glu Ile Lys				
	85	90	95	
Pro Leu Asn Phe Leu Asp Arg Glu Asn Ile Asp Gly His Ser Thr His				
	100	105	110	
Ala Leu Ala Ala Ala Leu Ala Val Ala Asp Ser Asn Asp Ala Thr Leu				
	115	120	125	
Tyr Trp Asn Phe Arg Ala Phe Leu Met Glu Asp Gln Ser Glu Ile Tyr				
	130	135	140	
Asn Gln Trp Ser Asp Asp Asp Phe Ala Asp Gly Val Glu Ala Leu Gly				
	145	150	155	160
Ala Asp Ser Ser Val Val Asp Ala Ile Arg Thr Ala Thr Thr Ser Ser				
	165	170	175	
Ala His Thr Thr Trp Gln Pro Gln Thr Val Lys Asn Ser Leu Lys Lys				
	180	185	190	
Pro Ala Ala Cys Ser Tyr His Ala Phe Phe Lys Thr Ala Arg Met Leu				
	195	200	205	
Lys Ala				
	210			

<210> 823

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<211> 915
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(892)  
<223> RXN01815
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4400> 823																																			
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ttctgctgtt	tttctcgggg	tgccggtcta	gaattgtaga	atg	aat	cgt	tca	aca								115																			
				Met	Asn	Arg	Ser	Thr																											
				1																															
att tcc cca gtt gaa gcc cgc cag caa ttc cgc gca ggc ctt atc caa																163																			
Ile Ser Pro Val Glu Ala Arg Gln Gln Phe																																			
				10											20																				
ccc acc tcc ggc tgg tcc gcg ggt ttt gcc caa gcc aac ctc att tcc																211																			
Pro Thr Ser Gly Trp Ser Ala Gly Phe																																			
				25											35																				
atg ccc cag gat ctg gct tat gat ttc ctg ctt ttt gct caa cgc aac																259																			
Met Pro Gln Asp Leu Ala Tyr Asp Phe Leu Leu Phe																																			
				40											50																				
ccc aag ccc tgc ccc atc ttg gaa gta tta aat gct ggc gaa acc ttc																307																			
Pro Lys Pro Cys Pro Ile Leu Glu Val Leu Asn																																			
				55											65																				
ggc gga att ttc ggc tca aac gcc acc gaa gca gac atc cgc acc gac																355																			
Gly Gly Ile Phe Gly Ser Asn Ala Thr Glu Ala Asp Ile Arg Thr Asp																																			
				70											85																				
gcg ccc caa tac cgc att tac gca cac gcc gaa ctt atc gat tcc ccc																403																			
Ala Pro Gln Gly Arg Ile Tyr Ala His Gly Glu Leu Ile Asp Ser Pro																																			
				90											100																				
gcc agc gcc gtc gat tat tgg cgc gac gac ctc gtc agt ttc atc atc																451																			
Ala Ser Ala Val Asp Tyr Trp Arg Asp Asp Leu Val Ser Phe Ile Ile																																			
				105																															

```

Ser Arg Tyr Pro Ala Val His Gly Ala Pro Val His Ile Gly Asp Pro
      185                      190                      195

tca ctg atc gga atc gat gac atc aac aac cct gat ttc gcc gat gcc 739
Ser Leu Ile Gly His Asp Asp Ile Asn Asn Pro Asp Phe Gly Asp Ala
      200                      205                      210

ccg ctg tcc gaa cca agc gac gtc ccc gtg ttt tgg gcc tgc gga gtt 787
Pro Leu Ser Glu Pro Ser Asp Val Pro Val Phe Trp Ala Cys Gly Val
      215                      220                      225

acc cct caa gca atg gtc atg tcc tcc aag cca ccg ctg gcg atc act 835
Thr Pro Gln Ala Met Val Met Ser Ser Lys Pro Pro Leu Ala Ile Thr
      230                      235                      240                      245

cac gca ccc gga cac atg ctg atc acc gac gcc cca gat ctg gga ttc 883
His Ala Pro Gly His Met Leu Ile Thr Asp Ala Pro Asp Leu Gly Phe
      250                      255                      260

cag gtt cct taaacctgga tccaccgatg tga 915
Gln Val Pro

```

<210> 824

<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 824

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Met Asn Arg Ser Thr Ile Ser Pro Val Glu Ala Arg Gln Gln Phe Arg
  1              5              10              15

```

```

Ala Gly Leu Ile Gln Pro Thr Ser Gly Trp Ser Ala Gly Phe Ala Gln
      20              25              30

```

```

Ala Asn Leu Ile Ser Met Pro Gln Asp Leu Ala Tyr Asp Phe Leu Leu
      35              40              45

```

```

Phe Ala Gln Arg Asn Pro Lys Pro Cys Pro Ile Leu Glu Val Leu Asn
      50              55              60

```

```

Ala Gly Glu Thr Phe Gly Gly Ile Phe Gly Ser Asn Ala Thr Glu Ala
      65              70              75              80

```

```

Asp Ile Arg Thr Asp Ala Pro Gln Tyr Arg Ile Tyr Ala His Gly Glu
      85              90              95

```

```

Leu Ile Asp Ser Pro Ala Ser Ala Val Asp Tyr Trp Arg Asp Asp Leu
      100              105              110

```

```

Val Ser Phe Ile Ile Gly Cys Ser Phe Thr Phe Glu His Pro Met Val
      115              120              125

```

```

Gln Ala Gly Val Pro Val Arg His Leu Glu Ala Gly Arg Asn Val Pro
      130              135              140

```

```

Met Tyr Glu Thr Ser Leu Ala Cys Arg Pro Ala Gly Ser Leu Ser Gly
      145              150              155              160

```

```

Asn Leu Val Val Ser Leu Arg Met Ile Pro Ala Ser Gln Val Ala Asp

```


165 170 175
 Ala Val Arg Ile Thr Ser Arg Tyr Pro Ala Val His Gly Ala Pro Val
 180 185 190
 His Ile Gly Asp Pro Ser Leu Ile Gly Ile Asp Asp Ile Asn Asn Pro
 195 200 205
 Asp Phe Gly Asp Ala Pro Leu Ser Glu Pro Ser Asp Val Pro Val Phe
 210 215 220
 Trp Ala Cys Gly Val Thr Pro Gln Ala Met Val Met Ser Ser Lys Pro
 225 230 235 240
 Pro Leu Ala Ile Thr His Ala Pro Gly His Met Leu Ile Thr Asp Ala
 245 250 255
 Pro Asp Leu Gly Phe Gln Val Pro
 260

<210> 825
 <211> 915
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(892)
 <223> FRXA01815

<400> 825
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 ttctgctgtt ttctcggga tgcggctcta gaattgtaga atg aat cgt tca aca 115
 Met Asn Arg Ser Thr
 1 5
 att tcc cca gtt gaa gcc cgc cag caa ttc cgc gca ggc ctt atc caa 163
 Ile Ser Pro Val Glu Ala Arg Gln Gln Phe Arg Ala Gly Leu Ile Gln
 10 15 20
 ccc acc tcc ggc tgg tcc gcg ggt ttt gcc caa gcc aac ctc att tcc 211
 Pro Thr Ser Gly Trp Ser Ala Gly Phe Ala Gln Ala Asn Leu Ile Ser
 25 30 35
 atg ccc cag gat ctg gct tat gat ttc ctg ctt ttt gct caa cgc aac 259
 Met Pro Gln Asp Leu Ala Tyr Asp Phe Leu Leu Phe Ala Gln Arg Asn
 40 45 50
 ccc aag ccc tgc ccc atc ttg gaa gta tta aat gct ggc gaa acc ttc 307
 Pro Lys Pro Cys Pro Ile Leu Glu Val Leu Asn Ala Gly Glu Thr Phe
 55 60 65
 ggc gga att ttc ggc tca aac gcc acc gaa gca gac atc cgc acc gac 355
 Gly Gly Ile Phe Gly Ser Asn Ala Thr Glu Ala Asp Ile Arg Thr Asp
 70 75 80 85
 ggc ccc caa tac cgc att tac gca cac ggc gaa ctt atc gat tcc ccc 403
 Ala Pro Gln Tyr Arg Ile Tyr Ala His Gly Glu Leu Ile Asp Ser Pro
 90 95 100

gcc agc gcc gtc gat tat tgg cgc gac gac ctc gtc agt ttc atc atc 451
 Ala Ser Ala Val Asp Tyr Trp Arg Asp Asp Leu Val Ser Phe Ile Ile
 105 110 115

ggc tgc tcc ttt act ttt gaa cat ccc atg gtc caa gca ggc gtt ccc 499
 Gly Cys Ser Phe Thr Phe Glu His Pro Met Val Gln Ala Gly Val Pro
 120 125 130

gtc cgc cac ctc gag gcc ggc cgc aac gtc ccc atg tat gaa acc tca 547
 Val Arg His Leu Glu Ala Gly Arg Asn Val Pro Met Tyr Glu Thr Ser
 135 140 145

ctt gcc tgc cga cca gcc ggt tcc cta tca gga aac ctc gtg gtg tca 595
 Leu Ala Cys Arg Pro Ala Gly Ser Leu Ser Gly Asn Leu Val Val Ser
 150 155 160 165

ctg cgc atg atc ccc gca tcc caa gtc gcg gat gcc gtc cgc att acc 643
 Leu Arg Met Ile Pro Ala Ser Gln Val Ala Asp Ala Val Arg Ile Thr
 170 175 180

tcc cgc tac ccc gcg gtt cac gga gca cca gtc cac atc ggc gat cct 691
 Ser Arg Tyr Pro Ala Val His Gly Ala Pro Val His Ile Gly Asp Pro
 185 190 195

tca ctg atc gga atc gat gac atc aac aac cct gat ttc ggc gat gcc 739
 Ser Leu Ile Gly Ile Asp Asp Ile Asn Asn Pro Asp Phe Gly Asp Ala
 200 205 210

ccg ctg tcc gaa cca agc gac gtc ccc gtg ttt tgg gcc tgc gga gtt 787
 Pro Leu Ser Glu Pro Ser Asp Val Pro Val Phe Trp Ala Cys Gly Val
 215 220 225

acc cct caa gca atg gtc atg tcc tcc aag cca ccg ctg gcg atc act 835
 Thr Pro Gln Ala Met Val Met Ser Ser Lys Pro Pro Leu Ala Ile Thr
 230 235 240 245

cac gca ccc gga cac atg ctg atc acc gac gcc cca gat ctg gga ttc 883
 His Ala Pro Gly His Met Leu Ile Thr Asp Ala Pro Asp Leu Gly Phe
 250 255 260

cag gtt cct taaacctgga tccaccgatg tga 915
 Gln Val Pro

<210> 826

<211> 264

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 826

Met Asn Arg Ser Thr Ile Ser Pro Val Glu Ala Arg Gln Gln Phe Arg
 1 5 10 15

Ala Gly Leu Ile Gln Pro Thr Ser Gly Trp Ser Ala Gly Phe Ala Gln
 20 25 30

Ala Asn Leu Ile Ser Met Pro Gln Asp Leu Ala Tyr Asp Phe Leu Leu
 35 40 45

```

Phe Ala Gln Arg Asn Pro Lys Pro Cys Pro Ile Leu Glu Val Leu Asn
 50                      55                      60

Ala Gly Glu Thr Phe Gly Gly Ile Phe Gly Ser Asn Ala Thr Glu Ala
 65                      70                      75                      80

Asp Ile Arg Thr Asp Ala Pro Gln Tyr Arg Ile Tyr Ala His Gly Glu
 85                      90                      95

Leu Ile Asp Ser Pro Ala Ser Ala Val Asp Tyr Trp Arg Asp Asp Leu
100                      105                      110

Val Ser Phe Ile Ile Gly Cys Ser Phe Thr Phe Glu His Pro Met Val
115                      120                      125

Gln Ala Gly Val Pro Val Arg His Leu Glu Ala Gly Arg Asn Val Pro
130                      135                      140

Met Tyr Glu Thr Ser Leu Ala Cys Arg Pro Ala Gly Ser Leu Ser Gly
145                      150                      155                      160

Asn Leu Val Val Ser Leu Arg Met Ile Pro Ala Ser Gln Val Ala Asp
165                      170                      175

Ala Val Arg Ile Thr Ser Arg Tyr Pro Ala Val His Gly Ala Pro Val
180                      185                      190

His Ile Gly Asp Pro Ser Leu Ile Gly Ile Asp Asp Ile Asn Asn Pro
195                      200                      205

Asp Phe Gly Asp Ala Pro Leu Ser Glu Pro Ser Asp Val Pro Val Phe
210                      215                      220

Trp Ala Cys Gly Val Thr Pro Gln Ala Met Val Met Ser Ser Lys Pro
225                      230                      235                      240

Pro Leu Ala Ile Thr His Ala Pro Gly His Met Leu Ile Thr Asp Ala
245                      250                      255

Pro Asp Leu Gly Phe Gln Val Pro
260

<210> 827
<211> 393
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(370)
<223> RXN01825

<400> 827
gtcaaggtag ctggcccggc aactgatacg ttaagctcaa acaagataag taccagttgc 60
tggggttttt ccaagacaat aaattatgaa ggtgtgaaca atg cca aag gca aga 115
Met Pro Lys Ala Arg
1 5

gta act aaa aac gag acc gca ccg gtt tca agc aac cca agc gca aac 163

```

```

Val Thr Lys Asn Glu Thr Ala Pro Val Ser Ser Asn Pro Ser Ala Asn
      10                      15                      20

cgc acc ccg gtt aag atc aat tcc gcc gga acc cca atg tgg tac aag 211
Arg Thr Pro Val Lys Ile Asn Ser Ala Gly Thr Pro Met Trp Tyr Lys
      25                      30                      35

gtc atc atg ttt gcc ttc atg atc gtc gcc cta gcc tgg ttg atc att 259
Val Ile Met Phe Ala Phe Met Ile Val Gly Leu Ala Trp Leu Ile Ile
      40                      45                      50

aac tac ctc gtg gcc cca cag atc cca ttc atg gct gat ctt ggt gca 307
Asn Tyr Leu Val Gly Pro Gln Ile Pro Phe Met Ala Asp Leu Gly Ala
      55                      60                      65

tgg aac tat gcc atc gcc ttc ggt ctg atg atc atc gcc cta ctc atg 355
Trp Asn Tyr Gly Ile Gly Phe Gly Leu Met Ile Ile Gly Leu Leu Met
      70                      75                      80                      85

acc atg ggt tgg cgt taatccttca aaaaagtgc tgc 393
Thr Met Gly Trp Arg
      90

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<210> 828

<211> 90

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 828

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Met Pro Lys Ala Arg Val Thr Lys Asn Glu Thr Ala Pro Val Ser Ser
  1                      5                      10                      15

Asn Pro Ser Ala Asn Arg Thr Pro Val Lys Ile Asn Ser Ala Gly Thr
      20                      25                      30

Pro Met Trp Tyr Lys Val Ile Met Phe Ala Phe Met Ile Val Gly Leu
      35                      40                      45

Ala Trp Leu Ile Ile Asn Tyr Leu Val Gly Pro Gln Ile Pro Phe Met
      50                      55                      60

Ala Asp Leu Gly Ala Trp Asn Tyr Gly Ile Gly Phe Gly Leu Met Ile
      65                      70                      75                      80

Ile Gly Leu Leu Met Thr Met Gly Trp Arg
      85                      90

```

<210> 829

<211> 393

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}..(370)

<223> FRXA01825

<400> 829

gtcaaggtag ctggccggc aactgatacg ttaagctcaa acaagataag taccagttgc 60

tgggggtttt ccaagacaat aaattatgaa ggtgtgaaca atg cca aag gca aga 115
Met Pro Lys Ala Arg
1 5

gta act aaa aac gag acc gca ccg gtt tca agc aac cca agc gca aac 163
Val Thr Lys Asn Glu Thr Ala Pro Val Ser Ser Asn Pro Ser Ala Asn
10 15 20

cgc acc ccg gtt aag atc aat tcc gcc gga acc cca atg tgg tac aag 211
Arg Thr Pro Val Lys Ile Asn Ser Ala Gly Thr Pro Met Trp Tyr Lys
25 30 35

gtc atc atg ttt gcc ttc atg atc gtc gcc cta gcc tgg ttg atc att 259
Val Ile Met Phe Ala Phe Met Ile Val Gly Leu Ala Trp Leu Ile Ile
40 45 50

aac tac ctc gtg gcc cca cag atc cca ttc atg gct gat ctt ggt gca 307
Asn Tyr Leu Val Gly Pro Gln Ile Pro Phe Met Ala Asp Leu Gly Ala
55 60 65

tgg aac tat gcc atc gcc ttc ggt ctg atg atc atc gcc cta ctc atg 355
Trp Asn Tyr Gly Ile Gly Phe Gly Leu Met Ile Ile Gly Leu Leu Met
70 75 80 85

acc atg ggt tgg cgt taatccttca aaaaagtgc tgc 393
Thr Met Gly Trp Arg
90

<210> 830

<211> 90

<212> PRT

<213> Corynebacterium glutamicum

<400> 830

Met Pro Lys Ala Arg Val Thr Lys Asn Glu Thr Ala Pro Val Ser Ser
1 5 10 15

Asn Pro Ser Ala Asn Arg Thr Pro Val Lys Ile Asn Ser Ala Gly Thr
20 25 30

Pro Met Trp Tyr Lys Val Ile Met Phe Ala Phe Met Ile Val Gly Leu
35 40 45

Ala Trp Leu Ile Ile Asn Tyr Leu Val Gly Pro Gln Ile Pro Phe Met
50 55 60

Ala Asp Leu Gly Ala Trp Asn Tyr Gly Ile Gly Phe Gly Leu Met Ile
65 70 75 80

Ile Gly Leu Leu Met Thr Met Gly Trp Arg
85 90

<210> 831

<211> 585

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS
 <222> (101)..(562)
 <223> RXN01831

<400> 831
 cctgtggata attggttggtt ggctgatggt gatgtcatta cgggtgggtca ttccaatatc 60
 gaagttcgta ttgttagtcc cttagaggag aggttgatca atg gat tct ctg gtc 115
 Met Asp Ser Leu Val
 1 5
 ctt ctt ggg ctt cgc atc gct ttg ctt gtg gtg ttg tgg ttt ttc gtc 163
 Leu Leu Gly Leu Arg Ile Ala Leu Leu Val Val Leu Trp Phe Phe Val
 10 15 20
 ttg atg gcg ctg cgc gct atg agg gca gat ttg aaa gtg acg ggt caa 211
 Leu Met Ala Thr Arg Ala Met Arg Ala Asp Leu Lys Val Thr Gly Gln
 25 30 35
 gcg tgc aca agc agc tcc tcc gtc gcg gca ccg cag gcc ctt gcc cgg 259
 Ala Ser Thr Ser Ser Ser Ser Val Ala Ala Pro Gln Gly Leu Ala Arg
 40 45 50
 gct ttt aat cgc tcc agc ccg cct cgt ctt ttg acg gtg gtc gag ggc 307
 Ala Phe Asn Arg Ser Ser Pro Pro Arg Leu Leu Thr Val Val Glu Gly
 55 60 65
 ccg ttg gcg ggc tcc tgc att gag gtg tgc gag gat atg acg atg gcc 355
 Pro Leu Ala Gly Ser Ser Ile Glu Val Ser Glu Asp Met Thr Met Gly
 70 75 80 85
 cgt agc cct gag tgc acg ttt gtg gtg gcc gat gat tac gcc tcc gcc 403
 Arg Ser Pro Glu Cys Thr Phe Val Val Gly Asp Asp Tyr Ala Ser Gly
 90 95 100
 atg cat gcg ccg gtg ttt aag cgt ggt tgc gag tgg ttt gtg gag gat 451
 Met His Ala Arg Val Phe Lys Arg Gly Ser Glu Trp Phe Val Glu Asp
 105 110 115
 ctg gat tgc cgc aac gcc act ttt gtc ggt ggt acg cgc att gat cag 499
 Leu Asp Ser Arg Asn Gly Thr Phe Val Gly Gly Thr Arg Ile Asp Gln
 120 125 130
 cct gag cag att gcg gtg gcc acg gat atc cgt att ggt cgt aca gca 547
 Pro Glu Gln Ile Ala Val Gly Thr Asp Ile Arg Ile Gly Arg Thr Ala
 135 140 145
 gtg agg ctt gtt ccc tgaatgtgaa acttaaatat gcg 585
 Val Arg Leu Val Pro
 150

<210> 832
 <211> 154
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 832
 Met Asp Ser Leu Val Leu Leu Gly Leu Arg Ile Ala Leu Leu Val Val
 1 5 10 15

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Leu Trp Phe Phe Val Leu Met Ala Leu Arg Ala Met Arg Ala Asp Leu
      20                      25                      30
Lys Val Thr Gly Gln Ala Ser Thr Ser Ser Ser Ser Val Ala Ala Pro
      35                      40                      45
Gln Gly Leu Ala Arg Ala Phe Asn Arg Ser Ser Pro Pro Arg Leu Leu
      50                      55                      60
Thr Val Val Glu Gly Pro Leu Ala Gly Ser Ser Ile Glu Val Ser Glu
      65                      70                      75
Asp Met Thr Met Gly Arg Ser Pro Glu Cys Thr Phe Val Val Gly Asp
      85                      90                      95
Asp Tyr Ala Ser Gly Met His Ala Arg Val Phe Lys Arg Gly Ser Glu
      100                     105                     110
Trp Phe Val Glu Asp Leu Asp Ser Arg Asn Gly Thr Phe Val Gly Gly
      115                     120                     125
Thr Arg Ile Asp Gln Pro Glu Gln Ile Ala Val Gly Thr Asp Ile Arg
      130                     135                     140
Ile Gly Arg Thr Ala Val Arg Leu Val Pro
      145                     150

```

<210> 833

<211> 585

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(562)

<223> FRXA01831

<400> 833

cctgtggata attggttgtt ggctgatggt gatgtcatta cgggtgggtca ttccaatattc 60

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gaagttcgtat ttgttagtcc cttagaggag aggttgatca atg gat tct ctg gtc 115
              Met Asp Ser Leu Val
              1                      5

```

```

ctt ctt ggg ctt cgc atc gct ttg ctt gtg gtg ttg tgg ttt ttc gtc 163
Leu Leu Gly Leu Arg Ile Ala Leu Leu Val Val Leu Trp Phe Phe Val
              10                      15                      20

```

```

ttg atg gcg ctg cgc gct atg agg gca gat ttg aaa gtg acg ggt caa 211
Leu Met Ala Leu Arg Ala Met Arg Ala Asp Leu Lys Val Thr Gly Gln
              25                      30                      35

```

```

gcg tcg aca agc agc tcc tcc gtc gcg gca cgg cag ggc ctt gcc cgg 259
Ala Ser Thr Ser Ser Ser Ser Val Ala Ala Pro Gln Gly Leu Ala Arg
              40                      45                      50

```

```

gct ttt aat cgc tcc agc ccg cct cgt ctt ttg acg gtg gtc gag ggc 307
Ala Phe Asn Arg Ser Ser Pro Pro Arg Leu Leu Thr Val Val Glu Gly
              55                      60                      65

```

ccg ttg gcg ggc tcc tgc att gag gtg tgc gag gat atg acg atg ggc 355
 Pro Leu Ala Gly Ser Ser Ile Glu Val Ser Glu Asp Met Thr Met Gly
 70 75 80 85

cgt agc cct gag tgc acg ttt gtg gtg ggc gat gat tac gcc tcc ggc 403
 Arg Ser Pro Glu Cys Thr Phe Val Val Gly Asp Asp Tyr Ala Ser Gly
 90 95 100

atg cat gcg cgg gtg ttt aag cgt ggt tgc gag tgg ttt gtg gag gat 451
 Met His Ala Arg Val Phe Lys Arg Gly Ser Glu Trp Phe Val Glu Asp
 105 110 115

ctg gat tgc cgc aac ggc act ttt gtc ggt ggt acg cgc att gat cag 499
 Leu Asp Ser Arg Asn Gly Thr Phe Val Gly Gly Thr Arg Ile Asp Gln
 120 125 130

cct gag cag att gcg gtg ggc acg gat atc cgt att ggt cgt aca gca 547
 Pro Glu Gln Ile Ala Val Gly Thr Asp Ile Arg Ile Gly Arg Thr Ala
 135 140 145

gtg agg ctt gtt ccc tgatgttgaa acttaaatat gcg 585
 Val Arg Leu Val Pro
 150

<210> 834

<211> 154

<212> PRT

<213> Corynebacterium glutamicum

<400> 834

Met Asp Ser Leu Val Leu Leu Gly Leu Arg Ile Ala Leu Leu Val Val
 1 5 10 15

Leu Trp Phe Phe Val Leu Met Ala Leu Arg Ala Met Arg Ala Asp Leu
 20 25 30

Lys Val Thr Gly Gln Ala Ser Thr Ser Ser Ser Ser Val Ala Ala Pro
 35 40 45

Gln Gly Leu Ala Arg Ala Phe Asn Arg Ser Ser Pro Pro Arg Leu Leu
 50 55 60

Thr Val Val Glu Gly Pro Leu Ala Gly Ser Ser Ile Glu Val Ser Glu
 65 70 75 80

Asp Met Thr Met Gly Arg Ser Pro Glu Cys Thr Phe Val Val Gly Asp
 85 90 95

Asp Tyr Ala Ser Gly Met His Ala Arg Val Phe Lys Arg Gly Ser Glu
 100 105 110

Trp Phe Val Glu Asp Leu Asp Ser Arg Asn Gly Thr Phe Val Gly Gly
 115 120 125

Thr Arg Ile Asp Gln Pro Glu Gln Ile Ala Val Gly Thr Asp Ile Arg
 130 135 140

Ile Gly Arg Thr Ala Val Arg Leu Val Pro
 145 150

<210> 835
 <211> 825
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(802)
 <223> RXN01834

<400> 835
 actaagaacg tgagcttggt ttcataatac cccccagggt attgttagcc aggtgattct 60
 agcccttctt ggccgcctaa taataggcct acttcttggc atg ctc ggt ggt ggc 115
 Met Leu Gly Gly Gly
 1 5
 ggt gcc atc ctt gcc att cgg ctg ctt att tat tat tct ttt agc 163
 Gly Ala Ile Leu Ala Ile Pro Leu Leu Ile Tyr Gly Phe Ser Phe Ser
 10 15 20
 gcc acg caa gct act gca gct tca tta atc atc atc gga ctt ggc gcc 211
 Ala Thr Gln Ala Thr Ala Ala Ser Leu Ile Ile Ile Gly Leu Gly Ala
 25 30 35
 ctc att gga ctg atc agc caa tac gct gcc ggg cac gtc cgc ctt aaa 259
 Leu Ile Gly Leu Ile Ser Gln Tyr Ala Ala Gly His Val Arg Leu Lys
 40 45 50
 gag ggt cta agc ttt ggc ctt tta ggg ttg gtc ggc tca ttt gtg ggc 307
 Glu Gly Leu Ser Phe Gly Leu Leu Gly Leu Val Gly Ser Phe Val Gly
 55 60 65
 agt cac ctt gct agc aat atc ccc gat tcc cta ctc ctg agc ggc ttt 355
 Ser His Leu Ala Ser Asn Ile Pro Asp Ser Leu Leu Leu Ser Gly Phe
 70 75 80 85
 gcc atc ctc acg ctc gtg gtg gcg ttg acc atg att tct aaa tta aga 403
 Ala Ile Leu Thr Leu Val Val Ala Leu Thr Met Ile Ser Lys Leu Arg
 90 95 100
 agc acc cga gaa tac ata acc aga agg cca agc atc ctt gcc att gct 451
 Ser Thr Arg Glu Tyr Ile Thr Arg Arg Pro Ser Ile Leu Ala Ile Ala
 105 110 115
 ctt agt gcc acc ggc gtg gga ttt ttg acg gga ttt ttt ggt gtg ggt 499
 Leu Ser Ala Thr Gly Val Gly Phe Leu Thr Gly Phe Gly Val Gly
 120 125 130
 ggc ggt ttt gcc att gtg cca gcc ttg att ttt gcg ctc ggt ttt tcc 547
 Gly Gly Phe Ala Ile Val Pro Ala Leu Ile Phe Ala Leu Gly Phe Ser
 135 140 145
 atg cgg cag gct agc gcc act tcc cta gtg gtg atc gcc gtt aac agc 595
 Met Arg Gln Ala Ser Ala Thr Ser Leu Val Val Ile Ala Val Asn Ser
 150 155 160 165
 gct att gcc atg gga ttt aga tat tcc gat ttg gca agt att gac tgg 643
 Ala Ile Ala Met Gly Phe Arg Tyr Ser Asp Leu Ala Ser Ile Asp Trp
 170 175 180

tca gtg atc tcg cca att atc atc acc acc gta ttg ggc gct ttt agt 691
 Ser Val Ile Ser Pro Ile Ile Ile Thr Thr Val Leu Gly Ala Phe Ser
 185 190 195

ggc gta aaa cta gcc aaa aag gtc aaa gca tca tca ctg caa cta ggt 739
 Gly Val Lys Leu Ala Lys Lys Val Lys Ala Ser Ser Leu Gln Leu Gly
 200 205 210

ttt gct ggc ttc ttg atc ttc att tcg atc tat atg gga ttt cag aat 787
 Phe Ala Gly Phe Leu Ile Phe Ile Ser Ile Tyr Met Gly Phe Gln Asn
 215 220 225

ttc ccg gac ctt ttt taaaacttca aaatataccc ccc 825
 Phe Pro Asp Leu Phe
 230

<210> 836

<211> 234

<212> PRT

<213> Corynebacterium glutamicum

<400> 836

Met Leu Gly Gly Gly Gly Ala Ile Leu Ala Ile Pro Leu Leu Ile Tyr
 1 5 10 15

Gly Phe Ser Phe Ser Ala Thr Gln Ala Thr Ala Ala Ser Leu Ile Ile
 20 25 30

Ile Gly Leu Gly Ala Leu Ile Gly Leu Ile Ser Gln Tyr Ala Ala Gly
 35 40 45

His Val Arg Leu Lys Glu Gly Leu Ser Phe Gly Leu Leu Gly Leu Val
 50 55 60

Gly Ser Phe Val Gly Ser His Leu Ala Ser Asn Ile Pro Asp Ser Leu
 65 70 75 80

Leu Leu Ser Gly Phe Ala Ile Leu Thr Leu Val Val Ala Leu Thr Met
 85 90 95

Ile Ser Lys Leu Arg Ser Thr Arg Glu Tyr Ile Thr Arg Arg Pro Ser
 100 105 110

Ile Leu Ala Ile Ala Leu Ser Ala Thr Gly Val Gly Phe Leu Thr Gly
 115 120 125

Phe Phe Gly Val Gly Gly Gly Phe Ala Ile Val Pro Ala Leu Ile Phe
 130 135 140

Ala Leu Gly Phe Ser Met Arg Gln Ala Ser Ala Thr Ser Leu Val Val
 145 150 155 160

Ile Ala Val Asn Ser Ala Ile Ala Met Gly Phe Arg Tyr Ser Asp Leu
 165 170 175

Ala Ser Ile Asp Trp Ser Val Ile Ser Pro Ile Ile Ile Thr Thr Val
 180 185 190

Leu Gly Ala Phe Ser Gly Val Lys Leu Ala Lys Lys Val Lys Ala Ser

195 200 205

Ser Leu Gln Leu Gly Phe Ala Gly Phe Leu Ile Phe Ile Ser Ile Tyr
210 215 220

Met Gly Phe Gln Asn Phe Pro Asp Leu Phe
225 230

<210> 837
<211> 825
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(802)
<223> FRXA01834

<400> 837
actaagaacg tgagcttggt ttcataatac cccccagggt attgttagcc aggtgattct 60

agcccttctt ggcgcctaa taataggcct acttcttgcc atg ctc ggt ggt ggc 115
Met Leu Gly Gly Gly 5
1

ggt gcc atc ctt gcc att ccg ctg ctt att tat gga ttt tct ttt agc 163
Gly Ala Ile Leu Ala Ile Pro Leu Leu Ile Tyr Gly Phe Ser Phe Ser 20
10 15

gcc acg caa gct act gca gct tca tta atc atc atc gga ctt ggc gcc 211
Ala Thr Gln Ala Thr Ala Ala Ser Leu Ile Ile Ile Gly Leu Gly Ala 35
25 30

ctc att gga ctg atc agc caa tac gct gcc ggg cac gtc cgc ctt aaa 259
Leu Ile Gly Leu Ile Ser Gln Tyr Ala Ala Gly His Val Arg Leu Lys 50
40 45

gag ggt cta agc ttt ggc ctt tta ggg ttg gtc ggc tca ttt gtg ggc 307
Glu Gly Leu Ser Phe Gly Leu Leu Gly Leu Val Gly Ser Phe Val Gly 65
55 60

agt cac ctt gct agc aat atc ccc gat tcc cta ctc ctg agc ggc ttt 355
Ser His Leu Ala Ser Asn Ile Pro Asp Ser Leu Leu Ser Gly Phe 85
70 75 80

gcc atc ctc acg ctc gtg gtg gcg ttg acc atg att tct aaa tta aga 403
Ala Ile Leu Thr Leu Val Val Ala Leu Thr Met Ile Ser Lys Leu Arg 100
90 95

agc acc cga gaa tac ata acc aga agg cca agc atc ctt gcc att gct 451
Ser Thr Arg Glu Tyr Ile Thr Arg Arg Pro Ser Ile Leu Ala Ile Ala 115
105 110

ctt agt gcc acc ggc gtg gga ttt ttg acg gga ttt ttt ggt gtg ggt 499
Leu Ser Ala Thr Gly Val Gly Phe Leu Thr Gly Phe Phe Gly Val Gly 130
120 125

ggc ggt ttt gcc att gtg cca gcc ttg att ttt ggc ctc ggt ttt tcc 547
Gly Gly Phe Ala Ile Val Pro Ala Leu Ile Phe Ala Leu Gly Phe Ser 145
135 140

atg cgg cag gct agc gcc act tcc cta gtg gtg atc gcc gtt aac agc 595
 Met Arg Gln Ala Ser Ala Thr Ser Leu Val Val Ile Ala Val Asn Ser
 150 155 160 165

gct att gcc atg gga ttt aga tat tcc gat ttg gca agt att gac tgg 643
 Ala Ile Ala Met Gly Phe Arg Tyr Ser Asp Leu Ala Ser Ile Asp Trp
 170 175 180

tca gtg atc tcg cca att atc atc acc acc gta ttg ggc gct ttt agt 691
 Ser Val Ile Ser Pro Ile Ile Ile Thr Thr Val Leu Gly Ala Phe Ser
 185 190 195

ggc gta aaa cta gcc aaa aag gtc aaa gca tca tca ctg caa cta ggt 739
 Gly Val Lys Leu Ala Lys Lys Val Lys Ala Ser Ser Leu Gln Leu Gly
 200 205 210

ttt gct ggc ttc ttg atc ttc att tcg atc tat atg gga ttt cag aat 787
 Phe Ala Gly Phe Leu Ile Phe Ile Ser Ile Tyr Met Leu Gly Phe Gln Asn
 215 220 225

ttc ccg gac ctt ttt taaaaacttca aaatataccc ccc 825
 Phe Pro Asp Leu Phe
 230

<210> 838
 <211> 234
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 838
 Met Leu Gly Gly Gly Gly Ala Ile Leu Ala Ile Pro Leu Leu Ile Tyr
 1 5 10 15
 Gly Phe Ser Phe Ser Ala Thr Gln Ala Thr Ala Ala Ser Leu Ile Ile
 20 25 30
 Ile Gly Leu Gly Ala Leu Ile Gly Leu Ile Ser Gln Tyr Ala Ala Gly
 35 40 45
 His Val Arg Leu Lys Glu Gly Leu Ser Phe Gly Leu Leu Gly Leu Val
 50 55 60
 Gly Ser Phe Val Gly Ser His Leu Ala Ser Asn Ile Pro Asp Ser Leu
 65 70 75
 Leu Leu Ser Gly Phe Ala Ile Leu Thr Leu Val Val Ala Leu Thr Met
 85 90 95
 Ile Ser Lys Leu Arg Ser Thr Arg Glu Tyr Ile Thr Arg Arg Pro Ser
 100 105 110
 Ile Leu Ala Ile Ala Leu Ser Ala Thr Gly Val Gly Phe Leu Thr Gly
 115 120 125
 Phe Phe Gly Val Gly Gly Gly Phe Ala Ile Val Pro Ala Leu Ile Phe
 130 135 140
 Ala Leu Gly Phe Ser Met Arg Gln Ala Ser Ala Thr Ser Leu Val Val
 145 150 155 160

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Ile Ala Val Asn Ser Ala Ile Ala Met Gly Phe Arg Tyr Ser Asp Leu
      165                      170                      175

Ala Ser Ile Asp Trp Ser Val Ile Ser Pro Ile Ile Ile Thr Thr Val
      180                      185                      190

Leu Gly Ala Phe Ser Gly Val Lys Leu Ala Lys Lys Val Lys Ala Ser
      195                      200                      205

Ser Leu Gln Leu Gly Phe Ala Gly Phe Leu Ile Phe Ile Ser Ile Tyr
      210                      215                      220

Met Gly Phe Gln Asn Phe Pro Asp Leu Phe
      225                      230

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<210> 839
<211> 382
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(382)
<223> RXN01846

<400> 839
gtatttagga attgaaaccc actaaaaaac agactaagtt actaggtgat aacaaaagtt 60

gtttattact tatgggaata gtgtggaaag taggggtgaat atg tca att cct gga 115
Met Ser Ile Pro Gly
1 5

aat gtt agt tat gtt gca cag ggt ggc acc ggt tgg gat ggt gct gat 163
Asn Val Ser Tyr Val Ala Gln Gly Gly Thr Gly Trp Asp Gly Ala Asp
10 15 20

cag tac acc acg ggt gag agt tgg gat cta cag tcg ttc ctt gaa aac 211
Gln Tyr Thr Thr Gly Glu Ser Trp Asp Leu Gln Ser Phe Leu Glu Asn
25 30 35

tcg act gac tac ctc atg att att ggt ggt tcg ctg ctg gca ctt gtt 259
Ser Thr Asp Tyr Leu Met Ile Ile Gly Gly Ser Leu Ala Leu Val
40 45 50

ggg ggt gct gct gtg att tgg ggc ttt gtc aac gtg atg cgc aag ctc 307
Gly Gly Ala Ala Val Ile Trp Gly Phe Val Asn Val Met Arg Lys Leu
55 60 65

ttc ggt ggt cag agt ggt cag cag att cag tgg ttc acc act att ttg 355
Phe Gly Gly Gln Ser Gly Gln Gln Ile Gln Trp Phe Thr Thr Ile Leu
70 75 80 85

ctc atc att gtc ggt ggt ggc ttg cct 382
Leu Ile Ile Val Gly Gly Ala Leu Pro
90

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<210> 840
<211> 94

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<212> PRT

<213> Corynebacterium glutamicum

<400> 840

Met	Ser	Ile	Pro	Gly	Asn	Val	Ser	Tyr	Val	Ala	Gln	Gly	Gly	Thr	Gly
1				5					10					15	

Trp	Asp	Gly	Ala	Asp	Gln	Tyr	Thr	Thr	Gly	Glu	Ser	Trp	Asp	Leu	Gln
			20					25					30		

Ser	Phe	Leu	Glu	Asn	Ser	Thr	Asp	Tyr	Leu	Met	Ile	Ile	Gly	Gly	Ser
		35					40					45			

Leu	Leu	Ala	Leu	Val	Gly	Gly	Ala	Ala	Val	Ile	Trp	Gly	Phe	Val	Asn
	50					55					60				

Val	Met	Arg	Lys	Leu	Phe	Gly	Gly	Gln	Ser	Gly	Gln	Gln	Ile	Gln	Trp
	65				70					75					80

Phe	Thr	Thr	Ile	Leu	Leu	Ile	Ile	Val	Gly	Gly	Ala	Leu	Pro
				85						90			

<210> 841

<211> 358

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(358)

<223> FRXA01846

<400> 841

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				Met	Ser	Ile	Pro	Gly	
				1				5	

aat	gtt	agt	tat	gtt	gca	cag	ggt	ggc	acc	ggt	tgg	gat	ggt	gct	gat	163
Asn	Val	Ser	Tyr	Val	Ala	Gln	Gly	Gly	Thr	Gly	Trp	Asp	Gly	Ala	Asp	
				10				15					20			

cag	tac	acc	acg	ggt	gag	agt	tgg	gat	cta	cag	tcg	ttc	ctt	gaa	aac	211
Gln	Tyr	Thr	Thr	Gly	Glu	Ser	Trp	Asp	Leu	Gln	Ser	Phe	Leu	Glu	Asn	
			25				30					35				

tcg	act	gac	tac	ctc	atg	att	att	ggt	ggt	tcg	ctg	ctg	gca	ctt	gtt	259
Ser	Thr	Asp	Tyr	Leu	Met	Ile	Ile	Gly	Gly	Ser	Leu	Leu	Ala	Leu	Val	
		40				45					50					

ggt	ggt	gct	gct	gtg	att	tgg	ggc	ttt	gtc	aac	gtg	atg	cgc	aag	ctc	307
Gly	Gly	Ala	Ala	Val	Ile	Trp	Gly	Phe	Val	Asn	Val	Met	Arg	Lys	Leu	
		55				60					65					

ttc	ggt	ggt	cag	agt	ggt	cag	cag	att	cag	tgg	ttc	acc	act	att	ttg	355
Phe	Gly	Gly	Gln	Ser	Gly	Gln	Gln	Ile	Gln	Trp	Phe	Thr	Thr	Ile	Leu	
		70			75					80					85	

ctc

358

Leu

<210> 842

<211> 86

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 842

Met Ser Ile Pro Gly Asn Val Ser Tyr Val Ala Gln Gly Gly Thr Gly
1 5 10 15Trp Asp Gly Ala Asp Gln Tyr Thr Thr Gly Glu Ser Trp Asp Leu Gln
20 25 30Ser Phe Leu Glu Asn Ser Thr Asp Tyr Leu Met Ile Ile Gly Gly Ser
35 40 45Leu Leu Ala Leu Val Gly Gly Ala Ala Val Ile Trp Gly Phe Val Asn
50 55 60Val Met Arg Lys Leu Phe Gly Gly Gln Ser Gly Gln Gln Ile Gln Trp
65 70 75 80Phe Thr Thr Ile Leu Leu
85

<210> 843

<211> 858

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(835)

<223> RXN01847

<400> 843

gacgtgtgat cataggtgac aaatataccc tctcaacttg gcttcgactg ccctgcccc 60

tcgatttaag aggcaaggct tttacagtat cctctcatgc atg ctt att gtg ttg 115
Met Leu Ile Val Leu
1 5cct ccc tca gaa act aag acc cac ggc ggt tca gga aaa cct ctg gat 163
Pro Pro Ser Glu Thr Lys Thr His Gly Gly Ser Gly Lys Pro Leu Asp
10 15 20ttt cac cat ttg agt ttc ccg tcg etc acc aag gca cgc caa aca ata 211
Phe His His Leu Ser Phe Pro Ser Leu Thr Lys Ala Arg Gln Thr Ile
25 30 35ctc gct gac ctg caa gct ttg gag gta gat gag gcg ctg aaa gtt ttg 259
Leu Ala Asp Leu Gln Ala Leu Glu Val Asp Glu Ala Leu Lys Val Leu
40 45 50ggc att tct gaa aag ctc cgc cct gag gcc gaa tcc aat cgc gcg ctg 307
Gly Ile Ser Glu Lys Leu Arg Pro Glu Ala Glu Ser Asn Arg Ala Leu
55 60 65

gag acc agc cct acg atg cct gcg att ttt cgg tat tcc gga gtg ctt 355
 Glu Thr Ser Pro Thr Met Pro Ala Ile Phe Arg Tyr Ser Gly Val Leu
 70 75 80 85
 tat gat gcg ctc gac gct gca acg ctg ccg gag aaa gca ctg gaa cgc 403
 Tyr Asp Ala Leu Asp Ala Ala Thr Leu Pro Glu Lys Ala Leu Glu Arg
 90 95 100
 ctc gcc atc ggc tgc gca ctt ttc ggc gtc atc cac gcc acc gat ccg 451
 Leu Ala Ile Gly Ser Ala Leu Phe Gly Val Ile His Ala Thr Asp Pro
 105 110 115
 atc ccg cat tac cgc ctg tcc ggc ggc aca aaa ctg ccc acc aaa agc 499
 Ile Pro His Tyr Arg Leu Ser Gly Gly Thr Lys Leu Pro Thr Lys Ser
 120 125 130
 ggc gag ctg ccc acc atg aag gcg cgt tgg ggc aca agc atc agc gaa 547
 Gly Glu Leu Pro Thr Met Lys Ala Arg Trp Gly Thr Ser Ile Ser Glu
 135 140 145
 gcg ctt atc gac gtc aac cag ctg gtg att gat ctt cgc agc ggg acc 595
 Ala Leu Ile Asp Val Asn Gln Leu Val Ile Asp Leu Arg Ser Gly Thr
 150 155 160 165
 tac caa cag ttg ggt cgc gta aaa gac gcc gtc acg gta cgc gtg gaa 643
 Tyr Gln Gln Leu Gly Arg Val Lys Asp Ala Val Thr Val Arg Val Glu
 170 175 180
 tca gtc atg gag gat ggc tcc cgc aaa gta gtc agc cac ttt aac aaa 691
 Ser Val Met Glu Asp Gly Ser Arg Lys Val Val Ser His Phe Asn Lys
 185 190 195
 cac tac aaa ggt gaa ctc gcc cgc gtg ctc gcg ctc tct gaa aaa gaa 739
 His Tyr Lys Gly Glu Leu Ala Arg Val Leu Ala Leu Ser Glu Lys Glu
 200 205 210
 gca cac acc gca gag gac gta atg agc att gcg cag gct gcg gcc ctt 787
 Ala His Thr Ala Glu Asp Val Met Ser Ile Ala Gln Ala Ala Gly Leu
 215 220 225
 gtg gtg gag gaa aac ccc aac cac aag gaa acc ctc act ctg gtt gtc 835
 Val Val Glu Glu Asn Pro Asn His Lys Glu Thr Leu Thr Leu Val Val
 230 235 240 245
 taggcgttaa tcaccatttt gat 858

<210> 844

<211> 245

<212> PRT

<213> Corynebacterium glutamicum

<400> 844

Met Leu Ile Val Leu Pro Pro Ser Glu Thr Lys Thr His Gly Gly Ser
 1 5 10 15

Gly Lys Pro Leu Asp Phe His His Leu Ser Phe Pro Ser Leu Thr Lys
 20 25 30

Ala Arg Gln Thr Ile Leu Ala Asp Leu Gln Ala Leu Glu Val Asp Glu


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      35              40              45
Ala Leu Lys Val Leu Gly Ile Ser Glu Lys Leu Arg Pro Glu Ala Glu
  50              55              60
Ser Asn Arg Ala Leu Glu Thr Ser Pro Thr Met Pro Ala Ile Phe Arg
  65              70              75              80
Tyr Ser Gly Val Leu Tyr Asp Ala Leu Asp Ala Ala Thr Leu Pro Glu
      85              90              95
Lys Ala Leu Glu Arg Leu Ala Ile Gly Ser Ala Leu Phe Gly Val Ile
  100              105              110
His Ala Thr Asp Pro Ile Pro His Tyr Arg Leu Ser Gly Gly Thr Lys
  115              120              125
Leu Pro Thr Lys Ser Gly Glu Leu Pro Thr Met Lys Ala Arg Trp Gly
  130              135              140
Thr Ser Ile Ser Glu Ala Leu Ile Asp Val Asn Gln Leu Val Ile Asp
  145              150              155              160
Leu Arg Ser Gly Thr Tyr Gln Gln Leu Gly Arg Val Lys Asp Ala Val
      165              170              175
Thr Val Arg Val Glu Ser Val Met Glu Asp Gly Ser Arg Lys Val Val
      180              185              190
Ser His Phe Asn Lys His Tyr Lys Gly Glu Leu Ala Arg Val Leu Ala
  195              200              205
Leu Ser Glu Lys Glu Ala His Thr Ala Glu Asp Val Met Ser Ile Ala
  210              215              220
Gln Ala Ala Gly Leu Val Val Glu Glu Asn Pro Asn His Lys Glu Thr
  225              230              235              240
Leu Thr Leu Val Val
      245

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<210> 845

<211> 809

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (52)..(786)

<223> FRXA01847

<400> 845

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gccctgcccc ctcgatttaa gaggcaaggc ttttacagta tcctctcatg catg ctt 57
                               Met Leu
                               1

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att gtg ttg cct ccc tca gaa act aag acc cac ggc ggt tca gga aaa 105
Ile Val Leu Pro Pro Ser Glu Thr Lys Thr His Gly Gly Ser Gly Lys
      5              10              15

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cct ctg gat ttt cac cat ttg agt ttc cgg tcg ctc acc aag gca cgc 153
 Pro Leu Asp Phe His His Leu Ser Phe Pro Ser Leu Thr Lys Ala Arg
 20 25 30

caa aca ata ctc gct gac ctg caa gct ttg gag gta gat gag gcg ctg 201
 Gln Thr Ile Leu Ala Asp Leu Gln Ala Leu Glu Val Asp Glu Ala Leu
 35 40 45 50

aaa gtt ttg ggc att tct gaa aag ctc cgc cct gag gcc gaa tcc aat 249
 Lys Val Leu Gly Ile Ser Glu Lys Leu Arg Pro Glu Ala Glu Ser Asn
 55 60 65

cgc gcg ctg gag acc agc cct acg atg cct gcg att ttt cgg tat tcc 297
 Arg Ala Leu Glu Thr Ser Pro Thr Met Pro Ala Ile Phe Arg Tyr Ser
 70 75 80

gga gtg ctt tat gat gcg ctc gac gct gca acg ctg ccg gag aaa gca 345
 Gly Val Leu Tyr Asp Ala Leu Asp Ala Ala Thr Leu Pro Glu Lys Ala
 85 90 95

ctg gaa cgc ctc gcc atc ggc tcg gca ctt ttc ggc gtc atc cac gcc 393
 Leu Glu Arg Leu Ala Ile Gly Ser Ala Leu Phe Gly Val Ile His Ala
 100 105 110

acc gat ccg atc ccg cat tac cgc ctg tcc ggc ggc aca aaa ctg ccc 441
 Thr Asp Pro Ile Pro His Tyr Arg Leu Ser Gly Gly Thr Lys Leu Pro
 115 120 125 130

acc aaa agc ggc gag ctg ccc acc atg aag gcg cgt tgg ggc aca agc 489
 Thr Lys Ser Gly Glu Leu Pro Thr Met Lys Ala Arg Trp Gly Thr Ser
 135 140 145

atc agc gaa gcg ctt atc gac gtc aac cag ctg gtg att gat ctt cgc 537
 Ile Ser Glu Ala Leu Ile Asp Val Asn Gln Leu Val Ile Asp Leu Arg
 150 155 160

agc ggg acc tac caa cag ttg ggt cgc gta aaa gac gcc gtc acg gta 585
 Ser Gly Thr Tyr Gln Gln Leu Gly Arg Val Lys Asp Ala Val Thr Val
 165 170 175

cgc gtg gaa tca gtc atg gag gat ggc tcc cgc aaa gta gtc agc cac 633
 Arg Val Glu Ser Val Met Glu Asp Gly Ser Arg Lys Val Val Ser His
 180 185 190

ttt aac aaa cac tac aaa ggt gaa ctc gcc cgc gtg ctc gcg ctc tct 681
 Phe Asn Lys His Tyr Lys Gly Glu Leu Ala Arg Val Leu Ala Leu Ser
 195 200 205 210

gaa aaa gaa gca cac acc gca gag gac gta atg agc att gcg cag gct 729
 Glu Lys Glu Ala His Thr Ala Glu Asp Val Met Ser Ile Ala Gln Ala
 215 220 225

gcg ggc ctt gtg gtg gag gaa aac ccc aac cac aag gaa acc ctc act 777
 Ala Gly Leu Val Val Glu Glu Asn Pro Asn His Lys Glu Thr Leu Thr
 230 235 240

ctg gtt gtc taggcggttaa tcaccatttt gat 809
 Leu Val Val
 245

<210> 846
 <211> 245
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 846
 Met Leu Ile Val Leu Pro Pro Ser Glu Thr Lys Thr His Gly Gly Ser
 1 5 10 15
 Gly Lys Pro Leu Asp Phe His His Leu Ser Phe Pro Ser Leu Thr Lys
 20 25 30
 Ala Arg Gln Thr Ile Leu Ala Asp Leu Gln Ala Leu Glu Val Asp Glu
 35 40 45
 Ala Leu Lys Val Leu Gly Ile Ser Glu Lys Leu Arg Pro Glu Ala Glu
 50 55 60
 Ser Asn Arg Ala Leu Glu Thr Ser Pro Thr Met Pro Ala Ile Phe Arg
 65 70 75 80
 Tyr Ser Gly Val Leu Tyr Asp Ala Leu Asp Ala Ala Thr Leu Pro Glu
 85 90 95
 Lys Ala Leu Glu Arg Leu Ala Ile Gly Ser Ala Leu Phe Gly Val Ile
 100 105 110
 His Ala Thr Asp Pro Ile Pro His Tyr Arg Leu Ser Gly Gly Thr Lys
 115 120 125
 Leu Pro Thr Lys Ser Gly Glu Leu Pro Thr Met Lys Ala Arg Trp Gly
 130 135 140
 Thr Ser Ile Ser Glu Ala Leu Ile Asp Val Asn Gln Leu Val Ile Asp
 145 150 155 160
 Leu Arg Ser Gly Thr Tyr Gln Gln Leu Gly Arg Val Lys Asp Ala Val
 165 170 175
 Thr Val Arg Val Glu Ser Val Met Glu Asp Gly Ser Arg Lys Val Val
 180 185 190
 Ser His Phe Asn Lys His Tyr Lys Gly Glu Leu Ala Arg Val Leu Ala
 195 200 205
 Leu Ser Glu Lys Glu Ala His Thr Ala Glu Asp Val Met Ser Ile Ala
 210 215 220
 Gln Ala Ala Gly Leu Val Val Glu Glu Asn Pro Asn His Lys Glu Thr
 225 230 235 240
 Leu Thr Leu Val Val
 245

<210> 847
 <211> 448
 <212> DNA
 <213> *Corynebacterium glutamicum*
 <220>

<221> CDS

<222> (101)..(448)

<223> RXN01874

<400> 847

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 agttccggag cgcaaaacgc ggtcagcctt tcgcgtcgca gtg atc gcg tat gtt 115
 Val Ile Ala Tyr Val
 1 5

gcc agc gcg tgc tgc ctg ccg ttt ggc gca ttt gcc gga gcg ttg ttg 163
 Ala Ser Ala Cys Cys Leu Pro Phe Gly Ala Phe Ala Gly Ala Leu Leu
 10 15 20

tcc aag gag ctg tcg gga cat ctc cag gaa cga gtc ctt ctc acc cac 211
 Ser Lys Glu Leu Ser Gly His Leu Gln Glu Arg Val Leu Leu Thr His
 25 30 35

acg gtg att aat ttt cta ggt ttc gtg gga ttt gct gcg ctc ggt tcg 259
 Thr Val Ile Asn Phe Leu Gly Phe Val Gly Phe Ala Ala Leu Gly Ser
 40 45 50

ctg tcg gtg ctg ttc gcc gcg att tgg cgc acc aaa att cgc cac aat 307
 Leu Ser Val Leu Phe Ala Ala Ile Trp Arg Thr Lys Ile Arg His Asn
 55 60 65

ttc acc cgg tgg tct gtg ggg atc atg gcg gtg agc ctg ccg atc atc 355
 Phe Thr Pro Trp Ser Val Gly Ile Met Ala Val Ser Leu Pro Ile Ile
 70 75 80 85

gtc acg ggc atc ctg ctc aac aac ggc tat gtc gcc gcc aca ggc ctg 403
 Val Thr Gly Ile Leu Leu Asn Asn Gly Tyr Val Ala Ala Thr Gly Leu
 90 95 100

gcc gcg tac gtg gca gca tgg ttg ctg gcc atg gtg ggg tgg ggg 448
 Ala Ala Tyr Val Ala Ala Trp Leu Leu Ala Met Val Gly Trp Gly
 105 110 115

<210> 848

<211> 116

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 848

Val Ile Ala Tyr Val Ala Ser Ala Cys Cys Leu Pro Phe Gly Ala Phe
 1 5 10 15

Ala Gly Ala Leu Leu Ser Lys Glu Leu Ser Gly His Leu Gln Glu Arg
 20 25 30

Val Leu Leu Thr His Thr Val Ile Asn Phe Leu Gly Phe Val Gly Phe
 35 40 45

Ala Ala Leu Gly Ser Leu Ser Val Leu Phe Ala Ala Ile Trp Arg Thr
 50 55 60

Lys Ile Arg His Asn Phe Thr Pro Trp Ser Val Gly Ile Met Ala Val
 65 70 75 80

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<210> 850
<211> 116
<212> PRT
<213> Corynebacterium glutamicum
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<400> 850

Val Ile Ala Tyr Val Ala Ser Ala Cys Cys Leu Pro Phe Gly Ala Phe
 1 5 10 15

Ala Gly Ala Leu Leu Ser Lys Glu Leu Ser Gly His Leu Gln Glu Arg
 20 25 30

Val Leu Leu Thr His Thr Val Ile Asn Phe Leu Gly Phe Val Gly Phe
 35 40 45

Ala Ala Leu Gly Ser Leu Ser Val Leu Phe Ala Ala Ile Trp Arg Thr
 50 55 60

Lys Ile Arg His Asn Phe Thr Pro Trp Ser Val Gly Ile Met Ala Val
 65 70 75 80

Ser Leu Pro Ile Ile Val Thr Gly Ile Leu Leu Asn Asn Gly Tyr Val
 85 90 95

Ala Ala Gln Ala Trp Pro Arg Thr Trp Gln His Gly Cys Trp Pro Trp
 100 105 110

Trp Gly Gly Gly
 115

<210> 851

<211> 969

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(946)

<223> RXN01875

<400> 851

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ttcagttgtg tactttgaaac acacacgaat ggagcaagaa atg cgt att gca gta 115
 Met Arg Ile Ala Val
 1 5

act gga gca acg gga tct ttg ggt gga cat gtt gtg gat agt ctt cta 163
 Thr Gly Ala Thr Gly Ser Leu Gly Gly His Val Val Asp Ser Leu Leu
 10 15 20

aac aag ggc gtc gca gca tca gac atc gtt gcc att gtt cga aat gaa 211
 Asn Lys Gly Val Ala Ala Ser Asp Ile Val Ala Ile Val Arg Asn Glu
 25 30 35

gaa aag gca gca gac ctc aaa gcc cgt gga atc gct ctt ggt gtg gct 259
 Glu Lys Ala Ala Asp Leu Lys Ala Arg Gly Ile Ala Leu Gly Val Ala
 40 45 50

act ttt gaa gac gaa gcg gca ctg act gca gct ctt gaa ggt gtg gat 307
 Thr Phe Glu Asp Glu Ala Ala Leu Thr Ala Ala Leu Glu Gly Val Asp
 55 60 65

cgc ctt gtg ttt atc tct ggc agc gaa gtg ggg cag cgc gtt gcg cag 355
 Arg Leu Val Phe Ile Ser Gly Ser Glu Val Gly Gln Arg Val Ala Gln

70	75	80	85	
cac acc aat gtc atc aat gcc gct aaa gca gct ggc gtg aca ttc att				403
His Thr Asn Val Ile Asn Ala Ala Lys Ala Ala Gly Val Thr Phe Ile	90	95	100	
gca tac acc agc ttg ctc aac ctt ggt acc tca aag ctt gca ctt gct				451
Ala Tyr Thr Ser Leu Leu Asn Leu Gly Thr Ser Lys Leu Ala Leu Ala	105	110	115	
cca gag cac att gca acg gaa aag ctc ctg gca gaa agc ggc att gac				499
Pro Glu His Ile Ala Thr Glu Lys Leu Leu Ala Glu Ser Gly Ile Asp	120	125	130	
cac gcg ctg ctg cgc aat ggt tgg tac tgg gag aac tac gaa tct tca				547
His Ala Leu Leu Arg Asn Gly Trp Tyr Trp Glu Asn Tyr Glu Ser Ser	135	140	145	
att ggc gca gcg aag gcc acc ggg aag gta ttc ggc gca gct gaa ggc				595
Ile Gly Ala Ala Lys Ala Thr Gly Lys Val Phe Gly Ala Ala Glu Gly	150	155	160	165
gca cgc gtt tcc gca gcc gca cgt aag gac tac gca gag gca gct gct				643
Ala Arg Val Ser Ala Ala Ala Arg Lys Asp Tyr Ala Glu Ala Ala Ala	170	175	180	
gtt gtc atc acc agc gac aac cag gca ggc aag gtc tat gag ctc gca				691
Val Val Ile Thr Ser Asp Asn Gln Ala Gly Lys Val Tyr Glu Leu Ala	185	190	195	
ggc gca cca gct ttg acc tac cca gag atc gca got ggc att ggt gag				739
Gly Ala Pro Ala Leu Thr Tyr Pro Glu Ile Ala Ala Gly Ile Gly Glu	200	205	210	
gtc att ggt tct gag gca gaa tac gtc aac ctc tcc gtg gag gag tac				787
Val Ile Gly Ser Glu Ala Glu Tyr Val Asn Leu Ser Val Glu Glu Tyr	215	220	225	
caa aat gcg ctg gag cag got ggc gtt cca gct gaa ttt gca gca ctt				835
Gln Asn Ala Leu Glu Gln Ala Gly Val Pro Ala Glu Phe Ala Ala Leu	230	235	240	245
ctc gca ggc atg gat ccc atc att gca gag ggc gcg ctg tac tcc gac				883
Leu Ala Gly Met Asp Pro Ile Ile Ala Glu Gly Ala Leu Tyr Ser Asp	250	255	260	
agc acc gac cta cag gat ctc atc gga cgc ccg agc acc tca atc gtt				931
Ser Thr Asp Leu Gln Asp Leu Ile Gly Arg Pro Ser Thr Ser Ile Val	265	270	275	
gag gcc ctg agc tca taacctgcta ctcacctaaa atg				969
Glu Ala Leu Ser Ser	280			

<210> 852

<211> 282

<212> PRT

<213> Corynebacterium glutamicum

<400> 852

Met Arg Ile Ala Val Thr Gly Ala Thr Gly Ser Leu Gly Gly His Val
 1 5 10 15

Val Asp Ser Leu Leu Asn Lys Gly Val Ala Ala Ser Asp Ile Val Ala
 20 25 30

Ile Val Arg Asn Glu Glu Lys Ala Ala Asp Leu Lys Ala Arg Gly Ile
 35 40 45

Ala Leu Gly Val Ala Thr Phe Glu Asp Glu Ala Ala Leu Thr Ala Ala
 50 55 60

Leu Glu Gly Val Asp Arg Leu Val Phe Ile Ser Gly Ser Glu Val Gly
 65 70 75 80

Gln Arg Val Ala Gln His Thr Asn Val Ile Asn Ala Ala Lys Ala Ala
 85 90 95

Gly Val Thr Phe Ile Ala Tyr Thr Ser Leu Leu Asn Leu Gly Thr Ser
 100 105 110

Lys Leu Ala Leu Ala Pro Glu His Ile Ala Thr Glu Lys Leu Leu Ala
 115 120 125

Glu Ser Gly Ile Asp His Ala Leu Leu Arg Asn Gly Trp Tyr Trp Glu
 130 135 140

Asn Tyr Glu Ser Ser Ile Gly Ala Ala Lys Ala Thr Gly Lys Val Phe
 145 150 155 160

Gly Ala Ala Glu Gly Ala Arg Val Ser Ala Ala Ala Arg Lys Asp Tyr
 165 170 175

Ala Glu Ala Ala Ala Val Val Ile Thr Ser Asp Asn Gln Ala Gly Lys
 180 185 190

Val Tyr Glu Leu Ala Gly Ala Pro Ala Leu Thr Tyr Pro Glu Ile Ala
 195 200 205

Ala Gly Ile Gly Glu Val Ile Gly Ser Glu Ala Glu Tyr Val Asn Leu
 210 215 220

Ser Val Glu Glu Tyr Gln Asn Ala Leu Glu Gln Ala Gly Val Pro Ala
 225 230 235 240

Glu Phe Ala Ala Leu Leu Ala Gly Met Asp Pro Ile Ile Ala Glu Gly
 245 250 255

Ala Leu Tyr Ser Asp Ser Thr Asp Leu Gln Asp Leu Ile Gly Arg Pro
 260 265 270

Ser Thr Ser Ile Val Glu Ala Leu Ser Ser
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<210> 853

<211> 921

<212> DNA

<213> Corynebacterium glutamicum

<220>


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<221> CDS
<222> (101)..(898)
<223> FRXA01875

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syaaacwggr gtcartcscg gatctttggg tggacatgtt gtg gat agt ctt cta 115
                                         Val Asp Ser Leu Leu
                                         1                               5

aac aag ggc gtc gca gca tca gac atc gtt gcc att gtt cga aat gaa 163
Asn Lys Gly Val Ala Ala Ser Asp Ile Val Ala Ile Val Arg Asn Glu
                               10                               15                               20

gaa aag gca gca gac ctc aaa gcc cgt gga atc gct ctt ggt gtg gct 211
Glu Lys Ala Ala Asp Leu Lys Ala Arg Gly Ile Ala Leu Gly Val Ala
                               25                               30                               35

act ttt gaa gac gaa gcg gca ctg act gca gct ctt gaa ggt gtg gat 259
Thr Phe Glu Asp Glu Ala Ala Leu Thr Ala Ala Leu Glu Gly Val Asp
                               40                               45                               50

cgc ctt gtg ttt atc tct ggc agc gaa gtg ggg cag cgc gtt gcg cag 307
Arg Leu Val Phe Ile Ser Gly Ser Glu Val Gly Gln Arg Val Ala Gln
                               55                               60                               65

cac acc aat gtc atc aat gcc gct aaa gca gct ggc gtg aca ttc att 355
His Thr Asn Val Ile Asn Ala Ala Lys Ala Ala Gly Val Thr Phe Ile
                               70                               75                               80                               85

gca tac acc agc ttg ctc aac ctt ggt acc tca aag ctt gca ctt gct 403
Ala Tyr Thr Ser Leu Leu Asn Leu Gly Thr Ser Lys Leu Ala Leu Ala
                               90                               95                               100

cca gag cac att gca acg gaa aag ctc ctg gca gaa agc ggc att gac 451
Pro Glu His Ile Ala Thr Glu Lys Leu Leu Ala Glu Ser Gly Ile Asp
                               105                               110                               115

cac gcg ctg ctg cgc aat ggt tgg tac tgg gag aac tac gaa tct tca 499
His Ala Leu Leu Arg Asn Gly Trp Tyr Trp Glu Asn Tyr Glu Ser Ser
                               120                               125                               130

att ggc gca gcg aag gcc acc ggg aag gta ttc ggc gca gct gaa ggc 547
Ile Gly Ala Ala Lys Ala Thr Gly Lys Val Phe Gly Ala Ala Glu Gly
                               135                               140                               145

gca cgc gtt tcc gca gcc gca cgt aag gac tac gca gag gca gct gct 595
Ala Arg Val Ser Ala Ala Ala Arg Lys Asp Tyr Ala Glu Ala Ala Ala
                               150                               155                               160                               165

gtt gtc atc acc agc gac aac cag gca ggc aag gtc tat gag ctc gca 643
Val Val Ile Thr Ser Asp Asn Gln Ala Gly Lys Val Tyr Glu Leu Ala
                               170                               175                               180

ggc gca cca gct ttg acc tac cca gag atc gca gct ggc att ggt gag 691
Gly Ala Pro Ala Leu Thr Tyr Pro Glu Ile Ala Ala Gly Ile Gly Glu
                               185                               190                               195

gtc att ggt tct gag gca gaa tac gtc aac ctc tcc gtg gag gag tac 739
Val Ile Gly Ser Glu Ala Glu Tyr Val Asn Leu Ser Val Glu Glu Tyr

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200	205	210	
caa aat gcg ctg gag cag gct ggc gtt cca gct gaa ttt gca gca ctt			787
Gln Asn Ala Leu Glu Gln Ala Gly Val Pro Ala Glu Phe Ala Ala Leu			
215	220	225	
ctc gca ggc atg gat ccc atc att gca gag ggc gcg ctg tac tcc gac			835
Leu Ala Gly Met Asp Pro Ile Ile Ala Glu Gly Ala Leu Tyr Ser Asp			
230	235	240	245
agc acc gac cta cag gat ctc atc gga cgc ccg agc acc tca atc gtt			883
Ser Thr Asp Leu Gln Asp Leu Ile Gly Arg Pro Ser Thr Ser Ile Val			
250	255	260	
gag gcc ctg agc tca taacctgcta ctcacctaaa atg			921
Glu Ala Leu Ser Ser			
265			

<210> 854

<211> 266

<212> PRT

<213> Corynebacterium glutamicum

<400> 854

Val Asp Ser Leu Leu Asn Lys Gly Val Ala Ala Ser Asp Ile Val Ala		
1	5	10

Ile Val Arg Asn Glu Glu Lys Ala Ala Asp Leu Lys Ala Arg Gly Ile		
20	25	30

Ala Leu Gly Val Ala Thr Phe Glu Asp Glu Ala Ala Leu Thr Ala Ala		
35	40	45

Leu Glu Gly Val Asp Arg Leu Val Phe Ile Ser Gly Ser Glu Val Gly		
50	55	60

Gln Arg Val Ala Gln His Thr Asn Val Ile Asn Ala Ala Lys Ala Ala		
65	70	75

Gly Val Thr Phe Ile Ala Tyr Thr Ser Leu Leu Asn Leu Gly Thr Ser		
85	90	95

Lys Leu Ala Leu Ala Pro Glu His Ile Ala Thr Glu Lys Leu Leu Ala		
100	105	110

Glu Ser Gly Ile Asp His Ala Leu Leu Arg Asn Gly Trp Tyr Trp Glu		
115	120	125

Asn Tyr Glu Ser Ser Ile Gly Ala Ala Lys Ala Thr Gly Lys Val Phe		
130	135	140

Gly Ala Ala Glu Gly Ala Arg Val Ser Ala Ala Ala Arg Lys Asp Tyr		
145	150	155

Ala Glu Ala Ala Ala Val Val Ile Thr Ser Asp Asn Gln Ala Gly Lys		
165	170	175

Val Tyr Glu Leu Ala Gly Ala Pro Ala Leu Thr Tyr Pro Glu Ile Ala		
180	185	190

Ala Gly Ile Gly Glu Val Ile Gly Ser Glu Ala Glu Tyr Val Asn Leu
 195 200 205

Ser Val Glu Glu Tyr Gln Asn Ala Leu Glu Gln Ala Gly Val Pro Ala
 210 215 220

Glu Phe Ala Ala Leu Leu Ala Gly Met Asp Pro Ile Ile Ala Glu Gly
 225 230 235 240

Ala Leu Tyr Ser Asp Ser Thr Asp Leu Gln Asp Leu Ile Gly Arg Pro
 245 250 255

Ser Thr Ser Ile Val Glu Ala Leu Ser Ser
 260 265

<210> 855

<211> 484

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(484)

<223> FRXA02734

<400> 855

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ttcaggtgtg tacttgaaac acacacgaat ggagcaagaa atg cgt att gca gta 115
 Met Arg Ile Ala Val
 1 5

act gga gca acg gga tct ttg ggt gga cat gtt gtg gat agt ctt cta 163
 Thr Gly Ala Thr Gly Ser Leu Gly Gly His Val Val Asp Ser Leu Leu
 10 15 20

aac aag ggc gtc gca gca tca gac atc gtt gcc att gtt cga aat gaa 211
 Asn Lys Gly Val Ala Ala Ser Asp Ile Val Ala Ile Val Arg Asn Glu
 25 30 35

gaa aag gca gca gac ctc aaa gcc cgt gga atc gct ctt ggt gtg gct 259
 Glu Lys Ala Ala Asp Leu Lys Ala Arg Gly Ile Ala Leu Gly Val Ala
 40 45 50

act ttt gaa gac gaa acg gca ctg act gca gct ctt gaa ggt gtg gat 307
 Thr Phe Glu Asp Glu Thr Ala Leu Thr Ala Ala Leu Glu Gly Val Asp
 55 60 65

cgc ctt gtg ttt atc tct ggc agc gaa gtg ggg cag cgc gtt gcg caa 355
 Arg Leu Val Phe Ile Ser Gly Ser Glu Val Gly Gln Arg Val Ala Gln
 70 75 80 85

cac acc aat gtc atc aat gcc gct aaa gca act ggc gtg aca ttc att 403
 His Thr Asn Val Ile Asn Ala Ala Lys Ala Thr Gly Val Thr Phe Ile
 90 95 100

gca tac acc agc ttg ctc aac ctt ggt cct caa agc ttg cac ttg ctc 451
 Ala Tyr Thr Ser Leu Leu Asn Leu Gly Pro Gln Ser Leu His Leu Leu
 105 110 115

cag agc aca ttg caa ccg gaa aag ctc ctg gca 484
 Gln Ser Thr Leu Gln Pro Glu Lys Leu Leu Ala
 120 125

<210> 856
 <211> 128
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 856
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 Val Asp Ser Leu Leu Asn Lys Gly Val Ala Ala Ser Asp Ile Val Ala
 20 25 30
 Ile Val Arg Asn Glu Glu Lys Ala Ala Asp Leu Lys Ala Arg Gly Ile
 35 40 45
 Ala Leu Gly Val Ala Thr Phe Glu Asp Glu Thr Ala Leu Thr Ala Ala
 50 55 60
 Leu Glu Gly Val Asp Arg Leu Val Phe Ile Ser Gly Ser Glu Val Gly
 65 70 75 80
 Gln Arg Val Ala Gln His Thr Asn Val Ile Asn Ala Ala Lys Ala Thr
 85 90 95
 Gly Val Thr Phe Ile Ala Tyr Thr Ser Leu Leu Asn Leu Gly Pro Gln
 100 105 110
 Ser Leu His Leu Leu Gln Ser Thr Leu Gln Pro Glu Lys Leu Leu Ala
 115 120 125

<210> 857
 <211> 1194
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1171)
 <223> RXN01877

<400> 857
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 Val Pro Leu Arg Leu
 1 5
 gct acc ggt ggc gtg ctc gcc acc ttg ctt atc ggc gga gtc acc gct 163
 Ala Thr Gly Gly Val Leu Ala Thr Leu Leu Ile Gly Gly Val Thr Ala
 10 15 20
 gca gct acc aaa aag gac atc att gtt gat gtc aac ggc gag cag atg 211

Ala	Ala	Thr	Lys	Lys	Asp	Ile	Ile	Val	Asp	Val	Asn	Gly	Glu	Gln	Met	
			25					30					35			
tcc	cta	gtg	act	atg	tcc	ggc	act	gtt	gaa	ggg	gtg	ctg	gcg	caa	gct	259
Ser	Leu	Val	Thr	Met	Ser	Gly	Thr	Val	Glu	Gly	Val	Leu	Ala	Gln	Ala	
	40						45				50					
ggg	gtg	gaa	ctt	ggg	gac	cag	gac	att	gtt	tcc	cct	tca	ctg	gat	tca	307
Gly	Val	Glu	Leu	Gly	Asp	Gln	Asp	Ile	Val	Ser	Pro	Ser	Leu	Asp	Ser	
	55					60					65					
tcc	atc	agt	gat	gaa	gac	act	gtg	act	gtt	cgt	act	gcc	aag	cag	gtg	355
Ser	Ile	Ser	Asp	Glu	Asp	Thr	Val	Thr	Val	Arg	Thr	Ala	Lys	Gln	Val	
	70				75					80					85	
gcg	ctc	gtg	gtg	gaa	ggg	caa	atc	caa	aac	gtg	acc	acc	act	gcg	gtt	403
Ala	Leu	Val	Val	Gly	Gln	Ile	Gln	Asn	Val	Thr	Thr	Thr	Thr	Ala	Val	
				90				95						100		
tcc	gtg	gag	gac	ctc	ctg	cag	gaa	gtc	ggg	ggc	att	acc	ggg	gct	gat	451
Ser	Val	Glu	Asp	Leu	Leu	Gln	Glu	Val	Gly	Gly	Ile	Thr	Gly	Ala	Asp	
			105					110					115			
gcg	gtg	gac	gct	gat	ctt	tca	gag	acc	atc	cca	gaa	tct	ggg	ttg	aag	499
Ala	Val	Asp	Ala	Asp	Leu	Ser	Glu	Thr	Ile	Pro	Glu	Ser	Gly	Leu	Lys	
			120				125					130				
gtg	agt	gtt	acc	aag	cgg	aag	att	att	tcc	atc	aat	gat	ggg	ggc	aag	547
Val	Ser	Val	Thr	Lys	Pro	Lys	Ile	Ile	Ser	Ile	Asn	Asp	Gly	Gly	Lys	
	135				140						145					
gtc	act	tac	gtt	tct	tgg	gca	gct	cag	aac	gta	cag	gaa	gcc	cta	gag	595
Val	Thr	Tyr	Val	Ser	Leu	Ala	Ala	Gln	Asn	Val	Gln	Glu	Ala	Leu	Glu	
	150				155					160				165		
ctg	cgg	gat	att	gag	ctg	ggg	gct	cag	gac	cgc	att	aat	gtg	cct	ctg	643
Leu	Arg	Asp	Ile	Glu	Leu	Gly	Ala	Gln	Asp	Arg	Ile	Asn	Val	Pro	Leu	
				170					175					180		
gat	cag	cag	ctg	aag	aac	aac	gct	gcg	atc	cag	atc	gac	cgc	gtt	gac	691
Asp	Gln	Gln	Leu	Lys	Asn	Asn	Ala	Ala	Ile	Gln	Ile	Asp	Arg	Val	Asp	
			185					190					195			
aac	acc	gaa	atc	act	gaa	act	gtg	tct	ttc	gat	gct	gag	cca	acc	tac	739
Asn	Thr	Glu	Ile	Thr	Glu	Thr	Val	Ser	Phe	Asp	Ala	Glu	Pro	Thr	Tyr	
		200					205					210				
gtg	gat	gat	cca	gaa	gct	cca	gct	ggc	gat	gaa	act	gtg	gtc	gaa	gaa	787
Val	Asp	Asp	Pro	Glu	Ala	Pro	Ala	Gly	Asp	Glu	Thr	Val	Val	Glu	Glu	
		215				220					225					
ggc	gct	cct	gga	acc	aag	gaa	gtt	act	cgc	acc	gta	aca	acc	gtt	aat	835
Gly	Ala	Pro	Gly	Thr	Lys	Glu	Val	Thr	Arg	Thr	Val	Thr	Thr	Val	Asn	
	230				235					240				245		
ggg	cag	gaa	gaa	tct	tcc	acg	gtg	atc	aat	gaa	gtt	gaa	atc	acc	gca	883
Gly	Gln	Glu	Glu	Ser	Ser	Thr	Val	Ile	Asn	Glu	Val	Glu	Ile	Thr	Ala	
				250					255					260		
gca	aag	cca	gca	acc	att	agc	cgt	ggc	acc	aaa	act	gtc	gct	gca	aac	931
Ala	Lys	Pro	Ala	Thr	Ile	Ser	Arg	Gly	Thr	Lys	Thr	Val	Ala	Ala	Asn	

265	270	275	
tcc gtg tgg gat cag ctg gca	cag tgt gaa tcc ggc gga aac tgg gca	979	
Ser Val Trp Asp Gln Leu Ala	Gln Cys Glu Ser Gly Gly Asn Trp Ala		
280	285	290	
atc aac aca ggt aat ggc ttc	tcc ggc ggc cta cag ttc cac cca cag	1027	
Ile Asn Thr Gly Asn Gly Phe	Ser Gly Gly Leu Gln Phe His Pro Gln		
295	300	305	
acc tgg ctg gca tac ggt ggt	gga gct ttc tcc ggt gac gct tcc ggt	1075	
Thr Trp Leu Ala Tyr Gly Gly	Gly Ala Phe Ser Gly Asp Ala Ser Gly		
310	315	320	325
gca agc cgt gaa cag caa atc	tcc atc gca gaa aag gtt cag gct gca	1123	
Ala Ser Arg Glu Gln Gln Ile	Ser Ile Ala Glu Lys Val Gln Ala Ala		
330	335	340	
caa ggt tgg gga gca tgg cct	gct tgc acc gca agc ttg ggc atc cga	1171	
Gln Gly Trp Gly Ala Trp Pro	Ala Cys Thr Ala Ser Leu Gly Ile Arg		
345	350	355	
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<210> 858			
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<213> Corynebacterium glutamicum			
<400> 858			
Val Pro Leu Arg Leu Ala Thr	Gly Gly Val Leu Ala Thr Leu Leu Ile		
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20	25	30	
Asn Gly Glu Gln Met Ser Leu	Val Thr Met Ser Gly Thr Val Glu Gly		
35	40	45	
Val Leu Ala Gln Ala Gly Val	Glu Leu Gly Asp Gln Asp Ile Val Ser		
50	55	60	
Pro Ser Leu Asp Ser Ser Ile	Ser Asp Glu Asp Thr Val Thr Val Arg		
65	70	75	80
Thr Ala Lys Gln Val Ala Leu	Val Val Glu Gly Gln Ile Gln Asn Val		
85	90	95	
Thr Thr Thr Ala Val Ser Val	Glu Asp Leu Leu Gln Glu Val Gly Gly		
100	105	110	
Ile Thr Gly Ala Asp Ala Val	Asp Ala Asp Leu Ser Glu Thr Ile Pro		
115	120	125	
Glu Ser Gly Leu Lys Val Ser	Val Thr Lys Pro Lys Ile Ile Ser Ile		
130	135	140	
Asn Asp Gly Gly Lys Val Thr	Tyr Val Ser Leu Ala Ala Gln Asn Val		
145	150	155	160

Gln Glu Ala Leu Glu Leu Arg Asp Ile Glu Leu Gly Ala Gln Asp Arg
 165 170 175
 Ile Asn Val Pro Leu Asp Gln Gln Leu Lys Asn Asn Ala Ala Ile Gln
 180 185 190
 Ile Asp Arg Val Asp Asn Thr Glu Ile Thr Glu Thr Val Ser Phe Asp
 195 200 205
 Ala Glu Pro Thr Tyr Val Asp Asp Pro Glu Ala Pro Ala Gly Asp Glu
 210 215 220
 Thr Val Val Glu Glu Gly Ala Pro Gly Thr Lys Glu Val Thr Arg Thr
 225 230 235 240
 Val Thr Thr Val Asn Gly Gln Glu Glu Ser Ser Thr Val Ile Asn Glu
 245 250 255
 Val Glu Ile Thr Ala Ala Lys Pro Ala Thr Ile Ser Arg Gly Thr Lys
 260 265 270
 Thr Val Ala Ala Asn Ser Val Trp Asp Gln Leu Ala Gln Cys Glu Ser
 275 280 285
 Gly Gly Asn Trp Ala Ile Asn Thr Gly Asn Gly Phe Ser Gly Gly Leu
 290 295 300
 Gln Phe His Pro Gln Thr Trp Leu Ala Tyr Gly Gly Ala Phe Ser
 305 310 315 320
 Gly Asp Ala Ser Gly Ala Ser Arg Glu Gln Gln Ile Ser Ile Ala Glu
 325 330 335
 Lys Val Gln Ala Ala Gln Gly Trp Gly Ala Trp Pro Ala Cys Thr Ala
 340 345 350
 Ser Leu Gly Ile Arg
 355

<210> 859

<211> 1188

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1165)

<223> FRXA01877

<400> 859

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 Leu Arg Leu Ala Thr 5
 1

ggt ggc gtg ctc gcc acc ttg ctt atc ggc gga gtc acc gct gca gct 163
 Gly Gly Val Leu Ala Thr Leu Leu Ile Gly Gly Val Thr Ala Ala Ala 20
 10 15

acc aaa aag gac atc att gtt gat gtc aac ggc gag cag atg tcc cta	211
Thr Lys Lys Asp Ile Ile Val Asp Val Asn Gly Glu Gln Met Ser Leu	
25 30 35	
gtg act atg tcc ggc act gtt gaa ggt gtg ctg gcg caa gct ggt gtg	259
Val Thr Met Ser Gly Thr Val Glu Gly Val Leu Ala Gln Ala Gly Val	
40 45 50	
gaa ctt ggt gac cag gac att gtt tcc cct tca ctg gat tca tcc atc	307
Glu Leu Gly Asp Gln Asp Ile Val Ser Pro Ser Leu Asp Ser Ser Ile	
55 60 65	
agt gat gaa gac act gtg act gtt cgt act gcc aag cag gtg gcg ctc	355
Ser Asp Glu Asp Thr Val Thr Val Arg Thr Ala Lys Gln Val Ala Leu	
70 75 80 85	
gtg gtg gaa ggt caa atc caa aac gtg acc acc act gcg gtt tcc gtg	403
Val Val Glu Gly Gln Ile Gln Asn Val Thr Thr Thr Ala Val Ser Val	
90 95 100	
gag gac ctc ctg cag gaa gtc ggt ggc att acc ggt gct gat gcg gtg	451
Glu Asp Leu Leu Gln Glu Val Gly Gly Ile Thr Gly Ala Asp Ala Val	
105 110 115	
gac gct gat ctt tca gag acc atc cca gaa tct ggt ttg aag gtg agt	499
Asp Ala Asp Leu Ser Glu Thr Ile Pro Glu Ser Gly Leu Lys Val Ser	
120 125 130	
gtt acc aag ccg aag att att tcc atc aat gat ggt ggc aag gtc act	547
Val Thr Lys Pro Lys Ile Ile Ser Ile Asn Asp Gly Gly Lys Val Thr	
135 140 145	
tac gtt tct ttg gca gct cag aac gta cag gaa gcc cta gag ctg cgg	595
Tyr Val Ser Leu Ala Ala Gln Asn Val Gln Glu Ala Leu Glu Leu Arg	
150 155 160 165	
gat att gag ctg ggt gct cag gac cgc att aat gtg cct ctg gat cag	643
Asp Ile Glu Leu Gly Ala Gln Asp Arg Ile Asn Val Pro Leu Asp Gln	
170 175 180	
cag ctg aag aac aac gct gcg atc cag atc gac cgc gtt gac aac acc	691
Gln Leu Lys Asn Asn Ala Ala Ile Gln Ile Asp Arg Val Asp Asn Thr	
185 190 195	
gaa atc act gaa act gtg tct ttc gat gct gag cca acc tac gtg gat	739
Glu Ile Thr Glu Thr Val Ser Phe Asp Ala Glu Pro Thr Tyr Val Asp	
200 205 210	
gat cca gaa gct cca gct ggc gat gaa act gtg gtc gaa gaa ggc gct	787
Asp Pro Glu Ala Pro Ala Gly Asp Glu Thr Val Val Glu Glu Gly Ala	
215 220 225	
cct gga acc aag gaa gtt act cgc acc gta aca acc gtt aat ggt cag	835
Pro Gly Thr Lys Glu Val Thr Arg Thr Val Thr Thr Val Asn Gly Gln	
230 235 240 245	
gaa gaa tct tcc acg gtg atc aat gaa gtt gaa atc acc gca gca aag	883
Glu Glu Ser Ser Thr Val Ile Asn Glu Val Glu Ile Thr Ala Ala Lys	
250 255 260	
cca gca acc att agc cgt ggc acc aaa act gtc gct gca aac tcc gtg	931


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Pro Ala Thr Ile Ser Arg Gly Thr Lys Thr Val Ala Ala Asn Ser Val
265                               275

tgg gat cag ctg gca cag tgt gaa tcc ggc gga aac tgg gca atc aac 979
Trp Asp Gln Leu Ala Gln Cys Glu Ser Gly Gly Asn Trp Ala Ile Asn
280                               290

aca ggt aat ggc ttc tcc ggc ggc cta cag ttc cac cca cag acc tgg 1027
Thr Gly Asn Gly Phe Ser Ser Gly Gly Leu Gln Phe His Pro Gln Thr Trp
295                               305

ctc gca tac ggt ggt gga gct ttc tcc ggt gac gct tcc ggt gca agc 1075
Leu Ala Tyr Gly Gly Gly Ala Phe Ser Ser Gly Asp Ala Ser Gly Ala Ser
310                               325

cgt gaa cag caa atc tcc atc gca gaa aag gtt cag gct gca caa ggt 1123
Arg Glu Gln Gln Ile Ser Ile Ala Glu Lys Val Gln Ala Ala Gln Gly
330                               340

tgg gga gca tgg cct gct tgc acc gca agc ttg ggc atc cga 1165
Trp Gly Ala Trp Pro Ala Cys Thr Ala Ser Leu Gly Ile Arg
345                               355

tagtagaaat ctggcatcca ata 1188

<210> 860
<211> 355
<212> PRT
<213> Corynebacterium glutamicum

<400> 860
Leu Arg Leu Ala Thr Gly Gly Val Leu Ala Thr Leu Leu Ile Gly Gly
1 5 10 15

Val Thr Ala Ala Ala Thr Lys Lys Asp Ile Ile Val Asp Val Asn Gly
20 25 30

Glu Gln Met Ser Leu Val Thr Met Ser Gly Thr Val Glu Gly Val Leu
35 40 45

Ala Gln Ala Gly Val Glu Leu Gly Asp Gln Asp Ile Val Ser Pro Ser
50 55 60

Leu Asp Ser Ser Ile Ser Asp Glu Asp Thr Val Thr Val Arg Thr Ala
65 70 75 80

Lys Gln Val Ala Leu Val Val Glu Gly Gln Ile Gln Asn Val Thr Thr
85 90 95

Thr Ala Val Ser Val Glu Asp Leu Leu Gln Glu Val Gly Gly Ile Thr
100 105 110

Gly Ala Asp Ala Val Asp Ala Asp Leu Ser Glu Thr Ile Pro Glu Ser
115 120 125

Gly Leu Lys Val Ser Val Thr Lys Pro Lys Ile Ile Ser Ile Asn Asp
130 135 140

Gly Gly Lys Val Thr Tyr Val Ser Leu Ala Ala Gln Asn Val Gln Glu
145 150 155 160

```

$$4\pi\epsilon_0\epsilon_{\infty} \frac{e^2}{m^*} \frac{1}{\omega^2 - \omega_p^2} = \frac{4\pi\epsilon_0\epsilon_{\infty} e^2}{m^*} \frac{1}{\omega^2 - \omega_p^2} \quad (11)$$

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<220>
<221> CDS
<222> (101)..(1033)
<223> RXN01879
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<400> 861
ctttgcgggc cgctgatatt gatccaacgc ttctgtggcgga aaagcttgat gtcactgact 60

atgtgcgcct agctggggtg ttgcagcaaa aggatgagaaa      gtg aaa att acc gct    115
                  Val Lys Ile Thr Ala
                        1                5

aag gcg tgg cgc aaa acc aac ctg cat tta ggt gtg gga ccg gct cac    163
Lys Ala Trp Ala Lys Thr Asn Leu His Leu Gly Val Gly Pro Ala His
          10              15             20
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gac gat gga ttt cac gag ctc atg acg gtg ttt caa acc att gat ctg 211
 Asp Asp Gly Phe His Glu Leu Met Thr Val Phe Gln Thr Ile Asp Leu
 25 30 35

ttt gac acc gtc acc tta acc acc ctc gat gag gag ttg gtg gag gag 259
 Phe Asp Thr Val Thr Leu Thr Thr Leu Asp Glu Glu Leu Val Glu Glu
 40 45 50

ggg agc gtc gtc aag caa tta tct gtg acc ggt gcc cgt gcc gtg cct 307
 Gly Ser Val Val Lys Gln Leu Ser Val Thr Gly Ala Arg Gly Val Pro
 55 60 65

gag gac gcc agc aat ctt gcg tgg cgc gct gtg gat gcg ttg gtt aag 355
 Glu Asp Ala Ser Asn Leu Ala Trp Arg Ala Val Asp Ala Leu Val Lys
 70 75 80 85

cgg cgc gcg gaa aag acg ccg ctg tct gca gtt tcg ctg cat att tcc 403
 Arg Arg Ala Glu Lys Thr Pro Leu Ser Ala Val Ser Leu His Ile Ser
 90 95 100

aag ggg att ccg gtg gct gcc gcc atg gct gcc gcc tct gcg gat gcg 451
 Lys Gly Ile Pro Val Ala Gly Gly Met Ala Gly Gly Ser Ala Asp Ala
 105 110 115

gct gcg aca ctg cgc gca gtg gat gcc tgg att ggg cct ttc gcc gag 499
 Ala Ala Thr Leu Arg Ala Val Asp Ala Trp Ile Gly Pro Phe Gly Glu
 120 125 130

gac aca ttg ctg gag gtt gcc gcg gag ctc gcc tca gat gtg ccg ttt 547
 Asp Thr Leu Leu Glu Val Ala Ala Glu Leu Gly Ser Asp Val Pro Phe
 135 140 145

tgc ctg ctt ggt gcc acc atg cgc ggt acc ggt cgc gcc gag cag ctg 595
 Cys Leu Leu Gly Gly Thr Met Arg Gly Thr Gly Arg Gly Glu Gln Leu
 150 155 160 165

gta gat atg ttg acg cgc gcc aag cta cat tgg gtg gtg gcc gcg atg 643
 Val Asp Met Leu Thr Arg Gly Lys Leu His Trp Val Val Ala Ala Met
 170 175 180

gcg cat gcc ctg tcc acg cct gag gta ttc aaa aag cat gat gag ctg 691
 Ala His Gly Leu Ser Thr Pro Glu Val Phe Lys Lys His Asp Glu Leu
 185 190 195

aat ccg gaa tcg cat atg gat atc agc gac ctc agc gcc gca ctt ctc 739
 Asn Pro Glu Ser His Met Asp Ile Ser Asp Leu Ser Ala Ala Leu Leu
 200 205 210

acc gcc aac acc gcc gag gtg ggg cag tgg ctg cac aat gat ctg acc 787
 Thr Gly Asn Thr Ala Glu Val Gly Gln Trp Leu His Asn Asp Leu Thr
 215 220 225

agc gcc gca ctc agt ttg cgc cct gaa ctg cgc agc gtc ctc caa gaa 835
 Ser Ala Ala Leu Ser Leu Arg Pro Glu Leu Arg Ser Val Leu Gln Glu
 230 235 240 245

gcc atc cgc tcc gcc gcg cat gca gga att gtc tcc gcc tcc gcc ccg 883
 Gly Ile Arg Ser Gly Ala His Ala Gly Ile Val Ser Gly Ser Gly Pro
 250 255 260

```

acc acg gta ttc ttg tgc gaa tgc gag cac aaa gcg caa gac gtt aaa 931
Thr Thr Val Phe Leu Cys Glu Ser Glu His Lys Ala Gln Asp Val Lys
      265                      270                      275

gag gcg cta atc gac gcc gcc cag gtg tac gct gct tac acc gcc acc 979
Glu Ala Leu Ile Asp Ala Gly Gln Val Tyr Ala Ala Tyr Thr Ala Thr
      280                      285                      290

ggc cct gcg gcc tca acc gcc gac cag cgc gcc gca cac att ttg act 1027
Gly Pro Ala Ala Ser Thr Ala Asp Gln Arg Gly Ala His Ile Leu Thr
      295                      300                      305

gtt tca taataaagac aaacttaagt atc 1056
Val Ser
310

```

<210> 862

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 862

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Val Lys Ile Thr Ala Lys Ala Trp Ala Lys Thr Asn Leu His Leu Gly
  1              5              10              15

Val Gly Pro Ala His Asp Asp Gly Phe His Glu Leu Met Thr Val Phe
      20              25              30

Gln Thr Ile Asp Leu Phe Asp Thr Val Thr Leu Thr Thr Leu Asp Glu
      35              40              45

Glu Leu Val Glu Glu Gly Ser Val Val Lys Gln Leu Ser Val Thr Gly
      50              55              60

Ala Arg Gly Val Pro Glu Asp Ala Ser Asn Leu Ala Trp Arg Ala Val
      65              70              75              80

Asp Ala Leu Val Lys Arg Arg Ala Glu Lys Thr Pro Leu Ser Ala Val
      85              90              95

Ser Leu His Ile Ser Lys Gly Ile Pro Val Ala Gly Gly Met Ala Gly
      100              105              110

Gly Ser Ala Asp Ala Ala Ala Thr Leu Arg Ala Val Asp Ala Trp Ile
      115              120              125

Gly Pro Phe Gly Glu Asp Thr Leu Leu Glu Val Ala Ala Glu Leu Gly
      130              135              140

Ser Asp Val Pro Phe Cys Leu Leu Gly Gly Thr Met Arg Gly Thr Gly
      145              150              155              160

Arg Gly Glu Gln Leu Val Asp Met Leu Thr Arg Gly Lys Leu His Trp
      165              170              175

Val Val Ala Ala Met Ala His Gly Leu Ser Thr Pro Glu Val Phe Lys
      180              185              190

Lys His Asp Glu Leu Asn Pro Glu Ser His Met Asp Ile Ser Asp Leu
      195              200              205

```

Ser Ala Ala Leu Leu Thr Gly Asn Thr Ala Glu Val Gly Gln Trp Leu
 210 215 220

His Asn Asp Leu Thr Ser Ala Ala Leu Ser Leu Arg Pro Glu Leu Arg
 225 230 235 240

Ser Val Leu Gln Glu Gly Ile Arg Ser Gly Ala His Ala Gly Ile Val
 245 250 255

Ser Gly Ser Gly Pro Thr Thr Val Phe Leu Cys Glu Ser Glu His Lys
 260 265 270

Ala Gln Asp Val Lys Glu Ala Leu Ile Asp Ala Gly Gln Val Tyr Ala
 275 280 285

Ala Tyr Thr Ala Thr Gly Pro Ala Ala Ser Thr Ala Asp Gln Arg Gly
 290 295 300

Ala His Ile Leu Thr Val Ser
 305 310

<210> 863
 <211> 711
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(688)
 <223> FRXA01879

<400> 863
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 atgtgcgccct agctgggggtg ttgcagcaaaa aggatgagaa gtg aaa att acc gct 115
 Val Lys Ile Thr Ala
 1 5

aag gcg tgg gcg aaa acc aac ctg cat tta ggt gtg gga ccg gct cac 163
 Lys Ala Trp Ala Lys Thr Asn Leu His Leu Gly Val Gly Pro Ala His
 10 15 20

gac gat gga ttt cac gag ctc atg acg gtg ttt caa acc att gat ctg 211
 Asp Asp Gly Phe His Glu Leu Met Thr Val Phe Gln Thr Ile Asp Leu
 25 30 35

ttt gac acc gtc acc tta acc acc ctc gat gag gag ttg gtg gag gag 259
 Phe Asp Thr Val Thr Leu Thr Thr Leu Asp Glu Glu Thr Val Glu Glu
 40 45 50

ggg agc gtc gtc aag caa tta tct gtg acc ggt gcc cgt gcc gtg cct 307
 Gly Ser Val Val Lys Gln Leu Ser Val Thr Gly Ala Arg Gly Val Pro
 55 60 65

gag gac gcc agc aat ctt gcg tgg cgc gct gtg gat gcg ttg gtt aag 355
 Glu Asp Ala Ser Asn Leu Ala Trp Arg Ala Val Asp Ala Leu Val Lys
 70 75 80 85

cgg cgc gcg gaa aag acg ccg ctg tct gca gtt tcg ctg cat att tcc 403

```

Arg Arg Ala Glu Lys Thr Pro Leu Ser Ala Val Ser Leu His Ile Ser
          90          95          100

aag ggg att ccg gtg gct ggc ggc atg gct ggc ggc tct gcg gat gcg 451
Lys Gly Ile Pro Val Ala Gly Gly Met Ala Gly Gly Ser Ala Asp Ala
          105          110          115

get gcg aca ctg cgc gca gtg gat gcc tgg att ggg cct ttc ggc gag 499
Ala Ala Thr Leu Arg Ala Val Asp Ala Trp Ile Gly Pro Phe Gly Glu
          120          125          130

gac aca ttg ctg gag gtt gcc gcg gag ctc ggc tca gat gtg ccg ttt 547
Asp Thr Leu Leu Glu Val Ala Ala Glu Leu Gly Ser Asp Val Pro Phe
          135          140          145

tgc ctg ctt ggt ggc acc atg cgc ggt acc ggt cgc ggc gag cag ctg 595
Cys Leu Leu Gly Gly Thr Met Arg Gly Thr Gly Arg Gly Glu Gln Leu
          150          155          160          165

gta gat atg ttg acg cgc ggc aag cta cat tgg gtg gtg gcc gcg atg 643
Val Asp Met Leu Thr Arg Gly Lys Leu His Trp Val Val Ala Ala Met
          170          175          180

gcg cat ggc ctg tcc acc ctg agg tat tca aaa agc atg atg agc 688
Ala His Gly Leu Ser Thr Leu Arg Tyr Ser Lys Ser Met Met Ser
          185          190          195

tgaatccgga atcgcatatg gat 711

<210> 864
<211> 196
<212> PRT
<213> Corynebacterium glutamicum

<400> 864
Val Lys Ile Thr Ala Lys Ala Trp Ala Lys Thr Asn Leu His Leu Gly
  1          5          10          15

Val Gly Pro Ala His Asp Asp Gly Phe His Glu Leu Met Thr Val Phe
  20          25          30

Gln Thr Ile Asp Leu Phe Asp Thr Val Thr Leu Thr Leu Asp Glu
  35          40          45

Glu Leu Val Glu Glu Gly Ser Val Val Lys Gln Leu Ser Val Thr Gly
  50          55          60

Ala Arg Gly Val Pro Glu Asp Ala Ser Asn Leu Ala Trp Arg Ala Val
  65          70          75          80

Asp Ala Leu Val Lys Arg Arg Ala Glu Lys Thr Pro Leu Ser Ala Val
  85          90          95

Ser Leu His Ile Ser Lys Gly Ile Pro Val Ala Gly Gly Met Ala Gly
  100          105          110

Gly Ser Ala Asp Ala Ala Ala Thr Leu Arg Ala Val Asp Ala Trp Ile
  115          120          125

Gly Pro Phe Gly Glu Asp Thr Leu Leu Glu Val Ala Ala Glu Leu Gly

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130	135	140
Ser Asp Val Pro Phe Cys Leu Leu Gly Gly Thr Met Arg Gly Thr Gly		
145	150	155
Arg Gly Glu Gln Leu Val Asp Met Leu Thr Arg Gly Lys Leu His Trp		
	165	170
Val Val Ala Ala Met Ala His Gly Leu Ser Thr Leu Arg Tyr Ser Lys		
	180	185
Ser Met Met Ser		
195		

<210> 865

<211> 531

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(508)

<223> FRXA01880

<400> 865

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agctcggtc agatgtgccg ttttgctgc ttggtggcac catgcgcggt accggtcgcg 60
gcgagcagct ggtagatatg ttgacgcgcg gcaagctaca ttg ggt ggt ggc cgc 115
Leu Gly Gly Gly Arg
1 5

gat ggc gca tgg cct gtc cac cct gag gta ttc aaa aag cat gat gag 163
Asp Gly Ala Trp Pro Val His Pro Glu Val Phe Lys Lys His Asp Glu
10 15 20

ctg aat cgc gaa tcg cat atg gat atc agc gac ctc agc gcc gca ctt 211
Leu Asn Pro Glu Ser His Met Asp Ile Ser Asp Leu Ser Ala Ala Leu
25 30 35

ctc acc ggc aac acc gcc gag gtg ggg cag tgg ctg cac aat gat ctg 259
Leu Thr Gly Asn Thr Ala Glu Val Gly Gln Trp Leu His Asn Asp Leu
40 45 50

acc agc gcc gca ctc agt ttg cgc cct gaa ctg cgc agc gtc ctc caa 307
Thr Ser Ala Ala Leu Ser Leu Arg Pro Glu Leu Arg Ser Val Leu Gln
55 60 65

gaa ggc atc cgc tcc ggc gcg cat gca gga att gtc tcc ggc tcc ggc 355
Glu Gly Ile Arg Ser Gly Ala His Ala Gly Ile Val Ser Gly Ser Gly
70 75 80 85

cgc acc acg gta ttc ttg tgc gaa tcg gag cac aaa gcg caa gac gtt 403
Pro Thr Thr Val Phe Leu Cys Glu Ser Glu His Lys Ala Gln Asp Val
90 95 100

aaa gag gcg cta atc gac gcc gcc cag gtg tac gct gct tac acc gcc 451
Lys Glu Ala Leu Ile Asp Ala Gly Gln Val Tyr Ala Ala Tyr Thr Ala
105 110 115

acc ggc cct gcg gcc tca acc gcc gac cag cgc gcc gca cac att ttg 499

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Thr Gly Pro Ala Ala Ser Thr Ala Asp Gln Arg Gly Ala His Ile Leu
 120 125 130

act gtt tca taataaagac aaacttaagt atc
 Thr Val Ser
 135

531

<210> 866

<211> 136

<212> PRT

<213> Corynebacterium glutamicum

<400> 866

Leu Gly Gly Gly Arg Asp Gly Ala Trp Pro Val His Pro Glu Val Phe
 1 5 10 15

Lys Lys His Asp Glu Leu Asn Pro Glu Ser His Met Asp Ile Ser Asp
 20 25 30

Leu Ser Ala Ala Leu Leu Thr Gly Asn Thr Ala Glu Val Gly Gln Trp
 35 40 45

Leu His Asn Asp Leu Thr Ser Ala Ala Leu Ser Leu Arg Pro Glu Leu
 50 55 60

Arg Ser Val Leu Gln Glu Gly Ile Arg Ser Gly Ala His Ala Gly Ile
 65 70 75 80

Val Ser Gly Ser Gly Pro Thr Thr Val Phe Leu Cys Glu Ser Glu His
 85 90 95

Lys Ala Gln Asp Val Lys Glu Ala Leu Ile Asp Ala Gly Gln Val Tyr
 100 105 110

Ala Ala Tyr Thr Ala Thr Gly Pro Ala Ala Ser Thr Ala Asp Gln Arg
 115 120 125

Gly Ala His Ile Leu Thr Val Ser
 130 135

<210> 867

<211> 759

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(736)

<223> RXN01896

<400> 867

ttattgggca gctcttttgg accgcgaagt caccocgag ctgcgccaca gcattgotta 60

ttggatccgc gcgaaccaca tcaaacgcta gaggattcc atg acg cat gcg atc 115
 Met Thr His Ala Ile
 1 5

ctc ttt gac ctc gac gcc acc ctc gtt gat cac gct tcc gcc gcc cgc 163
 Leu Phe Asp Leu Asp Gly Thr Leu Val Asp His Ala Ser Ala Ala Arg

	10	15	20	
gcc gcc ctg cac gcc tgg tgg ccg acc gtg ggc gtc gac acg gat gtt				211
Ala Ala Leu His Ala Trp Ser Pro Thr Val Gly Val Asp Thr Asp Val	25	30	35	
gag cgc tgg att gag ctg gat aag tgg ggt ttt gcc cgt ttt gag cgc				259
Glu Arg Trp Ile Glu Leu Asp Lys Trp Gly Phe Ala Arg Phe Glu Arg	40	45	50	
ggc gaa acc acg cat tta ggt cag cgg cgc gac cgc atc agg cgc tac				307
Gly Glu Thr Thr His Leu Gly Gln Arg Arg Asp Arg Ile Arg Ala Tyr	55	60	65	
ctc aac aga gag ctt gac gac gcc acc tgc gat gat att tac tcc gcc				355
Leu Asn Arg Glu Leu Asp Asp Ala Thr Cys Asp Asp Ile Tyr Ser Gly	70	75	80	85
tac ctt aaa gca tat gag caa aac tgg act gcc tac ccc gat gcc aag				403
Tyr Leu Lys Ala Tyr Glu Gln Asn Trp Thr Ala Tyr Pro Asp Ala Lys	90	95	100	
ggc gtt ctc gat cgc gcg gta gcc acc ggt gcc cct gtg gga atc ctg				451
Gly Val Leu Asp Arg Ala Val Ala Thr Gly Ala Pro Val Gly Ile Leu	105	110	115	
acc aat ggc gca gcc ccc atg cag caa gac aag ctt gat cgc acc gcc				499
Thr Asn Gly Ala Ala Pro Met Gln Gln Asp Lys Leu Asp Arg Thr Gly	120	125	130	
ctt ggc ctg cca gaa ctc gtc atg ttg gcg gcg tcc act ctg gat tct				547
Leu Gly Leu Pro Glu Leu Val Met Leu Ala Ala Ser Thr Leu Asp Ser	135	140	145	
gcg aag cct cgc ccc gaa atg tat gcc cga gcg ctc acc cat ttg ggt				595
Ala Lys Pro Arg Pro Glu Met Tyr Ala Arg Ala Leu Thr His Leu Gly	150	155	160	165
gcc cga acc gca aca att atc ggc gat gat tgg acc aac gat gtc gca				643
Ala Arg Thr Ala Thr Ile Ile Gly Asp Asp Trp Thr Asn Asp Val Ala	170	175	180	
gct ccc cgc gaa ctt ggc tgg aat gct ctc tat tta gat cgt tcc gga				691
Ala Pro Arg Glu Leu Gly Trp Asn Ala Leu Tyr Leu Asp Arg Ser Gly	185	190	195	
acc gat cca cgc gcc gat atc cac tcc ctg gat gaa ctc ttt cac				736
Thr Asp Pro Arg Ala Asp Ile His Ser Leu Asp Glu Leu Phe His	200	205	210	
taggctggcc ttattgttt ccg				759

<210> 868

<211> 212

<212> PRT

<213> Corynebacterium glutamicum

<400> 868

Met Thr His His Ala Ile Leu Phe Asp Leu Asp Gly Thr Leu Val Asp His

1

5

10

15

Ala Ser Ala Ala Arg Ala Ala Leu His Ala Trp Ser Pro Thr Val Gly
 20 25 30

Val Asp Thr Asp Val Glu Arg Trp Ile Glu Leu Asp Lys Trp Gly Phe
 35 40 45

Ala Arg Phe Glu Arg Gly Glu Thr Thr His Leu Gly Gln Arg Arg Asp
 50 55 60

Arg Ile Arg Ala Tyr Leu Asn Arg Glu Leu Asp Asp Ala Thr Cys Asp
 65 70 75 80

Asp Ile Tyr Ser Gly Tyr Leu Lys Ala Tyr Glu Gln Asn Trp Thr Ala
 85 90 95

Tyr Pro Asp Ala Lys Gly Val Leu Asp Arg Ala Val Ala Thr Gly Ala
 100 105 110

Pro Val Gly Ile Leu Thr Asn Gly Ala Ala Pro Met Gln Gln Asp Lys
 115 120 125

Leu Asp Arg Thr Gly Leu Gly Leu Pro Glu Leu Val Met Leu Ala Ala
 130 135 140

Ser Thr Leu Asp Ser Ala Lys Pro Arg Pro Glu Met Tyr Ala Arg Ala
 145 150 155 160

Leu Thr His Leu Gly Ala Arg Thr Ala Thr Ile Ile Gly Asp Asp Trp
 165 170 175

Thr Asn Asp Val Ala Ala Pro Arg Glu Leu Gly Trp Asn Ala Leu Tyr
 180 185 190

Leu Asp Arg Ser Gly Thr Asp Pro Arg Ala Asp Ile His Ser Leu Asp
 195 200 205

Glu Leu Phe His
 210

<210> 869

<211> 602

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(579)

<223> FRXA01896

<400> 869

gcc cgc gcc gcc ctg cac gcc tgg tgc cgc acc gtg gcc gtc gac acg 48

Ala Arg Ala Ala Leu His Ala Trp Ser Pro Thr Val Gly Val Asp Thr

1

5

10

15

gat gtt gag cgc tgg att gag ctg gat aag tgg ggt ttt gcc cgt ttt 96

Asp Val Glu Arg Trp Ile Glu Leu Asp Lys Trp Gly Phe Ala Arg Phe

20

25

30

gag cgc gcc gaa acc acg cat tta ggt cag cgg cgc gac cgc atc agg 144

Glu Arg Gly Glu Thr Thr His Leu Gly Gln Arg Arg Asp Arg Ile Arg
 35 40 45
 gcg tac ctc aac aga gag ctt gac gac gcc acc tgc gat gat att tac 192
 Ala Tyr Leu Asn Arg Glu Leu Asp Asp Ala Thr Cys Asp Asp Ile Tyr
 50 55 60
 tcc ggc tac ctt aaa gca tat gag caa aac tgg act gcc tac ccc gat 240
 Ser Gly Tyr Leu Lys Ala Tyr Glu Gln Asn Trp Thr Ala Tyr Pro Asp
 65 70 75 80
 gcc aag ggc gtt ctc gat cgc gcg gta gcc acc ggt gcc cct gtg gga 288
 Ala Lys Gly Val Leu Asp Arg Ala Val Ala Thr Gly Ala Pro Val Gly
 85 90 95
 atc ctg acc aat ggc gca gcc ccc atg cag caa gac aag ctt gat cgc 336
 Ile Leu Thr Asn Gly Ala Ala Pro Met Gln Gln Asp Lys Leu Asp Arg
 100 105 110
 acc ggc ctt ggc ctg cca gaa ctc gtc atg ttg gcg gcg tcc act ctg 384
 Thr Gly Leu Gly Leu Pro Glu Leu Val Met Leu Ala Ala Ser Thr Leu
 115 120 125
 gat tct gcg aag cct cgc ccc gaa atg tat gcc cga gcg ctc acc cat 432
 Asp Ser Ala Lys Pro Arg Pro Glu Met Tyr Ala Arg Ala Leu Thr His
 130 135 140
 ttg ggt gcc cga acc gca aca att atc ggc gat gat tgg acc aac gat 480
 Leu Gly Ala Arg Thr Ala Thr Ile Ile Gly Asp Asp Trp Thr Asn Asp
 145 150 155 160
 gtc gca gct ccc cgc gaa ctt ggc tgg aat gct ctc tat tta gat cgt 528
 Val Ala Ala Pro Arg Glu Leu Gly Trp Asn Ala Leu Tyr Leu Asp Arg
 165 170 175
 tcc gga acc gat cca cgc gcc gat atc cac tcc ctg gat gaa ctc ttt 576
 Ser Gly Thr Asp Pro Arg Ala Asp Ile His Ser Leu Asp Glu Leu Phe
 180 185 190
 cac taggctggcc tttattgttt ccg 602
 His

<210> 870

<211> 193

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 870

Ala Arg Ala Ala Leu His Ala Trp Ser Pro Thr Val Gly Val Asp Thr
 1 5 10 15
 Asp Val Glu Arg Trp Ile Glu Leu Asp Lys Trp Gly Phe Ala Arg Phe
 20 25 30
 Glu Arg Gly Glu Thr Thr His Leu Gly Gln Arg Arg Asp Arg Ile Arg
 35 40 45
 Ala Tyr Leu Asn Arg Glu Leu Asp Asp Ala Thr Cys Asp Asp Ile Tyr
 50 55 60

Ser Gly Tyr Leu Lys Ala Tyr Glu Gln Asn Trp Thr Ala Tyr Pro Asp
65 70 75 80

Ala Lys Gly Val Leu Asp Arg Ala Val Ala Thr Gly Ala Pro Val Gly
85 90 95

Ile Leu Thr Asn Gly Ala Ala Pro Met Gln Gln Asp Lys Leu Asp Arg
100 105 110

Thr Gly Leu Gly Leu Pro Glu Leu Val Met Leu Ala Ala Ser Thr Leu
115 120 125

Asp Ser Ala Lys Pro Arg Pro Glu Met Tyr Ala Arg Ala Leu Thr His
130 135 140

Leu Gly Ala Arg Thr Ala Thr Ile Ile Gly Asp Asp Trp Thr Asn Asp
145 150 155 160

Val Ala Ala Pro Arg Glu Leu Gly Trp Asn Ala Leu Tyr Leu Asp Arg
165 170 175

Ser Gly Thr Asp Pro Arg Ala Asp Ile His Ser Leu Asp Glu Leu Phe
180 185 190

His

<210> 871

<211> 909

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(886)

<223> RXN01899

<400> 871

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cgaaggctac tacgaagaaa ccgctgcccgc cgaggccctaa atg tcc cgc act ctg 115
Met Ser Arg Thr Leu
1 5

tgg gcg gtt tca gat cta cac gtc acc ttc gcc caa aac caa aac acc 163
Trp Ala Val Ser Asp Leu His Val Thr Phe Ala Gln Asn Gln Asn Thr
10 15 20

gtt gat gcc ctc atg ccg cag gac ccc ggc gac tgg ctg atc gtc gct 211
Val Asp Ala Leu Met Pro Gln Asp Pro Gly Asp Trp Leu Ile Val Ala
25 30 35

ggc gat gta gca gag aaa atc ccc gat gtg gta cgt acc tta tcc gcg 259
Gly Asp Val Ala Glu Lys Ile Pro Asp Val Val Arg Thr Leu Ser Ala
40 45 50

ctg gtc aaa cgc ttt gac acc gtg att tgg gtg ccg ggc aac cac gaa 307
Leu Val Lys Arg Phe Asp Thr Val Ile Trp Val Pro Gly Asn His Glu
55 60 65

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ctc ttc aac cgg aaa aca gac cgc gtc aac ggc aaa gcc cgc tac cga 355
Leu Phe Asn Arg Lys Thr Asp Arg Val Asn Gly Lys Ala Arg Tyr Arg
70 75 80 85

gca tta gtc gga caa ctc cga gcc atc ggc gtg atc acc ccc gaa gat 403
Ala Leu Val Gly Gln Leu Arg Ala Ile Gly Val Ile Thr Pro Glu Asp
90 95 100

ccc tat ccg atc ttt ggt ggc gtc acc atc tgc cca ett ttc aca ett 451
Pro Tyr Pro Ile Phe Gly Gly Val Thr Ile Cys Pro Leu Phe Thr Leu
105 110 115

tac gat tac tct ttc cgt ccc ctc ggc ctc acc gcg aaa caa gcc ctc 499
Tyr Asp Tyr Ser Phe Arg Pro Leu Gly Leu Thr Ala Lys Gln Ala Leu
120 125 130

gcc caa gca aaa ata aag cta gac gac gaa cta gcc atc gcc ccc tac 547
Ala Gln Ala Lys Ile Lys Leu Asp Asp Glu Leu Ala Ile Ala Pro Tyr
135 140 145

gta gac atc ccc gcc tgg tgc gcc gaa cga gtc acc tac aca gaa gac 595
Val Asp Ile Pro Ala Trp Cys Ala Glu Arg Val Thr Tyr Thr Glu Asp
150 155 160 165

cgc cta aaa gcc acc aaa ggc cca aaa gtc ctg gtc aat cac tgg ccg 643
Arg Leu Lys Ala Thr Lys Gly Pro Lys Val Leu Val Asn His Trp Pro
170 175 180

ctg gtc att gag ccc acc cac cgg ctc ttc caa aaa gac atc gcg ctg 691
Leu Val Ile Glu Pro Thr His Arg Leu Phe Gln Lys Asp Ile Ala Leu
185 190 195

tgg tgt gga acc acc gcc acc agg gat tgg gcc gta cga ttc aac gct 739
Trp Cys Gly Thr Thr Ala Thr Arg Asp Trp Ala Val Arg Phe Asn Ala
200 205 210

ctc atg gcc att cac ggt cac cta cat att cct gcc gaa acc cgc gtt 787
Leu Met Ala Ile His Gly His Leu His Ile Pro Ala Glu Thr Arg Val
215 220 225

gat ggg gta agc cac gtg gag gtt tct ttg ggt tac ccc ttt gaa aaa 835
Asp Gly Val Ser His Val Glu Val Ser Leu Gly Tyr Pro Phe Glu Lys
230 235 240 245

cac cca cct cac atg aag cgt ccg tgg ccg ttt ccg gtc atg cag att 883
His Pro Pro His Met Lys Arg Pro Trp Pro Phe Pro Val Met Gln Ile
250 255 260

aac taactctggt gcttaaatgg ggg 909
Asn

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<210> 872

<211> 262

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 872

Met Ser Arg Thr Leu Trp Ala Val Ser Asp Leu His Val Thr Phe Ala

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Gln Asn Gln	Asn Thr Val Asp Ala Leu Met Pro Gln Asp Pro Gly Asp		
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Trp Leu Ile	Val Ala Gly Asp Val Ala Glu Lys Ile Pro Asp Val Val		
	35	40	45
Arg Thr Leu Ser Ala Leu Val Lys Arg Phe Asp Thr Val Ile Trp Val			
	50	55	60
Pro Gly Asn His Glu Leu Phe Asn Arg Lys Thr Asp Arg Val Asn Gly			
	65	70	75
Lys Ala Arg Tyr Arg Ala Leu Val Gly Gln Leu Arg Ala Ile Gly Val			
	85	90	95
Ile Thr Pro Glu Asp Pro Tyr Pro Ile Phe Gly Gly Val Thr Ile Cys			
	100	105	110
Pro Leu Phe Thr Leu Tyr Asp Tyr Ser Phe Arg Pro Leu Gly Leu Thr			
	115	120	125
Ala Lys Gln Ala Leu Ala Gln Ala Lys Ile Lys Leu Asp Asp Glu Leu			
	130	135	140
Ala Ile Ala Pro Tyr Val Asp Ile Pro Ala Trp Cys Ala Glu Arg Val			
	145	150	155
Thr Tyr Thr Glu Asp Arg Leu Lys Ala Thr Lys Gly Pro Lys Val Leu			
	165	170	175
Val Asn His Trp Pro Leu Val Ile Glu Pro Thr His Arg Leu Phe Gln			
	180	185	190
Lys Asp Ile Ala Leu Trp Cys Gly Thr Thr Ala Thr Arg Asp Trp Ala			
	195	200	205
Val Arg Phe Asn Ala Leu Met Ala Ile His Gly His Leu His Ile Pro			
	210	215	220
Ala Glu Thr Arg Val Asp Gly Val Ser His Val Glu Val Ser Leu Gly			
	225	230	235
Tyr Pro Phe Glu Lys His Pro Pro His Met Lys Arg Pro Trp Pro Phe			
	245	250	255
Pro Val Met Gln Ile Asn			
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<210> 873

<211> 909

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(886)

<223> FRXA01899

<400> 873																		
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				Met	Ser	Arg	Thr	Leu	5									
tgg	gcg	gtt	tca	gat	cta	cac	gtc	acc	ttc	gcc	caa	aac	caa	aac	acc	163		
Trp	Ala	Val	Ser	Asp	Leu	His	Val	Thr	Phe	Ala	Gln	Asn	Gln	Asn	Thr	20		
gtt	gat	gcc	ctc	atg	ccg	cag	gac	ccc	ggc	gac	tgg	ctg	atc	gtc	gct	211		
Val	Asp	Ala	Leu	Met	Pro	Gln	Asp	Pro	Gly	Asp	Trp	Leu	Ile	Val	Ala	35		
ggc	gat	gta	gca	gag	aaa	atc	ccc	gat	gtg	gta	cgt	acc	tta	tcc	gcg	259		
Gly	Asp	Val	Ala	Glu	Lys	Ile	Pro	Asp	Val	Val	Arg	Thr	Leu	Ser	Ala	40		
ctg	gtc	aaa	cgc	ttt	gac	acc	gtg	att	tgg	gtg	ccg	ggc	aac	cac	gaa	307		
Leu	Val	Lys	Arg	Phe	Asp	Thr	Val	Ile	Trp	Val	Pro	Gly	Asn	His	Glu	60		
ctc	ttc	aac	cgg	aaa	aca	gac	cgc	gtc	aac	ggc	aaa	gcc	cgc	tac	cga	355		
Leu	Phe	Asn	Arg	Lys	Thr	Asp	Arg	Val	Asn	Gly	Lys	Ala	Arg	Tyr	Arg	70		
gca	tta	gtc	gga	caa	ctc	cga	gcc	atc	ggc	gtg	atc	acc	ccc	gaa	gat	403		
Ala	Leu	Val	Gly	Gln	Leu	Arg	Ala	Ile	Gly	Val	Ile	Thr	Pro	Glu	Asp	90		
ccc	tat	ccg	atc	ttt	ggg	ggc	gtc	acc	atc	tgc	cca	ctt	ttc	aca	ctt	451		
Pro	Tyr	Pro	Ile	Phe	Gly	Gly	Val	Thr	Ile	Cys	Pro	Leu	Phe	Thr	Leu	105		
tac	gat	tac	tct	ttc	cgt	ccc	ctc	ggc	ctc	acc	gcg	aaa	caa	gcc	ctc	499		
Tyr	Asp	Tyr	Ser	Phe	Arg	Pro	Leu	Gly	Leu	Thr	Ala	Lys	Gln	Ala	Leu	120		
gcc	caa	gca	aaa	ata	aag	cta	gac	gac	gaa	cta	gcc	atc	gcc	ccc	tac	547		
Ala	Gln	Ala	Lys	Ile	Lys	Leu	Asp	Asp	Glu	Leu	Ala	Ile	Ala	Pro	Tyr	135		
gta	gac	atc	ccc	gcc	tgg	tgc	gcc	gaa	cga	gtc	acc	tac	aca	gaa	gac	595		
Val	Asp	Ile	Pro	Ala	Trp	Cys	Ala	Glu	Arg	Val	Thr	Tyr	Thr	Glu	Asp	150		
cgc	cta	aaa	gcc	acc	aaa	ggc	cca	aaa	gtc	ctg	gtc	aat	cac	tgg	ccg	643		
Arg	Leu	Lys	Ala	Thr	Lys	Gly	Pro	Lys	Val	Leu	Val	Asn	His	Trp	Pro	170		
ctg	gtc	att	gag	ccc	acc	cac	cgg	ctc	ttc	caa	aaa	gac	atc	gcg	ctg	691		
Leu	Val	Ile	Glu	Pro	Thr	His	Arg	Leu	Phe	Gln	Lys	Asp	Ile	Ala	Leu	185		
tgg	tgt	gga	acc	acc	gca	acc	agg	gat	tgg	gcc	gta	cga	ttc	aac	gct	739		
Trp	Cys	Gly	Thr	Thr	Ala	Thr	Arg	Asp	Trp	Ala	Val	Arg	Phe	Asn	Ala	200		
ctc	atg	gcc	att	cac	ggg	cac	cta	cat	att	cct	gcc	gaa	acc	cgc	gtt	787		
Leu	Met	Ala	Ile	His	Gly	His	Leu	His	Ile	Pro	Glu	Glu	Thr	Arg	Val			

215

220

225

gat ggg gta agc cac gtg gag gtt tct ttg ggt tac ccc ttt gaa aaa 835
 Asp Gly Val Ser His Val Glu Val Ser Leu Gly Tyr Pro Phe Glu Lys
 230 235 240 245

cac cca cct cac atg aag cgt ccg tgg ccg ttt ccg gtc atg cag att 883
 His Pro Pro His Met Lys Arg Pro Trp Pro Phe Pro Val Met Gln Ile
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aac taactctgtt gcttaaatgg ggg 909
 Asn

<210> 874

<211> 262

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 874

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 20 25 30

Trp Leu Ile Val Ala Gly Asp Val Ala Glu Lys Ile Pro Asp Val Val
 35 40 45

Arg Thr Leu Ser Ala Leu Val Lys Arg Phe Asp Thr Val Ile Trp Val
 50 55 60

Pro Gly Asn His Glu Leu Phe Asn Arg Lys Thr Asp Arg Val Asn Gly
 65 70 75 80

Lys Ala Arg Tyr Arg Ala Leu Val Gly Gln Leu Arg Ala Ile Gly Val
 85 90 95

Ile Thr Pro Glu Asp Pro Tyr Pro Ile Phe Gly Gly Val Thr Ile Cys
 100 105 110

Pro Leu Phe Thr Leu Tyr Asp Tyr Ser Phe Arg Pro Leu Gly Leu Thr
 115 120 125

Ala Lys Gln Ala Leu Ala Gln Ala Lys Ile Lys Leu Asp Asp Glu Leu
 130 135 140

Ala Ile Ala Pro Tyr Val Asp Ile Pro Ala Trp Cys Ala Glu Arg Val
 145 150 155 160

Thr Tyr Thr Glu Asp Arg Leu Lys Ala Thr Lys Gly Pro Lys Val Leu
 165 170 175

Val Asn His Trp Pro Leu Val Ile Glu Pro Thr His Arg Leu Phe Gln
 180 185 190

Lys Asp Ile Ala Leu Trp Cys Gly Thr Thr Ala Thr Arg Asp Trp Ala
 195 200 205

Val Arg Phe Asn Ala Leu Met Ala Ile His Gly His Leu His Ile Pro

210

215

220

Ala Glu Thr Arg Val Asp Gly Val Ser His Val Glu Val Ser Leu Gly
 225 230 235 240

Tyr Pro Phe Glu Lys His Pro Pro His Met Lys Arg Pro Trp Pro Phe
 245 250 255

Pro Val Met Gln Ile Asn
 260

<210> 875

<211> 1182

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(1159)

<223> RXN01902

<400> 875

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ttcttcggcg acaccagct gtacaacacc cactccaacc gtg cag aag aag tcc 115
 Val Gln Lys Lys Ser
 1 5

aga act ggg caa aca acc tgg aac ggc ggc cca cca atc gaa aac cca 163
 Arg Thr Gly Gln Thr Trp Asn Gly Gly Pro Pro Ile Glu Asn Pro
 10 15 20

gga acc tcc ttc atc ctc tcc gcg ggt gat cag gca aac cac tcc agc 211
 Gly Thr Ser Phe Ile Leu Ser Ala Gly Asp Gln Ala Asn His Ser Ser
 25 30 35

tgg gac gag cac tcc gca tac atc tcc cca gaa acc ctg cgc aac tac 259
 Trp Asp Glu His Ser Ala Tyr Ile Ser Pro Glu Thr Leu Arg Asn Tyr
 40 45 50

cgt ctg gcc gtg aac aat gga aac cac gac cag tac aac tac gac gcc 307
 Arg Leu Ala Val Asn Asn Gly Asn His Asp Gln Tyr Asn Tyr Asp Ala
 55 60 65

tac aac gcg atg tac cca cgc cct aac cag gtc gat gag aac tac ttc 355
 Tyr Asn Ala Met Tyr Pro Arg Pro Asn Gln Val Asp Glu Asn Tyr Phe
 70 75 80 85

ttc gag tac aac aat gca ctc ttc ctg tcc ctg gac tcc aac gac tac 403
 Phe Glu Tyr Asn Asn Ala Leu Phe Leu Ser Leu Asp Ser Asn Asp Tyr
 90 95 100

ttg gac atc gac gac gac atc gca ttc ctt cgc gac acc gtc gca gca 451
 Leu Asp Ile Asp Asp Ile Ala Phe Leu Arg Asp Thr Val Ala Ala
 105 110 115

cac ggt gac gac aag gac tgg atc gtc ctg acc tac cac cat tcc act 499
 His Gly Asp Asp Lys Asp Trp Ile Val Leu Thr Tyr His His Ser Thr
 120 125 130

ttc tcc cag gcc tac cac atg gat gac gct cgc att aag tac cag cgc 547
 Phe Ser Gln Ala Tyr His Met Asp Asp Ala Arg Ile Lys Tyr Gln Arg
 135 140 145

 gaa cgc ctc acc cca gtg atc tct gaa ctg aac gtt gac ttg gtt ctc 595
 Glu Arg Leu Thr Pro Val Ile Ser Glu Leu Asn Val Asp Leu Val Leu
 150 155 160 165

 ggt gga cac gac cac atc tac acc cgc tcc cac ctg atg aac ggc ttc 643
 Gly Gly His Asp His Ile Tyr Thr Arg Ser His Leu Met Asn Gly Phe
 170 175 180

 acc cca gtc gat gca ggc cgc gaa gca gtt gtc ggt gaa act ctg aac 691
 Thr Pro Val Asp Ala Gly Arg Glu Ala Val Val Gly Glu Thr Leu Asn
 185 190 195

 cct aag gcc ggc gaa gtt gtt tac ctt gca acc aac tct tcc tca ggc 739
 Pro Lys Ala Gly Glu Val Val Tyr Leu Ala Thr Asn Ser Ser Ser Gly
 200 205 210

 tcc aag ttc tac gac ttc tac gac ttc cag ctc ggc cag cgt tac gac 787
 Ser Lys Phe Tyr Asp Phe Tyr Asp Phe Gln Leu Gly Gln Arg Tyr Asp
 215 220 225

 acc gga ctg gat ttc cag gaa acc gtc gat cag aag aag atc cgc acc 835
 Thr Gly Leu Asp Phe Gln Glu Thr Val Asp Gln Lys Lys Ile Arg Thr
 230 235 240 245

 tac acc gca gtc tgg aac cag gac cag gtt cag gac tac acc aac gtt 883
 Tyr Thr Ala Val Trp Asn Gln Asp Gln Val Gln Asp Tyr Thr Asn Val
 250 255 260

 gaa ctg acc cca gaa ggc ctg act gtg acc act aag gac gca gtc tcc 931
 Glu Leu Thr Pro Glu Gly Leu Thr Val Thr Thr Lys Asp Ala Val Ser
 265 270 275

 ggc gag ctg gtt gac cag ttc acc ctg agc aag cag gac cgc gac gaa 979
 Gly Glu Leu Val Asp Gln Phe Thr Leu Ser Lys Gln Asp Arg Asp Glu
 280 285 290

 gaa tct gaa gtc cca gtt gaa gat gac aag gac gga gac aac gcg acc 1027
 Glu Ser Glu Val Pro Val Glu Asp Asp Lys Asp Gln Asp Asn Ala Thr
 295 300 305

 ggc tcc tcc aac ctt ggt cta gct gct atc ttg gct cca gtt ctg gcc 1075
 Gly Ser Ser Asn Leu Gly Leu Ala Ala Ile Leu Ala Pro Val Leu Ala
 310 315 320 325

 atc ttc ggt ttc gtc ggt gga ctc ttt gtt ggc ggc ggc tcc etc gct 1123
 Ile Phe Gly Phe Val Gly Gly Leu Phe Val Gly Gly Gly Ser Leu Ala
 330 335 340

 gag ttc ttt gcc aac ctc ggc gtg aag atg cct ttc taatactgtc 1169
 Glu Phe Phe Ala Asn Leu Gly Val Lys Met Pro Phe
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<210> 876

<211> 353

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 876

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			20					25						30	

Ala	Asn	His	Ser	Ser	Trp	Asp	Glu	His	Ser	Ala	Tyr	Ile	Ser	Pro	Glu
			35				40					45			

Thr	Leu	Arg	Asn	Tyr	Arg	Leu	Ala	Val	Asn	Asn	Gly	Asn	His	Asp	Gln
	50				55						60				

Tyr	Asn	Tyr	Asp	Ala	Tyr	Asn	Ala	Met	Tyr	Pro	Arg	Pro	Asn	Gln	Val
	65				70					75				80	

Asp	Glu	Asn	Tyr	Phe	Phe	Glu	Tyr	Asn	Asn	Ala	Leu	Phe	Leu	Ser	Leu
				85						90				95	

Asp	Ser	Asn	Asp	Tyr	Leu	Asp	Ile	Asp	Asp	Ile	Ala	Phe	Leu	Arg	
			100					105					110		

Asp	Thr	Val	Ala	Ala	His	Gly	Asp	Asp	Lys	Asp	Trp	Ile	Val	Leu	Thr
		115					120						125		

Tyr	His	His	Ser	Thr	Phe	Ser	Gln	Ala	Tyr	His	Met	Asp	Asp	Ala	Arg
		130				135					140				

Ile	Lys	Tyr	Gln	Arg	Glu	Arg	Leu	Thr	Pro	Val	Ile	Ser	Glu	Leu	Asn
	145				150					155					160

Val	Asp	Leu	Val	Leu	Gly	Gly	His	Asp	His	Ile	Tyr	Thr	Arg	Ser	His
			165						170					175	

Leu	Met	Asn	Gly	Phe	Thr	Pro	Val	Asp	Ala	Gly	Arg	Glu	Ala	Val	Val
		180						185					190		

Gly	Glu	Thr	Leu	Asn	Pro	Lys	Ala	Gly	Glu	Val	Val	Tyr	Leu	Ala	Thr
		195				200							205		

Asn	Ser	Ser	Ser	Gly	Ser	Lys	Phe	Tyr	Asp	Phe	Tyr	Asp	Phe	Gln	Leu
	210					215					220				

Gly	Gln	Arg	Tyr	Asp	Thr	Gly	Leu	Asp	Phe	Gln	Glu	Thr	Val	Asp	Gln
	225				230					235					240

Lys	Lys	Ile	Arg	Thr	Tyr	Thr	Ala	Val	Trp	Asn	Gln	Asp	Gln	Val	Gln
			245						250					255	

Asp	Tyr	Thr	Asn	Val	Glu	Leu	Thr	Pro	Glu	Gly	Leu	Thr	Val	Thr	Thr
		260						265					270		

Lys	Asp	Ala	Val	Ser	Gly	Glu	Leu	Val	Asp	Gln	Phe	Thr	Leu	Ser	Lys
		275					280					285			

Gln	Asp	Arg	Asp	Glu	Glu	Ser	Glu	Val	Pro	Val	Glu	Asp	Asp	Lys	Asp
		290				295					300				

Gly Asp Asn Ala Thr Gly Ser Ser Asn Leu Gly Leu Ala Ala Ile Leu
305 310 315 320

Ala Pro Val Leu Ala Ile Phe Gly Phe Val Gly Gly Leu Phe Val Gly
325 330 335

Gly Gly Ser Leu Ala Glu Phe Phe Ala Asn Leu Gly Val Lys Met Pro
340 345 350

Phe

<210> 877

<211> 887

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(864)

<223> FRXA01902

<400> 877

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gag aac tac ttc ttc gag tac aac aat gca ctc ttc ctg tcc ctg gac 96
Glu Asn Tyr Phe Phe Glu Tyr Asn Asn Ala Leu Phe Leu Ser Leu Asp
20 25 30

tcc aac gac tac ttg gac atc gac gac gac atc gca ttc ctt cgc gac 144
Ser Asn Asp Tyr Leu Asp Ile Asp Asp Asp Ile Ala Phe Leu Arg Asp
35 40 45

acc gtc gca gca cac ggt gac gac aag gac tgg atc gtc ctg acc tac 192
Thr Val Ala Ala His Gly Asp Asp Lys Asp Trp Ile Val Leu Thr Tyr
50 55 60

cac cat tcc act ttc tcc cag gcc tac cac atg gat gac gct cgc att 240
His His Ser Thr Phe Ser Gln Ala Tyr His Met Asp Asp Ala Arg Ile
65 70 75 80

aag tac cag cgc gaa cgc ctc acc cca gtg atc tct gaa ctg aac gtt 288
Lys Tyr Gln Arg Glu Arg Leu Thr Pro Val Ile Ser Glu Leu Asn Val
85 90 95

gac ttg gtt ctc ggt gga cac gac cac atc tac acc cgc tcc cac ctg 336
Asp Leu Val Leu Gly Gly His Asp His Ile Tyr Thr Arg Ser His Leu
100 105 110

atg aac ggc ttc acc cca gtc gat gca ggc cgc gaa gca gtt gtc ggt 384
Met Asn Gly Phe Thr Pro Val Asp Ala Gly Arg Glu Ala Val Val Gly
115 120 125

gaa act ctg aac cct aag gcc ggc gaa gtt gtt tac ctt gca acc aac 432
Glu Thr Leu Asn Pro Lys Ala Gly Glu Val Val Tyr Leu Ala Thr Asn
130 135 140

tct tcc tca ggc tcc aag ttc tac gac ttc tac gac ttc cag ctc ggc 480

Ser Ser Ser Gly Ser Lys Phe Tyr Asp Phe Tyr Asp Phe Gln Leu Gly
 145 150 155 160
 cag cgt tac gac acc gga ctg gat ttc cag gaa acc gtc gat cag aag 528
 Gln Arg Tyr Asp Thr Gly Leu Asp Phe Gln Glu Thr Val Asp Gln Lys 175
 aag atc cgc acc tac acc gca gtc tgg aac cag gac cag gtt cag gac 576
 Lys Ile Arg Thr Tyr Thr Ala Val Trp Asn Gln Asp Gln Val Gln Asp 180 185 190
 tac acc aac gtt gaa ctg acc cca gaa ggc ctg act gtg acc act aag 624
 Tyr Thr Asn Val Glu Leu Thr Pro Glu Gly Leu Thr Val Thr Thr Lys 195 200 205
 gac gca gtc tcc ggc gag ctg gtt gac cag ttc acc ctg agc aag cag 672
 Asp Ala Val Ser Gly Glu Leu Val Asp Gln Phe Thr Leu Ser Lys Gln 210 215 220
 gac cgc gac gaa gaa tct gaa gtc cca gtt gaa gat gac aag gac gga 720
 Asp Arg Asp Glu Glu Ser Glu Val Pro Val Glu Asp Asp Lys Asp Gly 225 230 235 240
 gac aac gcg acc ggc tcc tcc aac ctt ggt cta gct gct atc ttg gct 768
 Asp Asn Ala Thr Gly Ser Ser Asn Leu Gly Leu Ala Ala Ile Leu Ala 245 250 255
 cca gtt ctg gcc atc ttc ggt ttc gtc ggt gga ctc ttt gtt ggc ggc 816
 Pro Val Leu Ala Ile Phe Gly Phe Val Gly Gly Leu Phe Val Gly Gly 260 265 270
 ggc tcc ctc gct gag ttc ttt gcc aac ctc ggc gtg aag atg cct ttc 864
 Gly Ser Leu Ala Glu Phe Phe Ala Asn Leu Gly Val Lys Met Pro Phe 275 280 285
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 <210> 878
 <211> 288
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 878
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 Ser Asn Asp Tyr Leu Asp Ile Asp Asp Asp Ile Ala Phe Leu Arg Asp
 35 40 45
 Thr Val Ala Ala His Gly Asp Asp Lys Asp Trp Ile Val Leu Thr Tyr
 50 55 60
 His His Ser Thr Phe Ser Gln Ala Tyr His Met Asp Asp Ala Arg Ile
 65 70 75 80
 Lys Tyr Gln Arg Glu Arg Leu Thr Pro Val Ile Ser Glu Leu Asn Val
 85 90 95